36th World Congress of
Biomedical Laboratory Science

IFBLS 2026

Bridge to the future of BLS around the world

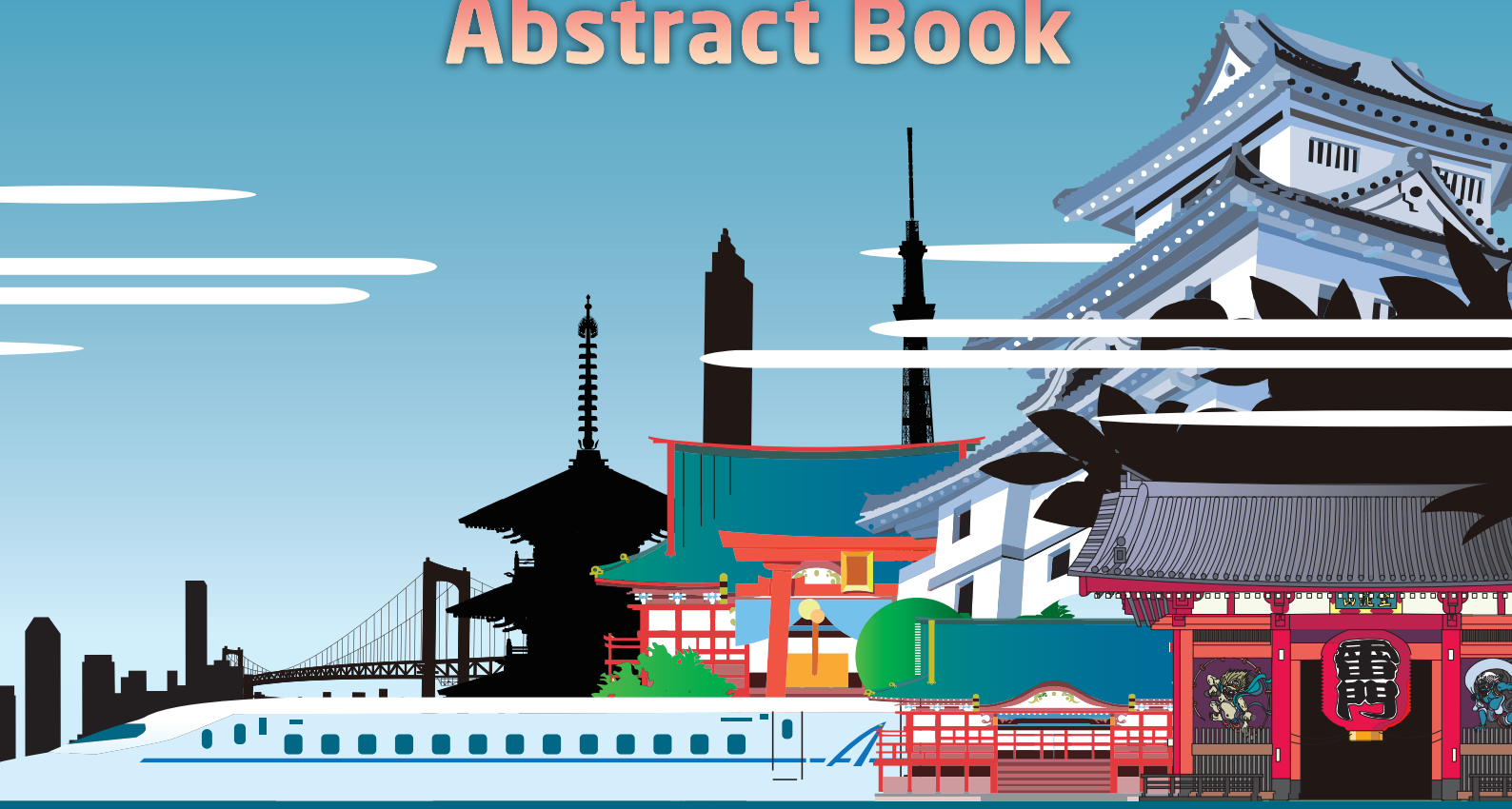
Date September 23rd – 27th 2026

Venue Makuhari Messe, Chiba JAPAN

Congress Organizers International Federation of Biomedical Laboratory Science (IFBLS)
Japanese Association of Medical Technologists (JAMT)

Congress Chairperson Mitsuaki Nagasawa
Vice Chairperson Kyoko Komatsu

Abstract Book



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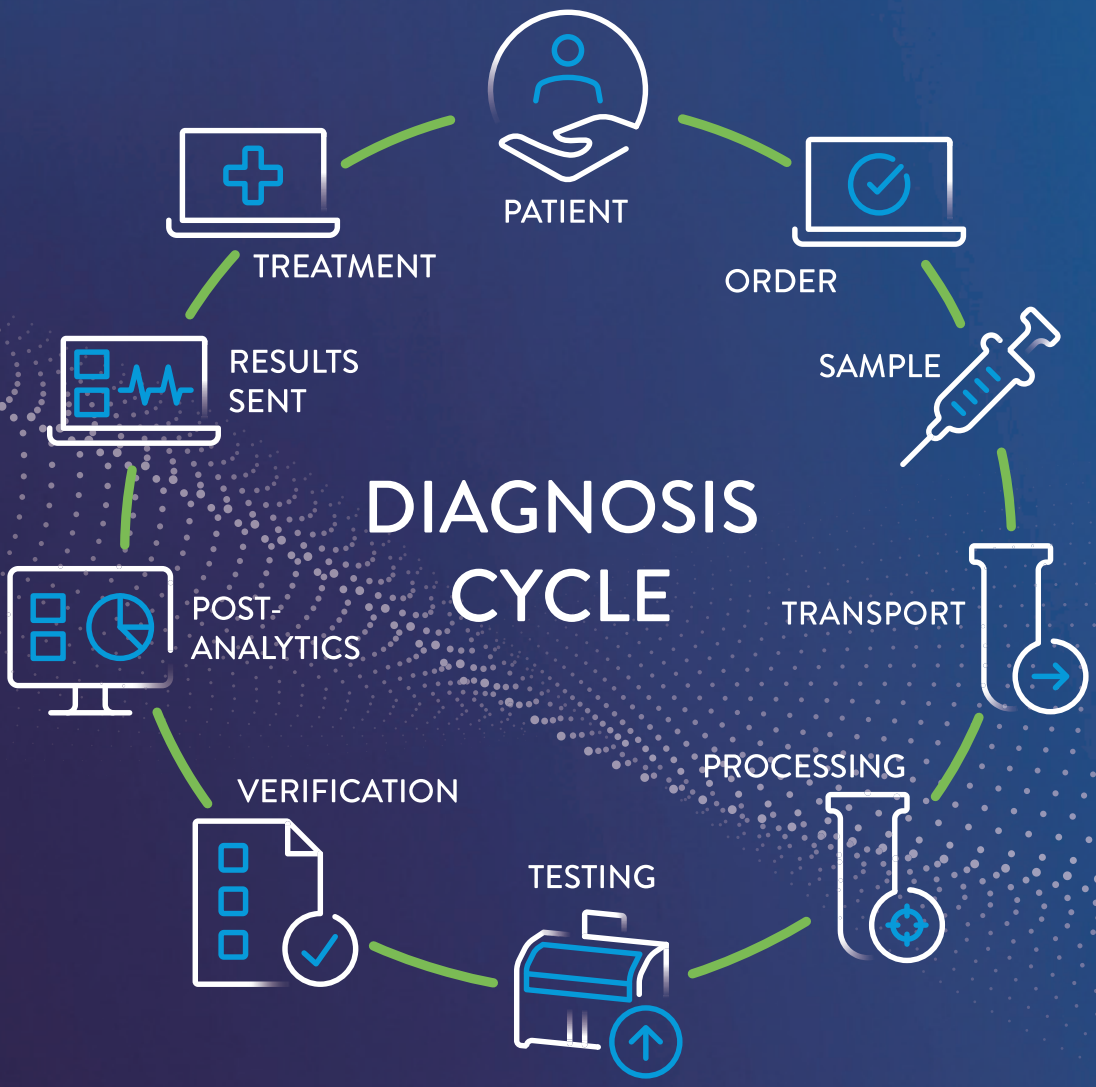

Abbott Japan LLC Core Diagnostics
3-5-27 Mita, Minato-ku, Tokyo 108-6305 Japan
TEL: +81-(0)3-4555-1000 URL: http://www.abbott.co.jp

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- MIZUHO MEDY Co.,Ltd.
- NIHON KOHDEN CORPORATION
- NIPRO CORPORATION
- PHC Corporation
- Pulstec Industrial Co.,Ltd.
- Q-may Laboratory Corporation
- QuidelOrtho Corporation
- Roche Diagnostics K.K.
- Sakura Finetek Japan Co., Ltd.
- SEKISUI MEDICAL CO., LTD.
- SENKO MEDICAL INSTRUMENT Mfg. CO., LTD.
- Shimadzu Diagnostics Corporation
- Shirai Electronics Indutrial Co.,Ltd.
- Siemens Healthcare Diagnostics K.K.
- SRL, Inc.
- SUGIYAMA-GEN CO., LTD.
- SYSMEX CORPORATION
- TAKANO Co.,Ltd.
- TAUNS Laboratories, Inc.
- Techno Medica Co., Ltd
- TEXeg CO., LTD.
- Thermo Fisher Scientific K.K.
- TOSOH CORPORATION
- TOYOBO CO.,LTD.
- YoukenScience Co.,Ltd.

Book Display

- Shigakushoten

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Congress Secretariat : Makuhari Messe 2-1 Nakase Mihama-ku Chiba, Japan

Email : info@ifbls2026.jp

URL : https://www.ifbls2026.jp

Welcome Message from IFBLS

Dear Colleagues and Friends,

On behalf of the International Federation of Biomedical Laboratory Science (IFBLS), it is my great honor and privilege to welcome you to the IFBLS 2026 World Congress, held under the inspiring theme: “Bridge to the Future of BLS Around the World.”

This theme reflects both our collective responsibility and our shared opportunity—to connect across borders, strengthen our global network, and ensure that biomedical laboratory science continues to advance in innovation, quality, and impact. Biomedical laboratory scientists are the foundation of diagnostic medicine, and by building bridges of knowledge, research, and collaboration, we create a healthier future for all.

The IFBLS World Congress provides a unique platform for professionals, educators, researchers, and students to come together to exchange knowledge, showcase achievements, and explore emerging challenges in our profession. It is also a celebration of our shared identity as biomedical laboratory scientists, united in our mission to improve healthcare worldwide.

I warmly invite you to join us for this landmark event. Your participation, expertise, and enthusiasm will help us shape the future of biomedical laboratory science and strengthen our voice in the global health community. Together, we will cross new bridges and inspire the next generation of leaders in our field.

I look forward to welcoming you to the IFBLS 2026 Congress and sharing what promises to be an unforgettable and transformative experience.

With warm regards,

Gabriella Lillsunde Larsson

President 2024-2026
International Federation of Biomedical Laboratory Science (IFBLS)

Welcome Message from IFBLS2026/JAMT

Dear Honorable guests from overseas and domestic professional members,

On behalf of the Japanese Association of Medical Technologists and the Organizing Committee of the 36th World Congress of Biomedical Laboratory science, I am delighted to extend my warmest welcome to our members from all around the world. We had an excellent time with you during the 32nd World Congress, in Japan, in 2016. It is a great pleasure for us to welcome you back to Japan, once again. The 36th World Congress of IFBLS will be held from September 23-27, 2026, at Makuhari Messe in Chiba, Japan.

Biomedical laboratory science is relevant to diagnostic work and public health care. As it had made remarkable progress, we need to get a new knowledge timely. The exchange of information at the global level is important. We strongly believe that this occasion will be a great opportunity to reconnect and deliver another fruitful scientific exchange. The Congress theme is “Bridge to the future of BLS around the world”. I hope that this Congress will serve as a bridge for knowledge sharing and meaningful interaction among participants.

There has been a hard time holding scientific meetings because of the COVID-19 pandemic. We are happy to offer ample opportunities to meet old friends and get acquainted with new ones. I wish you all a most pleasant stay in Japan and hope you will take home many rewarding memories of the Congress.

I look forward to meeting you Japan!

Mitsuaki Nagasawa

President of JAMT
President of the 36th World Congress of Biomedical Laboratory Science

About IFBLS

IFBLS is a global organization working to increase opportunities for debelopment of laboratory professionals through education and partnership.
Abiennial Congress provides networking opportunities in an education forum, while electronic communication facilitates and enhances professional development.

The objectives of IFBLS are:

1. To support, advance and promote good scientific laboratory practice through the development and adherence to high quality standards in diverse environments throughout the world;
2. To support and promote education and advancement of science and technology in the professional development of Biomedical Laboratory Scientists;
3. To support, advance and promote ethical and professional values in Biomedical Laboratory Science;
4. To facilitate the exchange of ideas through development of partnerships within the global healthcare community.

IFBLS Board of Directors 2024-2026

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About JAMT

The Japanese Association of Medical Technologists (JAMT) is a general incorporated association representing approximately 70,000 licensed biomedical laboratory scientists (BLSs) across Japan. Guided by our Ethical Code, which articulates our professional and social responsibilities, JAMT is committed to advancing public understanding of medical laboratory science, promoting high-quality laboratory practices, and safeguarding the professional interests of BLSs.

JAMT undertakes a wide range of activities to fulfill its mission, including:

1. Public Interest Programs (Core Ongoing Initiatives)
   1) Accreditation of quality assurance facilities and promotion of standardized laboratory practices
   2) National external quality assessment programs to ensure the accuracy and reliability of clinical testing
2. Additional Organizational Programs
   1) JAMT professional certification systems
   2) Academic promotion and research support
   3) International cooperation and global partnership initiatives
   4) Academic education programs and professional training workshops
   5) Publication of the official journal Medical Laboratory Science
   6) Development and distribution of professional publications
   7) Professional competency development programs
   8) Public health advancement and patient safety initiatives
   9) Policy advocacy and external relations
   10) Organizational development and governance activities
   11) Mutual aid and member support programs
   12) Research and survey projects related to clinical laboratory science

Through these activities, JAMT strives to contribute to the advancement of medical laboratory science, the improvement of public health, and the strengthening of professional practice both within Japan and internationally.

Local Organizing Committee(JAMT)

Executive Board

Congress President	Mitsuaki Nagasawa
Vice President	Kyoko Komatsu
Members	Hisashi Takino
	Hideo Maruta
	Masaaki Jitsuhara
Secretary General	Yoshio Hashizume

Executive Committee

Chair	Kyoko Komatsu
Vice Chair	Noriaki Harada
Members	Tomohito Yara
	Shuhei Ishii
	Satoshi Morito
	Kazunari Watahiki
	Hideo Sakamoto
	Yui Namikawa
	Ryosuke Kikuchi
	Keiji Fukasawa
	Tsunehiro Yokochi

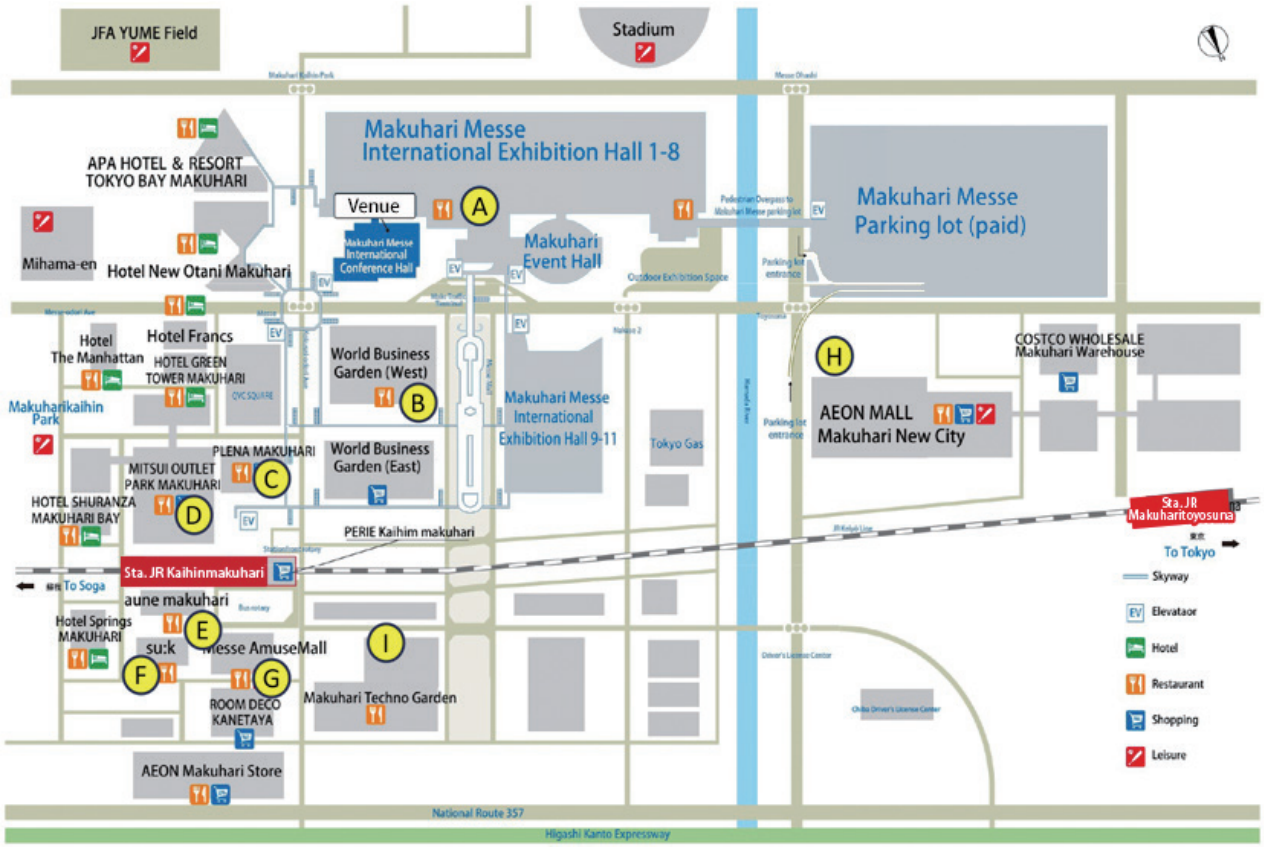
Program Committee

Chair	Ryosuke Kikuchi
Vice Chair	Kyoko Komatsu
Members	Atsuko Nakajima
	Hideo Sakamoto
	Hiromitsu Yokota
	Kenichiro Ohnuma
	Masahiro Jyouna
	Tatsuya Nakamura
	Youko Hidaka
	Yui Namikawa

Honorary Director

Yoshifumi Miyajima

Area Map



Venue Makuhari Messe

- About a 5-minute walk from “Kaihimmakuhari Station” on the JR Keiyo Line (about 30 minutes from Tokyo via the Rapid service)
- About a 20-minute walk from “Makuhari-Toyosuna Station” on the JR Keiyo Line
- About 17 minutes by bus bound for “Makuhari Messe Chuo” from “Makuhari-Hongo Station” on the JR Sobu Line and Keisei Line

Restaurant

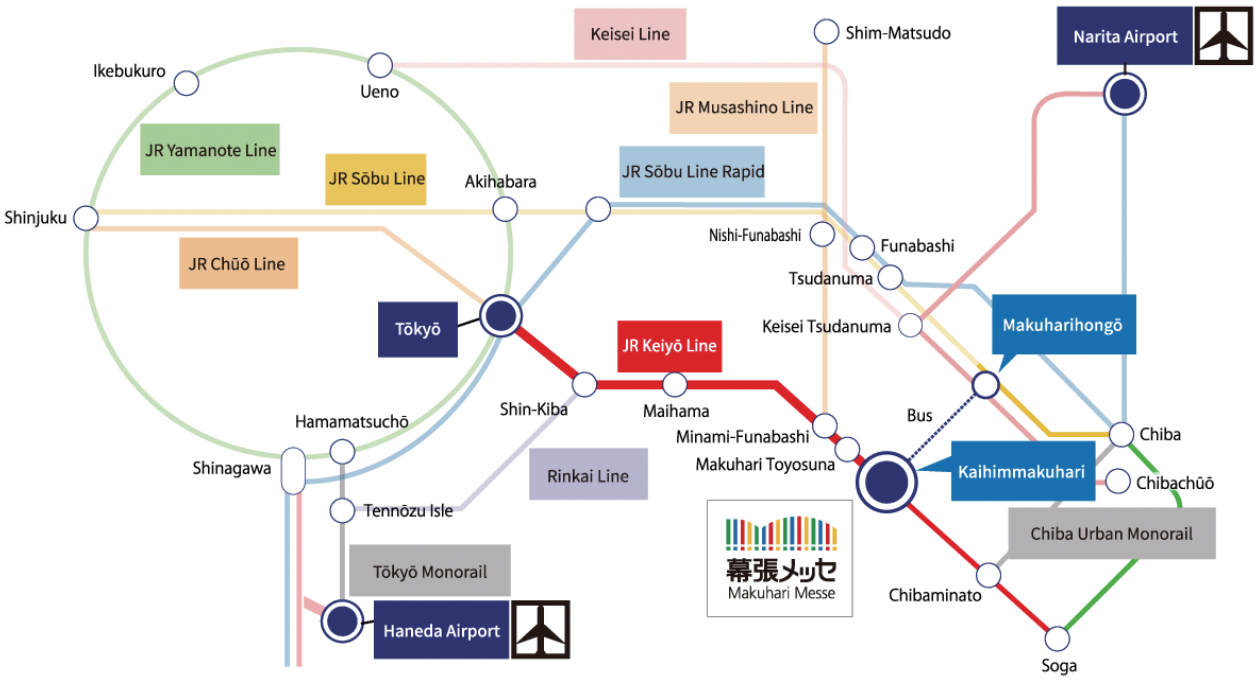
A : Makuhari messe
B : World business garden Marive Dining
C : PLENA Kaihin makuhari
D : Mitsui outlet park
E : Aune
F : Suk
G : Messe AmuseMall
H : AEON Mall Makuhari New city
I : Makuhari Techno garden

Hotel

- Hotel Springs MAKUHARI
- HOTEL GREEN TOWER MAKUHARI
- Hotel Francs
- Hotel The Manhattan
- Hotel New Otani Makuhari
- APA HOTE & RESORT TOKYO BAY MAKUHARI
- HOTEL SHURANZA MAKUHARI BAY

More Information for Shopping and Local specialities

Access MAP



Just a few train stops from **Kaihin-Makuhari Station**, you'll find a variety of exciting destinations for dining and shopping.

Explore Local Dining Areas:

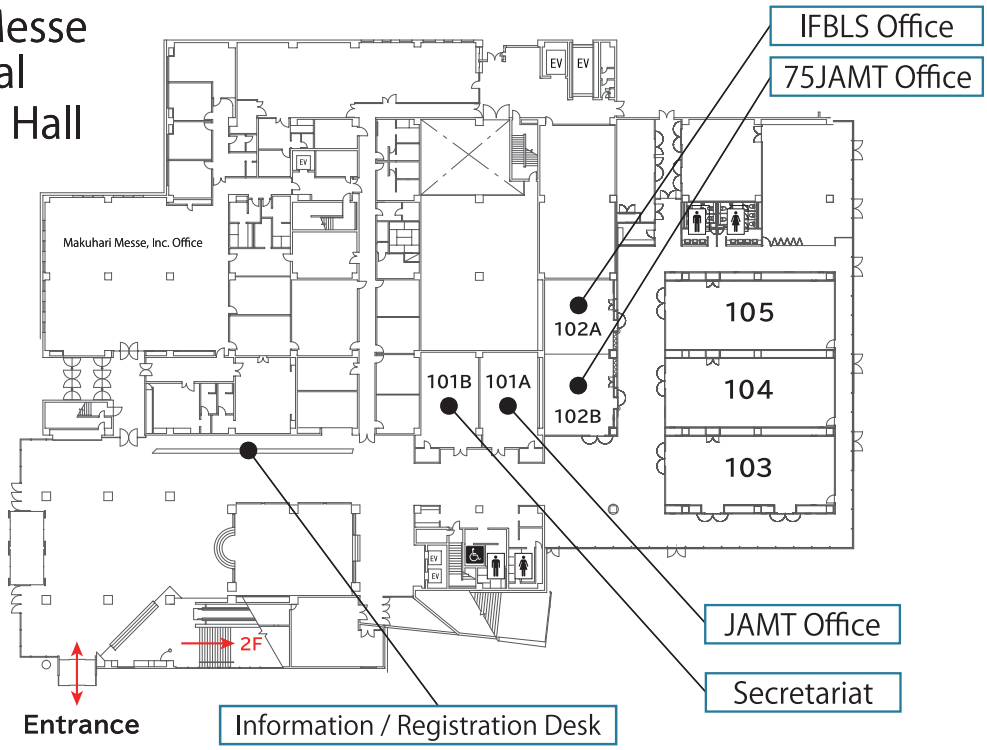
- Funabashi Station
- Nishi-Funabashi Station
- Chiba Station

Major Shopping Destinations:

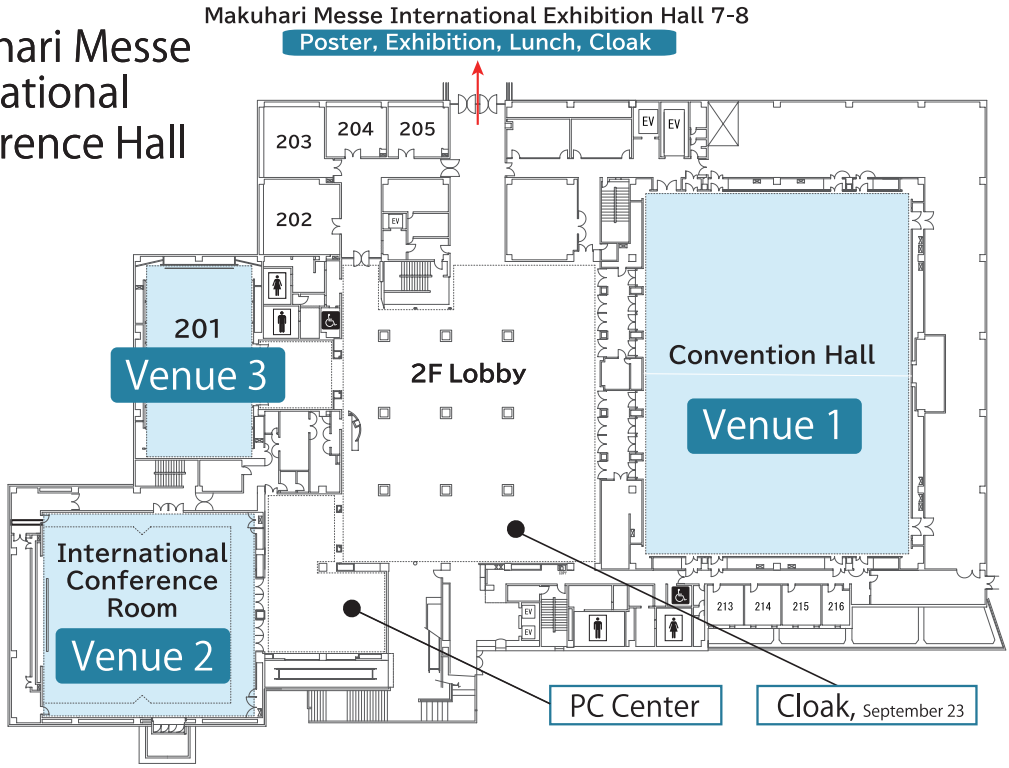
- **Makuhari-Toyosuna Station** – *AEON Mall Makuhari New City*
- **Minami-Funabashi Station** – *LaLaport TOKYO-BAY*
- **Maihama Station** – *Ikspiari*, a shopping and dining complex near Tokyo Disney Resort
- **Tokyo Station** – *Marunouchi Naka-dori, Tokyo Midtown Yaesu, and exclusive Tokyo Station sweets*

Venue Guide

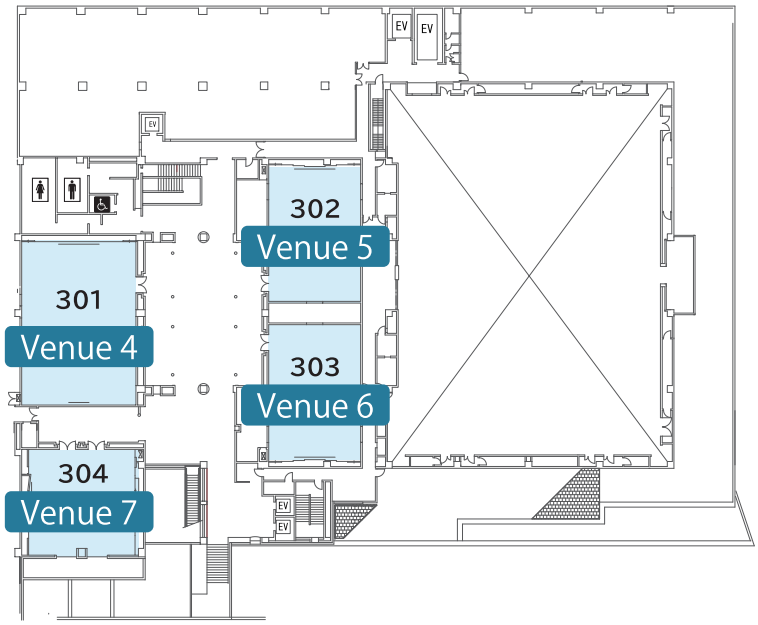
Makuhari Messe International Conference Hall 1F



Makuhari Messe International Conference Hall 2F

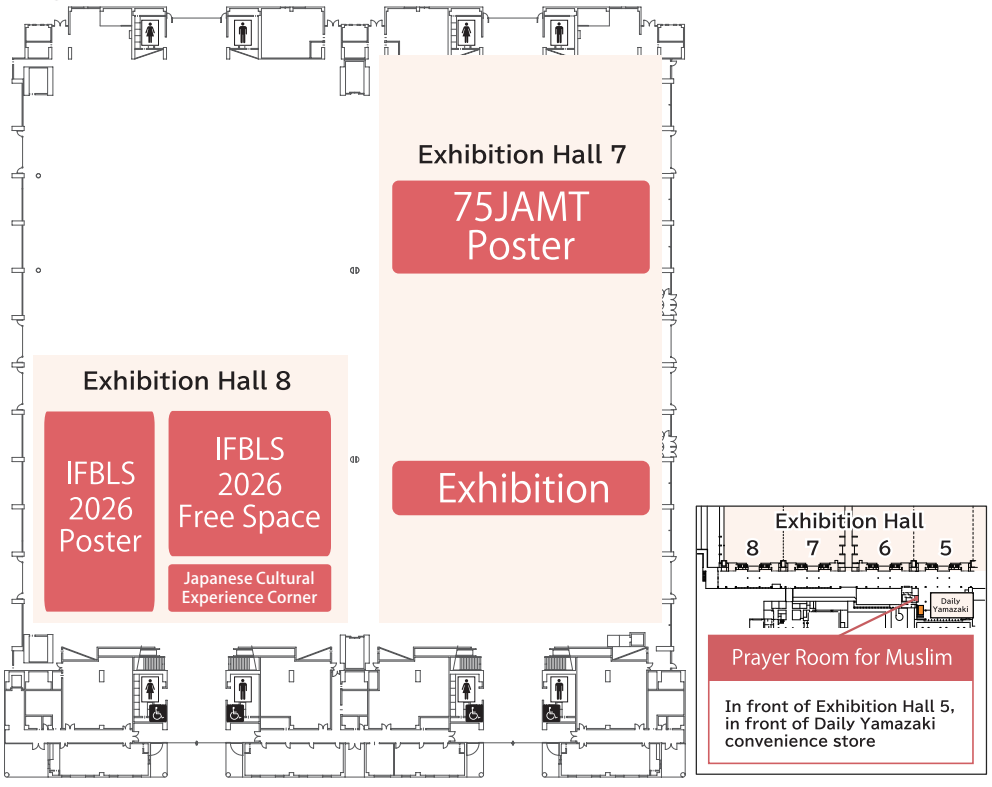


Makuhari Messe International Conference Hall 3F

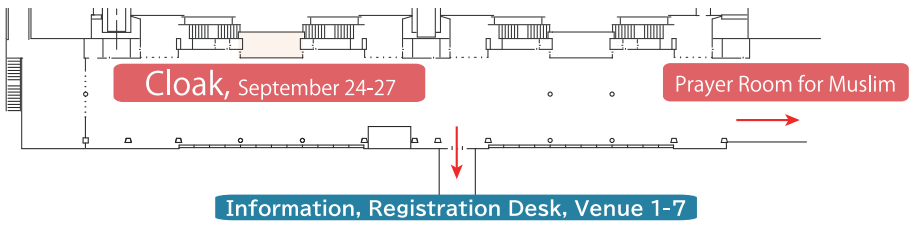


Makuhari Messe International Exhibition Hall 7-8

1F



2F

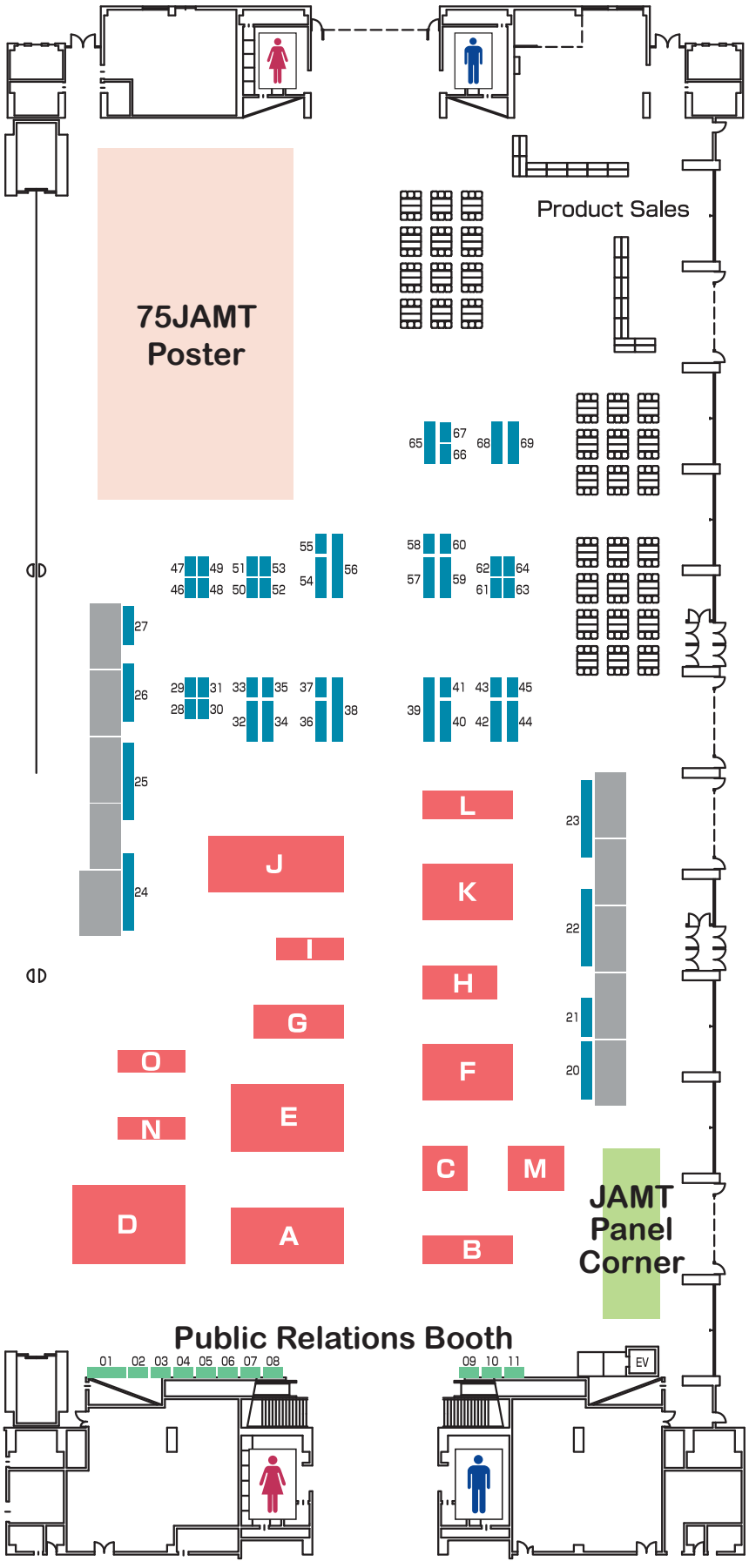


Information, Registration Desk, Venue 1-7

Makuhari Messe International Conference Hall

Exhibition Layout

Makuhari Messe International Exhibition Hall 7



Booth No.	Exhibitors
A	SYSMEX CORPORATION
B	Abbott Japan LLC
C	Roche Diagnostics K.K.
D	SEKISUI MEDICAL CO., LTD.
E	TOSOH CORPORATION
F	Hitachi High-Tech Corporation
G	H.U. Frontier, Inc./ SRL, Inc./ FUJIREBIO Inc.
H	NIHON KOHDEN CORPORATION
I	Beckman Coulter K.K. /Radiometer KK (Danaher)
J	Techno Medica Co. , Ltd.
K	EIKEN CHEMICAL CO., LTD
L	FUKUDA DENSHI CO., LTD.
M	Canon Medical Systems Corporation
N	NIPRO CORPORATION
O	QuidelOrtho Corporation
20	FUJIFILM Medical Co., Ltd.
21	FUJIFILM Wako Pure Chemical Corporation
22	JOKOH CO.,LTD.
23	Kobayashi Create Co.,Ltd.
24	BML, Inc.
25	CHEST M.I., INC.
26	Ansell Healthcare Japan, Inc.
27	Alfresa Pharma Corporation
28	Japan Lifeline Co.,Ltd.
29	Shimadzu Diagnostics Corporation
30	HONEST Co., Ltd.
31	Aglis Co., Ltd.
32	Bio-Rad Laboratories K.K.
33	Becton, Dickinson and Company
34	BIOTEC
35	TAUNS Laboratories, Inc.
36	YoukenScience Co.,Ltd.
37	ASAHI electrochemical Co., Ltd.
38	Thermo Fisher Scientific
39	Malcom Co.,Ltd.
40	KANTO CHEMICAL CO., INC
41	Minato Medical Science Co., Ltd.
42	-
43	Global Science Co., Ltd.
44	KYOKUTO PHARMACEUTICAL INDUSTRIAL CO., LTD./ TOYOBO CO., LTD.
45	Greiner Bio-One
46	SENKO MEDICAL INSTRUMENT Mfg. CO., LTD.
47	Eppendorf Co.,Ltd.
48	TEXeg CO., LTD.
49	SIemens Healthineers
50	BRAIN Co.,Ltd.
51	Japanese Association of Clinical Laboratory Systems (JACLaS)
52	Q-may Laboratory Corporation
53	FUJITSU JAPAN
54	Denka Co., Ltd.
55	Shirai Electronics Industrial Co., Ltd.
56	ARKRAY, Inc.
57	DAINIPPON SEIKI CO., LTD.
58	GramEye, Inc.
59	A&T Corporation
60	Pulstec Industrial Co.,Ltd.
61	TAKANO Co.,Ltd.
62	SUGIYAMA-GEN CO., LTD.
63	MIZUHO MEDY Co., Ltd.
64	Japan International Cooperation Agency (JICA)
65	PHC Corporation
66	FEATHER SAFETY RAZOR CO.,LTD.
67	Sakura Finetek Japan Co., Ltd.
68	Craif Inc.
69	ASIAKIZAI Inc.

Exhibiting Companies

Open Hours:

September 25 (Fri.)	11:20-17:00
September 26 (Sat.)	8:30-17:00
September 27 (Sun.)	8:30-15:00

Booth No.	Exhibitors	Major Exhibition Contents
A	SYSMEX CORPORATION	Exhibits: XR-Series Automated Hematology Analyzer / Automated Immunoassay System HISCL-800 / Fully Automated Urine Particle Analyzer UF-1500 and more
B	Abbott Japan LLC	Visit our booth to explore the Alinity ci-series, AlinIQ AMS, DSS, and the newly launched GLP systems Track. We welcome you.
C	Roche Diagnostics K.K.	We focus on sample workflows among our 5 pillars for the labs of tomorrow. Please experience next-gen workflows via AR ! (virtual display only)
D	SEKISUI MEDICAL CO., LTD.	We manufacture and sell essential products for clinical testing, focusing on blood coagulation, lifestyle-related diseases, and infectious diseases.
E	TOSOH CORPORATION	Automated chemiluminescent enzyme immunoassay system AIA-CL2400, AIA-CL1200 and AIA-CL300 / Tosoh Automated Glycohemoglobin Analyzer HLC-723® GR01
F	Hitachi High-Tech Corporation	① LABOSPECT 006 α HITACHI Automatic Analyzer ② Sample Preparation System LabFLEX 2600G ③ The Reaction Curve Fitting Method "MiRuDa"
G	H.U. Frontier, Inc./ SRL, Inc./ FUJIREBIO Inc.	Visit our booth to explore the LUMIPULSE® L2400 and learn about SRL's comprehensive laboratory testing services and diagnostic solutions.
H	NIHON KOHDEN CORPORATION	At this exhibition, we will showcase solutions that support quality management and optimize workflow efficiency in clinical physiology laboratories.
I	Beckman Coulter K.K. /Radiometer KK (Danaher)	“What Is Your Lab's Challenge?” (Beckman Coulter). Blood gas analyzers, Syringes, Immunoassay analyzer, Point-of-care IT solution (Radiometer)
J	Techno Medica Co. , Ltd.	• Automatic Tube Preparation System BC･ROBO-9000RFID • RFID Specimen Management System TRIPS • Blood Collection Support System Assist More･UA･ROBO-5000RFID
K	EIKEN CHEMICAL CO., LTD	Eiken will exhibit the new OC-SENSOR R70, OC-SENSOR Ceres, and the US Series, while introducing the LZ Series, Loopamp EXIA, POCT solutions, and more.
L	FUKUDA DENSHI CO., LTD.	Visit our booth. Explore our AI ECG, CAVI, Holter, pulmonary function, and other solutions. Some products are available only in Japan.
M	Canon Medical Systems Corporation	[Exhibit] Clinical Chemistry Automated Analyzers; TBA-400FR (Accute RX), Ultrasound; Aplio beyond, Others
N	NIPRO CORPORATION	POCT devices(Glucose meter,HbA1c meter),Biochemical diagnostic reagents,Antigen test kit,Blood collection tube

Booth No.	Exhibitors	Major Exhibition Contents
O	QuidelOrtho Corporation	VITROS Solutions(Clinical Chemistry and Immunoassay), ORTHO VISION System(Immunohematology), POCT Solutions
20	FUJIFILM Medical Co., Ltd.	Automated Clinical Chemistry Analyzer, FUJI DRI-CHEM NX700, FUJI DRI-CHEM NX600
21	FUJIFILM Wako Pure Chemical Corporation	LIMUSAVE MT-7500 : Quantitative β-D-glucan test. Ready-to-use single-test reagents, supporting early detection of invasive fungal infections.
22	JOKOH CO.,LTD.	• Smart Marker Series – Pathology Multi-Laser Printer • Smart Rate Series – ESR Analyzer • IoNEX – Electrolyte Analyzer
23	Kobayashi Create Co.,Ltd.	Support system for blood collecting duties, Testing tube preparation system for blood collecting duties
24	BML, Inc.	As a clinical laboratory center, we will showcase diagnostic tests and provide informational materials on our testing services.
25	CHEST M.I., INC.	CHEST expertly presents our spirometers, PFT system, FOT device, and PSG systems, delivering advanced, reliable, and precise respiratory solutions.
26	Ansell Healthcare Japan, Inc.	Ansell is a global leader in protective solutions, providing innovative gloves and PPE that help workers stay safe and productive worldwide.
27	Alfresa Pharma Corporation	Discrete Clinical Chemistry Analyzer AA01 Discrete Clinical Chemistry Analyzer NS-Prime® Rapid Tests
28	Japan Lifeline Co.,Ltd.	Japan Lifeline offers ATsens' AT-Patch. It features 7-day ECG recording, high-quality signals, and AT-Report software to streamline lab workflow.
29	Shimadzu Diagnostics Corporation	Ni-QCS Quality Control Management System and QC materials for clinical laboratories.
30	HONEST Co., Ltd.	
31	Aglis Co., Ltd.	Sealing film for laboratory containers. Hemostatic bandage for use after blood collection. Blood culture collection kit for standardized procedures.
32	Bio-Rad Laboratories K.K.	Visit the Bio-Rad booth to discover solutions for transfusion testing and quality control, featuring BRBTS NEXT, InteliQ, and Unity Next Peer QC.
33	Becton, Dickinson and Company	BD Vacutainer Barricor blood collection tube
34	BIOTEC	Demonstration of a versatile dispensing system for sample preparation prior to analysis.
35	TAUNS Laboratories, Inc.	ImmunoAce® Series:Rapid tests for respiratory pathogens,featuring a common extraction reagent shared by SARS-CoV-2,Flu,Adenovirus,hMPV and RSV assays.

Booth No.	Exhibitors	Major Exhibition Contents
36	YoukenScience Co.,Ltd.	
37	ASAHI electrochemical Co., Ltd.	Harun Kit: A new urine collection device that doesn't require paper cups.
38	Thermo Fisher Scientific	Visit our booth to explore the new Thermo Scientific™ FluidEase™ Pro ClipTip™ Electronic Pipette, calibration services, and laboratory solutions.
39	Malcom Co.,Ltd.	Exhibition and Presentation of In Vitro Diagnostic Medical Devices and Medical Devices
40	KANTO CHEMICAL CO., INC	① Reagent For Clinical Analyzer ② Products related to AMR : Chromogenic media , Genetic test kit ③ Automatic staining system ④ Liquid Handling Device
41	Minato Medical Science Co., Ltd.	Autospirometer System21
42	-	
43	Global Science Co., Ltd.	We manufacture and sell plastic consumables for clinical diagnostics, including urine sediment tubes, transfer pipettes, test tubes, and sample cups.
44	KYOKUTO PHARMACEUTICAL INDUSTRIAL CO., LTD. / TOYOBO CO., LTD.	POCT (Legionella urinary antigen, Bordetella pertussis etc.), GENECUBE Fully Automated Gene Analysis System, USCANNER Premio Urine Sediment Analyzer
45	Greiner Bio-One	Our exhibit features VACUETTE blood collection tubes with safety caps and MiniCollect capillary tubes
46	SENKO MEDICAL INSTRUMENT Mfg. CO., LTD.	
47	Eppendorf Co.,Ltd.	
48	TEXeg CO., LTD.	
49	SIemens Healthineers	
50	BRAIN Co.,Ltd.	We introduce an AI checking system that supports pathology laboratory operations by verifying slide folders and confirming the presence of specimens.
51	Japanese Association of Clinical Laboratory Systems (JACLaS)	
52	Q-may Laboratory Corporation	Blood coagulation-related reagents, D-dimer, FDP, Fibrinogen, vWF, etc

Booth No.	Exhibitors	Major Exhibition Contents
53	FUJITSU JAPAN	HOPE LifeMark-LAINS is a clinical laboratory system developed by an EMR vendor that contributes to improving the quality of medical care.
54	Denka Co., Ltd.	• Immunochromatographic Testing Devices & Readers • Clinical Chemistry Reagents
55	Shirai Electronics Industrial Co., Ltd.	The products on display are delivery robots and cleaning robots that can ride in elevators.
56	ARKRAY, Inc.	
57	DAINIPPON SEIKI CO., LTD.	Auto Slide Preparation System AS-410M and Automatic FFPE Tissue Block Facing Device AT-192M
58	GramEye, Inc.	Mycrium® is a Gram staining system automating staining, microscopy, imaging, and AI analysis. It standardizes workflows and optimizes lab efficiency.
59	A&T Corporation	A lineup of products that provide comprehensive solutions for clinical laboratories will be presented. Laboratory Information System – CLINILAN Series
60	Pulstec Industrial Co.,Ltd.	
61	TAKANO Co.,Ltd.	The analyzer (SiLIS-100) measures total IgE and 45 allergen-specific IgE from just 40 µL of serum or plasma, with results available in 15 minutes.
62	SUGIYAMA-GEN CO., LTD.	
63	MIZUHO MEDY Co., Ltd.	Point-of-Care PCR analyzer with 8 dedicated reagents, lateral flow reader compatible with 10 rapid antigen tests, and other diagnostic products
64	Japan International Cooperation Agency (JICA)	Introduction of Japan Disaster Relief Medical Team (JDR). Photo and video displays will illustrate our activities.
65	PHC Corporation	PATHFAST™ is a highly precise, fast and compact chemiluminescence immunoassay analyzer designed for confident decision-making at the point of care.
66	FEATHER SAFETY RAZOR CO.,LTD.	MICROTOME BLADE, MICROTOME HOLDER, TRIMMING KNIFE, DISSECTING BLADE, AUTOPSY BLAD, REPLACEABLE BLADE SCISSORSE
67	Sakura Finetek Japan Co., Ltd.	We are presenting a variety of information covering from “integration of staining and film embedding” to digitization.
68	Craif Inc.	Oyster is a next-generation LIMS that enables rigorous quality management and flexible laboratory workflows for testing and research.
69	ASIAKIZAI Inc.	

Makuhari Messe International Conference Hall 2F Lobby

Exhibitor	Contents
Shigaku Bookstore	Book

For Attendees

Basic Information

Language

The official language of the congress is English.

Congress Policy

- IFBLS has stated that the purpose of the Congress is to promote excellence in Biomedical Laboratory Science, foster professional development, provide networking opportunities within an educational forum, and advance Biomedical Laboratory Sciences globally. This mission holds significant international and scientific value. In alignment with this objective, JAMT will organize and implement the Congress.
- Please switch your mobile phones off or to vibration mode during all sessions.
- No photography and/or recording are allowed in any sessions, including posters.
- Smoking is prohibited at all times in the congress rooms and the entire building.

Congress Abstracts

Abstract books and program books are handed out to the registrants.
Abstracts can be downloaded from the congress website.

PC Preview

Special sessions speakers are requested to report to the PC Preview in the venue.
2nd floor Lobby, International Conference Hall (In front of Venue 2)

September 24 (Thu.)	8:30-15:30
September 25 (Fri.)	8:30-11:00

Prayer Room for Muslim

In front of Exhibition Hall 5, in front of Daily Yamazaki convenience store

Meals

The participation fee includes welcome reception, beer party, and lunch on September 23–26.
Lunch picks up area

September 23 (Wed.)	3rd floor Foyer, International conference hall
September 24 (Thu.) - 26 (Sat.)	International Exhibition Hall 8

Bookstore of JAMT Publishing

2nd floor Foyer, International conference hall (From September 25)

JAMT Office

Room 101A 1st floor, International Conference Hall

IFBLS Office

Room 102A 1st floor, International Conference Hall

Open Hours

Registration

September 23 (Wed.)	8:30-17:00	1st floor Lobby, International Conference Hall
September 24 (Thu.)	8:30-17:00	
September 25 (Fri.)	8:30-17:00	
September 26 (Sat.)	8:30-17:00	
September 27 (Sun.)	8:30-12:00	

Cloak

September 23 (Wed.)	8:30-20:30	2nd floor Hoyer, International Conference Hall
September 24 (Thu.)	8:30-20:30	2nd floor, entrance for International Exhibition Hall
September 25 (Fri.)	8:30-21:30	
September 26 (Sat.)	8:30-18:30	
September 27 (Sun.)	7:30-15:30	

Exhibition

September 25 (Fri.)	11:30-17:00	International Exhibition Hall 7
September 26 (Sat.)	8:30-17:00	
September 27 (Sun.)	8:30-15:00	

Coffee Break

September 23 (Wed.)	10:00-10:30 / 15:00-15:30	2nd floor Foyer, International conference hall
September 24 (Thu.)	10:00-10:30 / 15:00-15:30	2nd floor Foyer, International conference hall
September 25 (Fri.)	10:00-10:30	2nd floor Foyer, International conference hall / International Exhibition Hall 8
September 26 (Sat.)	10:00-10:30	International Exhibition Hall 8
September 27 (Sun.)	10:30-10:45	2nd floor Foyer, International conference hall

The 75th JAMT Congress 2026

The 75th JAMT Congress 2026 will be held from September 26 (Sat.) to 27 (Sun.), 2026.

Instructions for Presenters

Information for Special Program Speakers (Keynote, Educational Lecture, Symposium, Workshop, IFBLS Special Session, etc.)

All presentations will be discussed in English as oral presentations.
Please complete conference registration (or on-site registration) at the Registration Desk.

Preparing Presentation Data

Please note the following guidelines when preparing your presentation materials.

Fonts

To prevent character corruption and layout issues, please use standard fonts such as Arial, Century, Century Gothic, and Times New Roman.
If special fonts are used, we recommend converting the text to images before inserting it into your slides.

For Windows Users

* Please prepare your presentation using Microsoft PowerPoint.
* A slide size of 16:9 (widescreen format) is recommended.
* The presentation PCs and projectors provided at the venue support Full HD resolution (1920 × 1080).
* The operating system of the presentation PCs is Windows 11.
* Microsoft PowerPoint (Office 365) will be used for presentations at the venue.

For Mac Users

* If your presentation is created on a Mac, please thoroughly check in advance for any compatibility issues or layout changes when displayed in a Windows environment.
* If your presentation contains video files or if you are concerned about possible display issues, bringing your own laptop is recommended.
* The connection interface at the venue will be HDMI. If your device requires an adapter, please bring your own.
* Please test your presentation on a different computer in advance and prepare backup data.

Bringing Presentation Data

* Please save your presentation file on a USB flash drive and bring it with you.
* Ensure that your USB flash drive has been scanned for viruses before arrival.
* Please confirm that the presentation functions correctly on a computer other than the one used to create it.
* The file name should be saved in the following format: “Presentation Number_Presenter Name”
* Modifications to presentation data cannot be made at the venue. Please be sure to bring backup copies of your data.
* All presentation data received by the organizers will be securely deleted after the conference.

Use of Video and Audio

* If your presentation includes video or audio, please inform the staff at the time of registration.
* MP4 format is recommended for video files.
* In addition to embedding videos in your PowerPoint presentation, please bring the original video files as backup.
* Video files and any linked data should be stored in the same folder as the presentation file.

Presentation Data Check-in

1. Please complete data submission and preview testing at the PC preview room at least 60 minutes before your session begins (or 30 minutes before the first session of the day).
2. Presentation files should be brought on a USB flash drive. Files sent in advance by mail or courier cannot be accepted.
3. Presentation using a personal laptop is generally not permitted except in special circumstances. After completing the check-in process, presenters will receive a presentation confirmation slip.

Please present this slip to the audiovisual operator in your session room at least 30 minutes before the session begins (or immediately after PC reception for the first session of the day).

Presentation Time

Symposium	15–20 minutes per speaker/3–5 speakers per session Total session duration: 90 minutes includes FAQ time
Workshop	10–15 minutes per speaker/3–5 speakers per session Total session duration: 60 minutes includes FAQ time

- Presentation time begins when the Chair starts introducing the presentation, not when the speaker begins speaking.
- To maintain the schedule, presentations and discussions may be terminated if they exceed the allotted time.
- All presentation data copied to conference computers will be securely deleted by the organizers after the conference.

Information for General session Presenters

All general session presentations will be presented in English and presented in poster format.
All presenters must complete conference registration (or on-site registration) at the Registration Desk.

Poster Presentation Schedule

Venue:

Poster Area (Makuhari Messe International Exhibition Hall 8)

Schedule:

Poster Mounting	September 24 (Thu), 13:00–17:00
Poster Display	September 25 (Fri), 09:00–17:00 (Social Hours: 09:00–12:00) September 26 (Sat), 09:00–17:00 September 27 (Sun), 09:00–13:00
Poster Removal	September 27 (Sun), 13:00–15:00

Presentation Guidelines

- No individual presentation time slots will be assigned for poster presentations. “Social Hours” will be held on Friday, September 25, from 09:00 to 12:00. Presenters are encouraged to visit the poster area during this time to interact with attendees and discuss their work.
- Outstanding poster presentations will be considered for the Poster Award. Judges may visit your poster and ask questions regarding your research. Poster Award winners will be announced during the Closing Ceremony on September 27, Sunday morning.

Poster Setup

No check-in is required for poster presentations.
Thumbtacks will be provided at each poster board. Please mount your poster at the designated location according to your presentation number within the assigned setup period.
Presenters are requested to remain near their posters during the “Social Hours” and be available to answer questions from participants.

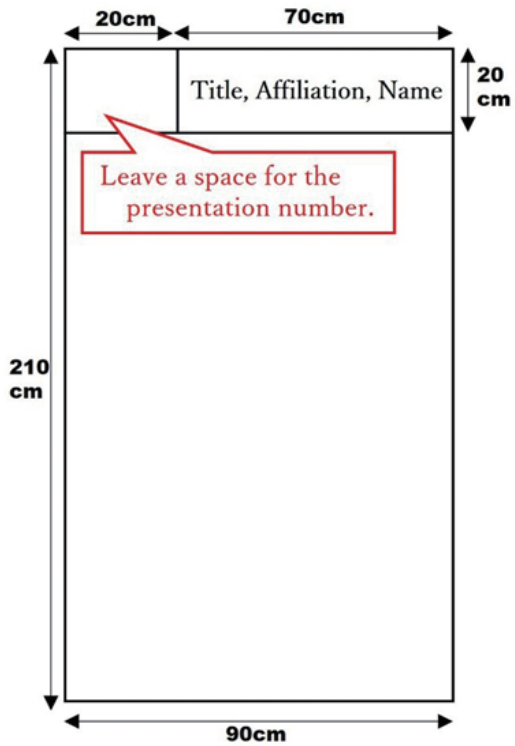
Please note: Posters must be removed during the designated removal period. Any posters remaining after the deadline will be removed and disposed of by the organizers.

Poster Specifications

Poster size	Length 190 cm x width 90 cm.
Font	Widely used font (Arial or Calibri recommended.)
Disclosure of COI	To avoid any commercial bias, all authors must disclose conflicts of interest in a statement at the bottom of the poster.

- Please prepare the title, affiliations, and author information within a space of 70 cm (W) × 20 cm (H).
- Poster numbers will be prepared by the congress Secretariat.
- The title, author names, affiliations, and poster content should be prepared by the presenter.

Sample Poster



September 23

Facility name	International Conference Hall									International Exhibition Hall	
Floor	2F				3F				1F	1F	
Room name	Convention Hall	International Conference Room	Lobby	201	301	302	303	304	Counter	Exhibition Hall 7	Exhibition Hall 8
Venue name	Venue 1	Venue 2		Venue 3	Venue 4	Venue 5	Venue 6	Venue 7	Registration Desk	Exhibition	Poster-Lunch
8:30 ▸									Registration		
9:00 ▸		Open Forum		Student Forum							
10:00 ▸			Coffee Break								
11:00 ▸											
12:00 ▸					Lunch	Lunch	Lunch				
13:00 ▸		Chief Delegates Meeting-Day 1		Student Forum							
14:00 ▸											
15:00 ▸			Coffee Break								
16:00 ▸											
17:00 ▸	Welcome Ceremony										
18:00 ▸		Welcome Reception									
19:00 ▸											
20:00 ▸											

• Welcome Ceremony: Smart Casual • Welcome Reception: Casual

September 24

Facility name	International Conference Hall									International Exhibition Hall	
Floor	2F				3F				1F	1F	
Room name	Convention Hall	International Conference Room	Lobby	201	301	302	303	304	Counter	Exhibition Hall 7	Exhibition Hall 8
Venue name	Venue 1	Venue 2		Venue 3	Venue 4	Venue 5	Venue 6	Venue 7	Registration Desk	Exhibition	Poster-Lunch
8:30 ▶									Registration		
9:00 ▶											
		WS01 Microbiology		WS02 Hematology	WS03 Transfusion Medicine	WS04 Genetics	Chief Delegates Meeting-Day 2	Student Forum			
10:00 ▶			Coffee Break								
		SY01 Hematology		SY02 Education	SY03 Immunology	SY04 Others (Physiology)					
11:00 ▶											
12:00 ▶								Lunch Seminar for students			Lunch
13:00 ▶											
		SY05 Microbiology		SY06 Cytology	SY07 Chemistry	SY08 Parasitosis					Poster Mounting
14:00 ▶											
15:00 ▶			Coffee Break								
		Educational Lecture2 Dr.Hayato Miyachi		WS05 Others (Management)	WS06 Cytology	WS07 Urinalysis					
16:00 ▶											
17:00 ▶											
18:00 ▶	Beer Party										
19:00 ▶											
20:00 ▶											

・Beer Party: Casual

September 25

Facility name	International Conference Hall									International Exhibition Hall	
Floor	2F				3F				1F	1F	
Room name	Convention Hall	International Conference Room	Lobby	201	301	302	303	304	Counter	Exhibition Hall 7	Exhibition Hall 8
Venue name	Venue 1	Venue 2		Venue 3	Venue 4	Venue 5	Venue 6	Venue 7	Registration Desk	Exhibition	Poster-Lunch
8:30 ▸									Registration		
9:00 ▸		IFBLS Special Session		WS08 Pathology	WS09 Education	WS10 Immunology					Poster viewing
10:00 ▸	Educational Lecture3 Dr.Kentaro Naoda		Coffee Break							10:00-10:30 Coffee Break	
11:00 ▸		Educational Lecture1 Dr. Amy Spiczka		SY09 Pathology	SY10 Genetics	SY11 Transfusion Medicine				Ribbon-cutting ceremony	Social Hours 9:00-12:00
12:00 ▸										Exhibition	Lunch
13:00 ▸											Poster viewing
14:00 ▸	Opening Ceremony										
15:00 ▸	Keynote Speech 1										
16:00 ▸	Keynote Speech 2										
17:00 ▸											
18:00 ▸											
19:00 ▸	Gala Dinner										
21:00 ▸											

• Opening Ceremony: Business Attire • Gala Dinner: Casual

September 26

Facility name	International Conference Hall									International Exhibition Hall	
Floor	2F				3F				1F	1F	
Room name	Convention Hall	International Conference Room	Lobby	201	301	302	303	304	Counter	Exhibition Hall 7	Exhibition Hall 8
Venue name	Venue 1	Venue 2		Venue 3	Venue 4	Venue 5	Venue 6	Venue 7	Registration Desk	Exhibition	Poster-Lunch
8:30 ▶											
9:00 ▶	Optional Tour								Registration	10:00-10:30 Coffee Break	Poster viewing
12:00 ▶										Exhibition	Lunch
13:00 ▶											Poster viewing
17:00 ▶											

September 27

Facility name	International Conference Hall									International Exhibition Hall	
Floor	2F				3F				1F	1F	
Room name	Convention Hall	International Conference Room	Lobby	201	301	302	303	304	Counter	Exhibition Hall 7	Exhibition Hall 8
Venue name	Venue 1	Venue 2		Venue 3	Venue 4	Venue 5	Venue 6	Venue 7	Registration Desk	Exhibition	Poster-Lunch
8:30 ▶											
9:00 ▶		GAD & Closing Ceremony		10:30-10:45 Coffee Break					Registration	Exhibition	Poster viewing
12:00 ▶											
13:00 ▶											
17:00 ▶											

September 25 (Fri.)

Keynote Speech 1

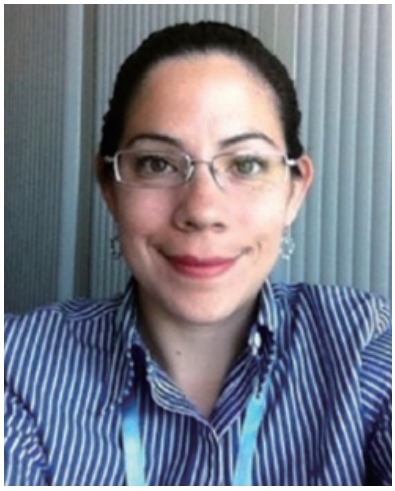
Convention Hall

Venue 1

September 25 (Fri.) 15:00-15:30

Chair: Kyoko Komatsu (Tsuchiura Kyodo General Hospital, Department of Pathology)

KS01 Building Bridges: Biomedical Laboratory Science Connecting People, Innovation and Global Health



Ana Aceves Capri

Medical Devices and Assistive Technology team. Department of Medicines and Health Products Policies and Standards. World Health Organization.

Keynote Speech 2

Convention Hall

Venue 1

September 25 (Fri.) 15:30-16:00

Chair: Hiromichi Matsushita (Japanese Society of Laboratory Medicine)

KS02 Regarding emerging infectious diseases such as COVID-19

Shigeru Omi

Chairman, Board of Directors Japan Anti-Tuberculosis Association(JATA)

September 24 (Thu.) - 25 (Fri.)

Educational Lecture 1

International Conference Room — Venue 2

September 25 (Fri.) 11:00-12:00

Chair: Hideo Sakamoto (Kobe Tokiwa University Medical Technology)

EL01 Advancing Global Laboratory Practice Through Examination Excellence and Data-Driven Insights: ASCP BOC's Commitment to Professionals and Patients Worldwide

Amy Spiczka

DHSc, MS, HTL(ASCP) CM, SCTCM, MBCM, CPHQ

Executive Director, Board of Certification, American Society for Clinical Pathology

Educational Lecture 2

International Conference Room — Venue 2

September 24 (Thu.) 15:30-16:30

Chair: Mohd Nazil Bin Salleh (Malaysian Institute of Medical Laboratory Science)

EL02 Quality Assurance Framework for Molecular Genetic Testing: International Standards and Risk Management for Laboratory Developed Tests

Hayato Miyachi

Professor, Department of Clinical Laboratory Science, Nitobe Bunka College

Educational Lecture 3

International Conference Room — Venue 2

September 25 (Fri.) 10:30-10:50

Chair: Hideo Sakamoto (Kobe Tokiwa University Medical Technology)

EL03 Disaster response supporting system by JAMT

Kentaro Naoda

Seirei Hamamatsu General Hospital (Japan)

September 24 (Thu.)

Lunch Seminar for students

Room 304

Venue 7
September 24 (Thu.) 12:00-13:00

Meet the IFBLS Leaders
Ask the IFBLS Leaders, Shape Your Future

Chair: Yui Namikawa (Toin University of Yokohama)

The future of Biomedical Laboratory Science begins with curiosity, dialogue, and inspiration.

This interactive lunch seminar offers students a unique opportunity to meet IFBLS Past Presidents and IFBLS leaders from around the world. Through an open Q&A session, participants are invited to ask questions about professional careers, international collaboration, leadership, education, and the future of the profession.

Rather than a traditional lecture, this session is designed as an engaging conversation between students and global leaders. By sharing their experiences, challenges, and visions, the speakers aim to inspire the next generation of biomedical laboratory professionals and encourage students to pursue leadership opportunities in an increasingly connected world.

Whether you are considering your future career, interested in international activities, or simply curious to hear from leaders who have shaped our profession, this session is for you.

Bring your questions. Meet the IFBLS leaders. Shape your future.

Speakers:

Marie Culliton
Past-President of IFBLS
(Ireland)

Gabriella Lillsunde Larsson
President of IFBLS
(Sweden)

Hassan Aziz
President-Elect of IFBLS
(United states of America)

Kyoko Komatsu
Former President of IFBLS
(Japan)

September 25 (Fri.)

IFBLS Special Session

International Conference Room — Venue 2

September 25 (Fri.) 09:00-10:00

IFBLS-A professional framework towards increased knowledge, advancement and visibility of the profession

Chair: Kyoko Komatsu (Tsuchiura Kyodo General Hospital, Department of Pathology)

IFBLS-A professional framework towards increased knowledge, advancement and visibility of the profession

Gabriella Lillsunde Larsson

President of IFBLS (Sweden)

Associate Professor, Örebro University, Örebro, Sweden

IFBLS Services to Members
International Directory of Biomedical Laboratory Science Education (IDBLSE) and IFBLS Professional Code of Ethics

Marie Nora Roald

Member at Large of IFBLS (Norway)

Laboratory Manager, Department of Medical Biochemistry and Blood Bank, Helse Møre and Romsdal Hospital Trust

ISCO Classification and Biomedical Laboratory Scientists

Marie Culliton

Past-President of IFBLS (Ireland)

MSc, MBA, FACSLM

September 24 (Thu.) - 25 (Fri.)

Symposium 1

International Conference Room — Venue 2

September 24 (Thu.) 10:30-12:00

The advancement of hematological analysis utilizing new technology (AI and big data, etc)

Hematology

Chairs: Yuya Tanabe (Hematology Laboratory, Clinical Laboratory, Japanese Red Cross Kyoto Daini Hospital)
Robyn Wells (Board Member of IFBLS (Australia))

SY01-1 A New Stage in Thrombosis and Hemostasis Testing
The Future of Thrombosis and Hemostasis Testing with Artificial Intelligence

Naoki Tokunaga

Department of Clinical Laboratory, Kawashima Hospital

SY01-2 Seeing Before Sequencing: Early AML Treatment
Morphology and flow cytometry as rapid surrogates for AML decision-making

Hui-Ling Chen, Li-Fong Hong, Yi-Chun Kuo, Chia-Yi Hou

Chi Mei Medical Center, Liouying

SY01-3 The *CALR* mutation in myeloproliferative neoplasms patients: a single institution experience

FRIKHA

University hospital of sfax; Department of Medical genetic Sfax-TUNISIA

SY01-4 p53 Expression by IHC and Cytogenetic-Morphological Findings in MDS

Mari Kunihiro

Fukuyama City Hospital, Hiroshima, Japan

SY01-5 Data-Derived D-dimer Cutoffs Corresponding to FDP Categories in the JAAM-2 DIC Criteria
A Large Real-World Analysis

Ryota Masutani

Dept. of Central Clinical Laboratory, Osaka Medical and Pharmaceutical Univ. Hosp

Symposium 2

Room 201 — Venue 3

September 24 (Thu.) 10:30-12:00

Career development for BLS students

Education

Chair: Hideo Sakamoto (Kobe Tokiwa University Medical Technology)

SY02-1 Current Career Paths After Studying Biomedical Laboratory Science

Kohki Okada

Department of Medical Technology and Sciences, Faculty of Health Sciences, Kyoto Tachibana University

SY02-2 BLS Education and Career Paths in Norway

Marie Nora Roald

Department of Medical Biochemistry and Blood Bank, Helse Møre and Romsdal Hospital Trust

SY02-3 Closing the Gap
DCLS Practice Model as the Key to Transforming Patient Care from Volume to Value

Hassan Aziz[1], Peter Hu[2], Yasmen Simonian[3], Marisa James[4]

1 The Rochester Institute of Technology (RIT), New York / IFBLS President-Elect
2 The University of Texas MD Anderson Cancer Center
3 Weber State University
4 National Accrediting Agency for Clinical Laboratory Science

SY02-4 The Swedish Biomedical Laboratory Scientist Research School for eXcellence (BioLabX)
A national initiative to increase the amount of university teachers and researchers within biomedical laboratory science

Gabriella Lillsunde Larsson

President IFBLS 2024–2026, associate professor at Örebro University, Örebro Sweden and node director (Örebro) of The Swedish Biomedical Laboratory Scientist Research School for eXcellence (BioLabX)

Symposium 3

Room 301 Venue 4

September 24 (Thu.) 10:30-12:00

The Future of Immuno-Serological Testing: Addressing Unexpected Pitfalls and Exploring New Horizons

Immunology

Chairs: Chiaki Sato (Clinical Laboratory, Showa Medical University Koto Toyosu Hospital)
Giseon Song (Board Member of IFBLS (Korea))

SY03-1 Future of Immunoserological Testing
Toward the Resolution of Pitfalls

Ryuji Miki

Department of Clinical Laboratory, Dokkyo Medical University Saitama Medical Center

SY03-2 Transition from intravenous to subcutaneous natalizumab treatment in persons with multiple sclerosis

Aage Winje Brustad

Department of Medical Biochemistry, Oslo University Hospital, Norway

Symposium 4

Room 302 — Venue 5

September 24 (Thu.) 10:30-12:00

Physiological Diagnostics in the Digital Age: new technology (AI and big data, etc) into Functional Testing

Others (Physiology)

Chair: Tomohito Yara (Central Clinical Laboratory, JIHS, Center Hospital of the National Center for Global Health and Medicine)

SY04-1 AI in Physiological Functional Diagnostics
To What Extent Can We Rely on It?

Nozomi Aoyama

Clinical Laboratory, NTT Medical Center Tokyo

SY04-2 Enhancing Clinical Laboratory Internship Training Through an Intelligent Image-Assisted Learning System
Application to Sperm Counting and Morphological Analysis in Microscopic Examination

Ming-Shu Chen[1], Chung-Chih Hung[2], Tsou-Chi Chen[3]

1 Department of Healthcare Administration, Asia Eastern University of Science and Technology, New Taipei City 220, Taiwan, (ROC)
2 Department of Laboratory Medicine, Taipei Hospital, Ministry of Health and Welfare, New Taipei City 220, Taiwan, (ROC)
3 Department of Health Promotion and Health Education, National Taiwan Normal University, Taipei City 106, Taiwan, (ROC)

SY04-3 Toward More Precise Neurophysiological Diagnosis: Motor Function Assessment Using the Second Lumbrical CMAP in Carpal Tunnel Syndrome

Keita Nishiwaki, Fuuki SUGIOKA, Yuu ISOMURA, Keitarou ITOU, Kenji INOUE, Yuudai SUZUKI, Eiji ITOU, Takeshi OOSHIMA

Department of Clinical Laboratory, Kariya Toyota General Hospital, Aichi

SY04-4 Invasive EEG versus Stereo-EEG for Epileptogenic Zone Localization
A Comparative Analysis of Invasive Monitoring Techniques in Presurgical Epilepsy Evaluation

Park Jin woo

Neurology Lap. Samsung Medical Center, Seoul Korea

Symposium 5

International Conference Room — Venue 2

September 24 (Thu.) 13:30-15:00

Advanced Technologies Revolutionizing Microbiological Testing

Microbiology

Chairs: Takeya Ohshiro (Department of Clinical Laboratory, Naha City Hospital, Okinawa)
Bitten Kaanbjerg Kristensen (Board Member of IFBLS (Denmark))

SY05-1 Toward the implementation of Bacterial WGS to Transform Clinical Practice
Proposing the Concept of Tracking Antimicrobial-Resistant Organisms Timely (TAROT)

Kotaro Aoki

Microbiology and Infectious Diseases, Toho University School of Medicine

SY05-2 Enhancing tuberculosis diagnosis and drug resistance detection in Thailand through next-generation sequencing (NGS)

Panan Ratthawongjirakul

1 Director of Center of Excellence for Innovative Diagnosis of Antimicrobial Resistance
2 Faculty of Allied Health Sciences, Chulalongkorn University
3 Scientific chairman of the Association of Medical Technology of Thailand

SY05-3 Clinical Determinants of Rapid Influenza Antigen Test Performance
Effects of Age and Symptom Duration on Diagnostic Accuracy

Suphara Manowong, Sujitra Kaewarree, Phakamat Saihikam, Tavitiya Sudjaritruk

Department of Pediatrics, Faculty of Medicine, Chiang Mai University, Chiang Mai, Thailand

SY05-4 Nomman: automated bacterial nomenclature management in the clinical microbiology laboratory

Herman Tse[1], Garnet Kwan-Yue Choi[2]

1 Department of Laboratory Medicine, Khoo Teck Puat Hospital, Singapore
2 Department of Pathology, Hong Kong Children's Hospital,Hong Kong, China

Symposium 6

Room 201 Venue 3

September 24 (Thu.) 13:30-15:00

Cytology Beyond Generations: What Today's Experts Want to Share with Tomorrow's Cytotechnologists

Cytology

Chairs: Shuhei Ishii (Pathology, The Cancer Institute Hospital, Japanese Foundation for Cancer Research)
Hwa Jeong Ha (Department of Hematology, Transfusiology and Laboratory Research, Tashkent State Medical University, Uzbekistan)

SY06-1 Immunocytochemistry Using the Cell Transfer Method in Cytological Specimens

Shinji Matsumoto

Department of Pathology, Fukuoka University Hospital

SY06-2 Diagnostic Clues in Pancreatic Cytology
Ancillary Findings Suggestive of Malignancy

Yuki Obara

Laboratory of Anatomic Pathology Toyama University Hospital

SY06-3 Cytology Beyond Generations: Integrating AI-driven Morphological Recognition with Lean Management in Clinical Practice and Education
Transforming Laboratory Workflows and Morphological Education in The Era of Digital Diagnostics

Wan-Ling Chiu

1 Technical Supervisor, Laboratory Medicine, Taipei City Hospital (Yang-Ming Branch), Taiwan
2 PhD. Student, Graduate Institute of Business Administration, Fu Jen Catholic University, Taiwan

SY06-4 Impact of BLS's Technical Proficiency on Cytologic Diagnosis
Focused on Specimen Processing in Central Nervous System Samples

Atsuko Suzuki[1], Tomoko Shimooka[1], Kazuyo Yoshida[1], Yuka Kagawa[1], Asuka Imai[1], Kyoko Komatsu[2], Hiroyuki Hao[3]

1 Pathology Laboratory, Nihon University Itabashi Hospital
2 Pathological diagnosis unit, Tsuchiura Kyodo General Hospital, Japan
3 Division of Human Pathology, Department of Pathology and Microbiology, Nihon University School of Medicine

SY06-5 Insights into Tenascin-C in MAPK inhibitor resistance in melanoma

Nina Zila[1], Christopher Gerner[2], Ossia M. Eichhoff[3], Verena Paulitschke[4]

1 Biomedical Science, University of Applied Sciences Campus Vienna; / Dept. of Dermatology, Medical Univ. of Vienna; Austria
2 Dept. of Analytical Chemistry, Univ. of Vienna; Austria
3 Dept. of Dermatology, Univ. Hospital Zurich, Univ. Zurich; Switzerland
4 Dept. of Dermatology, Medical Univ. of Vienna; Austria

Symposium 7

Room 301 Venue 4

September 24 (Thu.) 13:30-15:00

Global Landscape of Clinical Chemistry: Current Status and Future Perspectives

Chemistry

Chair: Ryunosuke Ohkawa (Clinical Bioanalysis and Molecular Biology, Institute of Science Tokyo)

SY07-1 Navigating Through Standardization, Digital Transformation, and Advanced Quality Control

Keita Yamashita

Department of Laboratory Medicine, Hamamatsu University Hospital

SY07-2 The development of POCT at Landspítalinn

Helga Sigrún Sigurjónsdóttir

Department of Clinical Biochemistry, Laboratory Core, Landspítali – The National University Hospital of Iceland, Reykjavík, Iceland

SY07-3 When challenges become opportunities: quality reviews in geographically distributed laboratories in accordance with ISO 15189:2022

Louise Spendrup

Biomedical Laboratory Scientist, Clinical Chemistry, Medical Diagnostics, Karolinska, Karolinska University Hospital

SY07-4 Falsely Low Total Bilirubin by Elevated Hyaluronic Acid

Yu Nagakura[1], Shinya Ueno[1], Yasuko Okui[1], Yoshiya Matsumoto[2], Takuya Asaoka[2], Kouji Abou[1], Tomoya Kawaguchi[2], Mika Nakamae[1]

1 Department of Central Clinical Laboratory, Osaka Metropolitan University Hospital
2 Department of Respiratory Medicine, GraduateSchool of Medicine, Osaka Metropolitan University

SY07-5 Artificial Intelligence for Clinical Chemistry in Low-Resource Laboratory Settings. Implementing Edge AI for Real-Time Diagnostic Support in Connectivity-Challenged Environments

Ahmed Salih[1], Hanem Haron[2]

1 Sudan Lab AI
2 Deep Solve medtech

Symposium 8

Room 302 Venue 5

September 24 (Thu.) 13:30-15:00

Global Trends in Parasitic Disease Detection and Innovations in Diagnostic Methods

Parasitosis

Chair: Kenichiro Ohnuma (Clinical Laboratory Kobe University Hospital)

SY08-1 Rapid Diagnostic Tests in Malaria
Confronting Drug and Diagnostic Resistance

Takaya Sakura

Institute of Tropical Medicine (NEKKEN), Nagasaki University

SY08-2 Molecular Detection of *Fasciola* spp. In Farmland Plants and Surrounding Water Samples from Selected *Barangays* in San Jose City, Nueva Ecija: A Corollary for One Health Approach

Somer Dame A. Basallote

1 Department of Medical Technology, Faculty of Pharmacy, University of Santo Tomas
2 Biosafety and Environment Section, Research and Department Division, Philippine Carabao Center National Headquarters and Gene Pool, Science City of Muñoz, Nueva Ecija 3120, Philippines
3 Local Government Unit, San Jose City, Nueva Ecija, Philippines

SY08-3 Evaluating the Diagnostic Accuracy of the Sysmex XN-31 Automated Malaria Analyzer Against Gold Standard Microscopy: A. cross-sectional study in Kumasi-Ghana

Edward Yaw Afriyie, Theophilus Arthur-Gyimah

Haematology Unit, Komfo Anokye Teaching Hospital, Kumasi-Ghana

SY08-4 Two Cases of Cryptosporidiosis: Oocysts Initially Detected by Gram Stain

Yusuke Nomura[1], Yoshimi Higurashi[1], Shinya Yamamoto[2], Kazuhiko Ikeuchi[2], Ryu Yoneda[1], Kazuya Okushin[1], Takeya Tsutsumi[1]

1 Department of Infection Control and Prevention, The University of Tokyo Hospital, Tokyo, Japan
2 Department of Infectious, Diseases, The University of Tokyo Hospital, Tokyo, Japan

Symposium 9

Room 201 Venue 3

September 25 (Fri.) 10:30-12:00

Next-Generation Histopathology: Bridging Fundamental Processing and Advanced Technologies

Pathology

Chair: Satoshi Morito (Department of Diagnostic Pathology, Hyogo Medical University Hospital)

SY09-1 Advanced Testing, Built on Strong Foundations
Perspectives on Pre-analytical Pathology in the Genomic Era

Yoshiki Shinomiya

Center for Development of Advanced Diagnostics, Hokkaido University Hospital, Sapporo, Japan

SY09-2 Integration of Artificial Intelligence (Ai) Technology in Histopathology Curriculum in Medical Technology

Mohd Nazil Bin Salleh

Department Forensic Law Enforcement, SAITO University College, Kuala Lumpur Malaysia

SY09-3 Implementation of MacroPATH MX SK C-Scan Image-Based Macroscopic Biopsy Documentation

Joergensen, Charlotte Salskov

Department of Pathology, Odense University Hospital

SY09-4 Digital Pathology Implementation in Remote Canadian Regions A summary of unique opportunities and challenges

Christine Bruce, Raj Saniasy

University Health Network

Symposium 10

Room 301 Venue 4

September 25 (Fri.) 10:30-12:00

Current Status of Genome Testing with NGS in Japan and Worldwide

Genetics

Chair: Yuka Fujimoto-Sato (Tokyo Healthcare University)

SY10-1 The Evolving Role of Laboratory Scientists in Genomic Medicine Education and Workforce Development for the Genomic Era in Japan

Asami Nishikori

Department of Molecular Hematopathology, Okayama University Graduate School of Health Sciences, Okayama, Japan

SY10-2 Current Status of Genome Testing with NGS in Japan and Worldwide From Companion Diagnostics to CGP: Practical Realities of Cancer Genomic Testing in Japan

Kaori Watanabe

Department of Laboratory Medicine, National Cancer Center Japan

SY10-3 Advanced Genomic Diagnostics: Current Status and the Vital Role of Medical Laboratory Professionals in the NGS Era Global Trends and Strategic Adaptations in South Korea's Healthcare Landscape

Jiwon Lee

Department of Laboratory Medicine, The Catholic University of Korea Seoul St. Mary's Hospital, Seoul, South Korea

SY10-4 Dual luciferase assays for miRNA target investigation in salmonid cells

Nardos Tesfaye Woldemariam[1], Hilde Sindre[2], Alice Shwe[1], Rune Andreassen[1]

1 Oslo Metropolitan University, Dept. of Life Sciences and Health, Biomedical Laboratory Sciences
2 Norwegian Veterinary Institute

Symposium 11

Room 302 Venue 5

September 25 (Fri.) 10:30-12:00

Clinical support in the field of blood transfusion across various countries

Transfusion medicine

Chairs: Ryosei Murai (Division of Laboratory Medicine, Sapporo Medical University Hospital)
Marie Culliton (Past-President of IFBLS (Ireland))

SY11-1 Clinical Support by Medical Technologists in Transfusion Medicine
Task Shifting and Task Sharing in Japan

Yuya Tashiro

Department of Transfusion Service, Tokai University Hospital, Kanagawa, Japan

SY11-2 Cis-AB Blood Group with Asian-type DEL (c.1227G>A): Serologic and Molecular Characterization of a Rare Case
A rare combination of ABO Cis-AB and RHD*01EL.01 alleles

Sumin Kim

Department of Laboratory Medicine, Seoul St. Mary's Hospital, College of Medicine, The Catholic University of Korea, Seoul, Republic of Korea

September 24 (Thu.) - 25 (Fri.)

Workshop 1

International Conference Room

Venue 2
September 24 (Thu.) 9:00-10:00

Resistance: Current Status and Strategic Responses

Microbiology

Chair: Kenichi Shizuno (Clinical Laboratory, Chiba Kaihin Municipal Hospital)

WS01-1 Current Status and Strategic Responses to AMR in Japan
Surveillance Systems and Epidemiological Trends of Antimicrobial-Resistant Bacteria

Kohei Uechi

Division of Clinical Laboratory and Infection Control Kanazawa University Hospital

WS01-2 A glance of carbapenem-resistant situation in Thailand

Pitak Santanirand

1 Head of Microbiology Laboratory, Department of Pathology, Faculty of Medicine Ramathibodi Hospital, Mahidol University, Thailand
2 President of the Royal College of Medical Technologists (RCMT), Thailand

WS01-3 The Importance of Establishing Testing Strategies Based on Risk Assessment of Drug-Resistant Bacteria
-Aligning Local Epidemiology, Facility Resources, and Regional Networks-

Hara Yuki

Japanese Red Cross Aichi Medical Center Nagoya Daini Hospital

Workshop 2

Room 201

Venue 3
September 24 (Thu.) 9:00-10:00

The current status and challenges of body cavity fluid analysis

Hematology

Chair: Naoko Hisasue (Clinical Laboratory, The University of Tokyo Hospital)

WS02-1 A Multi-Laboratory CSF Workflow for Rapid Hematologic Malignancy Detection

Yoshifumi Morita

Department of Clinical Laboratory, The University of Tokyo Hospitall, Tokyo, Japan

WS02-2 Evaluation of Body Fluid Analysis Using an Automated Hematology Analyzer

Kazuho Uchida

Department of Clinical Laboratory, Toyohashi Municipal Hospital

WS02-3 Cerebrospinal Fluid and Body Cavity Fluids Examination: A Hematological Approach
Current Status and Challenges in the Examination of Cerebrospinal Fluid and Body Cavity Fluids

Kei Shimbo

Clinical Laboratory Center, Dokkyo Medical University Hospital

Workshop 3

Room 301 Venue 4

September 24 (Thu.) 9:00-10:00

Quality control required for blood transfusion testing

Transfuion medicine

Chair: Junko Nishioka (Blood Group Section, Laboratory Division, Japanese Red Cross, Kanto-Koshinetsu Block Blood Center)

WS03-1 Quality management in blood transfusion testing

Shunsuke Kojima

Shinshu University Hospital Center for Advanced Cellular therapy

WS03-2 Strategies and Effectiveness of Improving Management Rh(D)-Negative Blood Components Returns
RhD-Negative Blood Component Return Reduction Strategies

Lin Cheng-Yu, Huang Chen-Tsai

National Taiwan University Hospital Hsin-Chu Branch Laboraory Medicine

WS03-3 Clinical Significance of Naturally Occurring Anti-Wr^{a}
IgG Subclass and Functional Analysis

Hidekazu Hasunuma[1], Tomoko ISHIDA[1], Hiroki OTAKI[1], Tamotsu MACHIDA[1], Sanshiro NAKAO[2], Naomi SHIMIZU[2]

1 Division of Transfusion, Toho University Sakura Medical Center, Sakura, Chiba, Japan
2 Department of Clinical Laboratory Medicine, Toho University Sakura Medical Center, Sakura, Chiba, Japan

Workshop 4

Room 302 Venue 5

September 24 (Thu.) 9:00-10:00

Quality Assurance in Genetic Testing Using Next-Generation Sequencing (NGS)

Genetics

Chair: Kenji Amemiya (Department of Medical Technology and Sciences, School of Health Sciences at Narita, International University of Health and Welfare)

WS04-1 Understanding technical limitations of genetic testing by short read NGS
Toward improving diagnostic accuracy

Takayuki Ishige

Department of Applied Genomics, Kazusa DNA Research Institute

WS04-2 How Biobanking enables Precision Oncology in the IMPRESS-Norway study
From Bench to Clinic: The importance of biobanking perspectives in the IMPRESS-Norway study

Britina Kjuul Danielsen*, Solveig Kokkvoll*, Ingrid Dyvik, Aaslaug Helland, Hege G. Russnes, Kajsa A, M. Johansson, Mona Otrebeski Nilsson, Gry A. Gjeitvik *Co-first authors.

Department of Cancer Genetics, Institute for Cancer research, Oslo University Hospital, Oslo, Norway

Workshop 5

Room 201 Venue 3

September 24 (Thu.) 15:30-16:30

Fostering a Culture of Safety in Healthcare: Effective Communication, Standardized Checklists, and Ongoing Quality Improvement

Others (Management)

Chairs: Tokiko Nishimura (Japan Accreditation Board (JAB))
Maria Klement (Board Member of IFBLS (Canada))

WS05-1 Fostering a Culture of Safety in Healthcare: A Japanese Perspective on Communication, Checklists, and Continuous Improvement

Shota Miyao

Department of Pathology Laboratory, Osaka Saiseikai Nakatsu Hospital, Osaka, Japan

WS05-2 Championing a safety culture
Good professional practice for the ISO 15189:2022 accredited medical laboratory

Dennis MOK

Faculty of Health, Southern Cross University, Bilinga, Queensland, Australia

WS05-3 From Reactive to Predictive
Data-Driven Risk Management Across the Clinical Laboratory Testing Process

Hidekazu Ishida

Division of Clinical Laboratory, Gifu University Hospital

Workshop 6

Room 301 Venue 4

September 24 (Thu.) 15:30-16:30

Global Cytology Case Conference: Sharing Diagnostic Perspectives Across Borders

Cytology

Chairs: Masami Nambu
Mirjana Stupnisek (University Hospital for Infectious Diseases, Zagreb, Croatia)

WS06-1 Kazuyo Yoshida
Nihon University Itabashi Hospital

WS06-2-1 Mirjana Stupnisek
1 University Hospital for Infectious Diseases, Zagreb, Croatia
2 Faculty of Dental Medicine and Health, J. J. Strossmayer University of Osijek, Croatia

WS06-2-2 Mirjana Stupnisek, Katarina Pajtak
University Hospital for Infectious Diseases, Zagreb, Croatia

WS06-3 Mei-Ling Wu
Department of Pathology and Laboratory Medicine, Koo Foundation Sun Yat-Sen Cancer Center, Taiwan

WS06-4 Kumi Nakatani
National Cancer Center Japan

WS06-5 Hitomi Kanno
Kyorin University Hospital

Workshop 7

Room 302 Venue 5

September 24 (Thu.) 15:30-16:30

Urinalysis Case Conference: The Impact of Urine Testing on the Management of Renal and Urological Diseases

Urinalysis

Chair: Takashi Yokoyama (Faculty of Medical Technology, Niigata University of Health and Welfare)

WS07-1 Adenovirus-Infected Cells Distinguishable in Urinary Sediment

Noriko Kawamitsu

Department of Clinical Chemistry, Laboratory Medicine, Kyushu University Hospital

WS07-2 The Impact of Acute Caffeine Consumption on Routine Urinalysis Parameters in Healthy Adults: A Cross-Sectional Observational Study
Clinical Implications of Caffeine as a Pre-Analytical Confounder in Spot Urine Testing

Jeffery Chan Tsz Him[1], CHEUNG Ka Tik*[1,2] *Corresponding author

1 School of Nursing and Health Sciences, Department of Diagnostic Sciences, Hong Kong Metropolitan University, Hong Kong SAR, China
2 Councils Member, Hong Kong Institute of Medical Laboratory Sciences Ltd., Hong Kong SAR, China

WS07-3 Quantitative Assessment of Macroscopic Haematuria Using Urinary RBC Counts

Tomoji Yuno, Hiaki SATOU

Hokuriku University, Faculty of Health and Medical Sciences

Workshop 8

Room 201 Venue 3

September 25 (Fri.) 9:00-10:00

Global Perspectives in Histopathology: Evolving Roles, Standards, and Expectations for BLS Professionals

Pathology

Chair: Yoshihiko Murata (Pathology, University of Tsukuba Hospital)

WS08-1 Evaluation of Immunofluorescence in Renal Biopsy and the Critical Role of Biomedical Laboratory Scientists

Shoji Takimoto[1], Kyoko Komatsu[1], Ito Hitoshi[2], Keiko Igarashi[1], Ryota Hanyu[1], Aya Shibata[1]

1 Pathological diagnosis unit,Tsuchiura Kyodo General Hospital, Japan
2 Shonan Fujisawa Tokushukai Hospital, Japan

WS08-2 Implementation of AT192: automated preparation of paraffin-embedded tissue-blocks An approach towards integrating more automated work processes in the laboratory

Hoerdum, Jill Moeller

Department of Pathology, Odense University Hospital

WS08-3 Rapid Fresh Pathology for Pulmonary Specimens
Whole-mount Gigapixel Imaging of Fresh Lung Surgical Tissue

Yao-Chen Tseng[1], Cheng-Hao Li[2], Hsuan Wang[2], Chung-Yen Huang[3], Jin-Shing Chen[4], Yi-Hua Liao[5], Chi-Kuang Sun[6], Min-Shu Hsieh[2]

1 Graduate Institute of Photonics and Optoelectronics and Department of Electrical Engineering, National Taiwan University, Taipei, Taiwan
2 Department of Pathology, National Taiwan University Cancer Center, Taipei, Taiwan
3 Department and Graduate Institute of Pathology, National Taiwan University Hospital, Taipei, Taiwan
4 Department of Surgery, National Taiwan University Hospital, Taipei, Taiwan
5 Department of Dermatology, National Taiwan University Hospital and National Taiwan University College of Medicine, Taipei, Taiwan
6 Graduate Institute of Photonics and Optoelectronics, National Taiwan University, Taipei, Taiwan

WS08-4 The Role of Biomedical Laboratory Scientists in Diagnostic Pathology and Medical Research Supporting Diverse Research Needs through High-Quality and Reproducible Tissue Preparation

Minako Suzuki

Department of Pathology, Keio University School of Medicine, Tokyo, Japan

Workshop 9

Room 301 Venue 4

September 25 (Fri.) 9:00-10:00

Continuing education to maintain professionalism for BLS

Education

Chairs: Nau Ishimine (Department of Laboratory Medicine, Shinshu University Hospital)
Hassan Aziz (The Rochester Institute of Technology (RIT), New York / IFBLS President-Elect)

WS09-1 Empowering the Next Generation: A Competency-Based Model for Lifelong Learning and Professionalism - Insights from Japan
Bridging Clinical Laboratory Excellence and Professional Leadership through Competency Development

Manjiro Yamanaka

Center for Advanced Cell Therapy, Shinshu University Hospital, Matsumoto, Japan

WS09-2 Using an Ethics Board Game in Biomedical Science Education
Experiences and Insights

Margrete Tennfjord

Working with Ethics in The Norwegian Association of Engineers and Technologists at The Norwegian Institute of Biomedical Science (NITO BFI)

WS09-3 Global Harmonization of Medical Laboratory Science Education: Bridging Education, Competencies, and Emerging Career Opportunities -Preparing a Future-Ready Medical Laboratory Workforce for Global Healthcare

Kaptan Singh Sehrawat

Department of Biochemistry, Kalawati Saran Children's Hospital, New Delhi (India)

WS09-4 Comparative Analysis of Cytotechnology Training Systems in East Asia
Current Status in Japan, Taiwan, and Korea.

Yukari Nishimura[1], Takeshi Nakamura[2], Akihiko Kawahara[3], Misao Yoneda[4], Kouichi Ikebata[5], Yi-Ju Lee, Jen-Sheng Ko[6], Shin Min Shik, Hwa-Jeong Ha[7], Hitoshi Abe[5]

1 Kitasato University,JAPAN
2 Kanagawa Cancer Center
3 Kurume University Hosp.
4 Suzuka University of Medical Science
5 Cancer Institute Hospital of JFCR
6 Taiwan Society of Clinical Cytology,TAIWAN
7 The Korean Specialist in Cytology,KOREA

Workshop 10

Room 302 Venue 5

September 25 (Fri.) 9:00-10:00

From Field Experience to Innovation: Rethinking POCT from Disaster Settings to Daily Clinical Practice

Immunology

Chair: Yoshiyuki Kanno (Faculty of Health Science, Kochi Gakuen University)

WS10-1 Disaster Field Hospital Overseas Clinical: Laboratory Activities, The Use of POCT, Challenges
Is it possible to conduct clinical laboratory during a disaster?This question is simply silly.

Chitoshi Sato

Okazaki Health Center

WS10-2 POCT related personnel certification systems in Japan
Roles of the POC Coordinator and Operator in POCT

Hideo Sakamoto

Department of Medical Technology, Faculty of Health Sciences, Kobe Tokiwa University

September 23 (Wed.) – 24 (Thu.)

Student Forum

Room 201 — Venue 3
September 23 (Wed.) 9:00-15:00

Room 304 — Venue 7
September 24 (Thu.) 9:00-12:00

Chairs: Yui Namikawa (Toin University of Yokohama)
Louise Spendrup (University of Iceland)
Marie Nora Roald (Member at Large of IFBLS (Norway))

Bridging Knowledge: Shaping the Future of Biomedical Laboratory Science Together

How can the next generation of biomedical laboratory scientists connect research, clinical practice, and global health needs?
By sharing perspectives across countries and cultures, what challenges can we identify, and what skills, values, and innovations will shape the future of healthcare?

Purpose and Concept of the Theme

This theme was developed to encourage meaningful international discussion among students in biomedical laboratory science.
The Student Forum aims to create an opportunity for participants from different countries and educational backgrounds to share their experiences, perspectives, and current challenges in laboratory medicine and healthcare systems.
Biomedical laboratory scientists play an essential role in modern healthcare by supporting diagnosis, treatment, disease prevention, and public health. In recent years, rapid advances in medical technology, globalization, aging populations, emerging infectious diseases, and healthcare disparities have highlighted the growing importance of international collaboration and interdisciplinary knowledge.
The main theme, “Bridging Knowledge,” represents the importance of connecting research, clinical practice, education, technology, and global health needs. It also emphasizes collaboration across countries, cultures, and future generations of healthcare professionals.
Through the subtheme, we hope students will:

- identify current and future challenges in biomedical laboratory science,
- discuss differences and similarities among countries and healthcare systems,
- explore the skills and professional values required for the next generation,
- consider how innovation and international cooperation can contribute to better patient care and global healthcare outcomes.

This forum is intended not only as a place for academic discussion, but also as an opportunity to inspire students to become globally minded biomedical laboratory scientists who can contribute to the future of healthcare worldwide.

Day1	
Time	Program
9:00–9:20	Welcome & Opening Remarks
9:20–9:40	Introduction of Forum Theme & Objectives
9:40–10:10	Ice-breaking & Networking Session
	Students are divided into 4 multicultural groups.
10:10–10:20	Break
10:20–11:00	Country Perspective Sharing
	Students briefly introduce laboratory science education, healthcare systems, and current challenges in their countries within mixed groups.
11:00–12:00	Group Discussion Session ①
	Topic: “Current Challenges in Biomedical Laboratory Science and Global Healthcare”
12:00–12:45	Lunch Break
12:45–13:45	Group Discussion Session ②
	Topic: “Future Skills, Values, and Innovations for Biomedical Laboratory Scientists”
13:45–14:50	Group Presentation Preparation
	Slide preparation and discussion summary in multicultural teams.
14:50–15:00	Day 1 Wrap-up

Day2	
Time	Program
9:00–9:15	Final Group Preparation
9:15–10:45	Group Presentations
	Each multicultural group presents discussion outcomes and future perspectives.
10:45–11:00	Break
11:00–11:35	Open Discussion & Reflection
	Topic: “How Can We Shape the Future of Global Healthcare Together?”
11:35–11:50	Student Forum Summary & Shared Message
11:50–12:00	Final Reflection & Farewell

September 25 (Fri.) – 27(Sun.)

International Exhibition Hall 8

Poster Presentation

Social Hours: September 25 (Fri.) 9:00-12:00

Microbiology

P-1-1 Comparing Autof MS and VITEK MS for Microbial Identification
Routine Clinical Isolates and Stored Isolates

Sang-Tae LEE, Akira KOIZUMI, Koji UI, Nobukazu UCHIIKE, Yuki NAKANO, Chiaki MACHINO, Eri TANIGUCHI, Masahito ONISHI
Nara Medical University Hospital

P-1-3 Integrating Genotypic and Phenotypic Data to Strengthen MRSA Resistance Surveillance
Evaluation of Emerging Resistance Patterns in MRSA Bloodstream Infections Using Integrated Diagnostics

Lemuel Uminga
Shared Health

P-1-4 Two Cases of Cryptosporidiosis: Oocysts Initially Detected by Gram Stain

Yusuke Nomura[1], Yoshimi Higurashi[1], Shinya Yamamoto[2], Kazuhiko Ikeuchi[2], Ryu Yoneda[1], Kazuya Okushin[1], Takeya Tsutsumi[1]
1 Department of Infection Control and Prevention, The University of Tokyo Hospital, Tokyo, Japan
2 Department of Infectious Diseases, The University of Tokyo Hospital, Tokyo, Japan

P-1-5 Vertical Transmission of Candida albicans
A Microbiological Perspective on Maternal Chorioamnionitis and Early-Onset Neonatal Candidemia

Ying-Tso Wang[1], Hsiu-Hsien Lin[1], Chih-Yi Yang[2], Po-Ren Hsueh[3]
1 Dept. of Laboratory Medicine, China Medical University Hospital
2 Dept. of Obstetrics and Gynecology, China Medical University Hospital
3 Dept. of Laboratory Medicine and Internal Medicine, China Medical University Hospital

P-1-6 *Hungatella effluvii* Bacteremia in a Hemodialysis Patient

Yukitaka Ito[1], Naomi Kaneko Ito[2], Nobuhiko Joki[3]
1 Division of Clinical Microbiology Laboratory, Toho University Ohashi Medical Center
2 Department of Clinical Laboratory, Kyorin University Suginami Hospital
3 Department of Nephrology, Toho University Ohashi Medical Center

P-1-7 Environmental Detection of *Balamuthia mandrillaris* in Bangladesh
Molecular Analysis of Soil and Water Samples to Assess Infection Risk

Kanako YAMANOUCHI[1], Karin KAKIHARA[1], Mitsuru CHIBA[1], Takakiyo TSUJIGUCHI[2], Chowdhury Rafiqul AHSAN[3], Tomoh MATSUMIYA[1]
1 Hirosaki University Graduate School of Health Sciences
2 Hirosaki University Education Center for Disaster and Radiation Emergency Medicine
3 Department of Microbiology, University of Dhaka

P-1-8 Validation of PCR for H. pylori and Clarithromycin Resistance Detection Enhancing Precision Therapy by Detecting Heteroresistance and Overcoming Culture Limitations in Clinical Practice

Tzu-Ying Lee[1], Ya-Lun Chuang[2], Li-Yuan Cheng[2], Hsin-Ching Cho[2], Yung-Li Yang[3], Jyh-Ming Liou[4]

1 Department of Laboratory Medicine, National Taiwan University, Cancer Center, Taipei, Taiwan.
2 Dept. of Laboratory Medicine, National Taiwan Univ. Cancer Center, Taipei, Taiwan.
3 Dept. of Laboratory Medicine, National Taiwan Univ. Cancer Center, Taipei, Taiwan; Dept. of Laboratory Medicine, National Taiwan Univ. Hosp., Taipei, Taiwan.
4 Dept. of Medicine, National Taiwan Univ. Cancer Center, Taipei, Taiwan; Dept. of Internal Medicine, National Taiwan Univ. Hosp., Taipei, Taiwan; Dept. of Internal Medicine, College of Medicine, National Taiwan Univ., Taipei, Taiwan.

P-1-9 Nomman: automated bacterial nomenclature management in the clinical microbiology laboratory

Herman Tse[1], Garnet Kwan-Yue Choi[2]

1 Department of Laboratory Medicine, Khoo Teck Puat Hospital, Singapore
2 Department of Pathology, Hong Kong Children's Hospital, Hong Kong, China

P-1-10 Rapid Bloodstream Pathogen Identification and Resistance Screening via FilmArray BCID

Ying-Ju Chen[1], Tze-Kiong Er[2]

1 Division of Laboratory Medicine, Asia University Hospital, Asia University
2 Division of Laboratory Medicine, Asia University Hospital

P-1-11 Identification of *Taenia* spp. in a Regional Hospital From Proglottids to Morphological Confirmation

FON-JU CHIEN, WAN-CHEN LIN

Department of Laboratory Medicine, Taiwan Adventist Hospital.

P-1-12 In vitro activity of macrolides against *Mycobacterium avium* complex Implications for macrolides resistance risk in long-term prophylactic therapy

Noriyuki ABE, Masaharu BIRUKAWA, Hiroko MATSUTANI, Daiki FUJIMOTO, Gaku MATSUMOTO, Daiki SHIMOMURA, Masashi SHIMADA, Mikio KAMIOKA

Department of Clinical Laboratory Medicine, Tenri Hospital, Tenri, Japan

P-1-13 Hospital Wastewater Biofilms as Antimicrobial Resistance Reservoirs In situ evidence for prevalence, expression, and spread of carbapenemases

Yusuke Ota[1], Yoko Nukui[2], Yoshiaki Gu[3], Ryoichi Saito[1]

1 Department of Molecular Microbiology and Immunology, Institute of Science Tokyo
2 Department of Infection Control and Laboratory Medicine, Kyoto Prefectural University of Medicine
3 Department of Infectious Diseases, Institute of Science Tokyo

P-1-14 Pathogenic *Bacillus cereus* Group from Hospital Wastewater in Ghana Genomic and phenotypic evidence of environmental adaptation and virulence traits

Yusuke Ota[1], Frederick Ofosu Appiah[1], Mitsunori Yoshida[2], Masato Suzuki[3], Yoshihiko Hoshino[2], Toshihiko Suzuki[1], Anthony Ablordey[4], Ryoichi Saito[1]

1 Institute of Science Tokyo
2 Leprosy Research Center, National Institute of Infectious Diseases
3 Antimicrobial Resistance Research Center, National Institute of Infectious Diseases
4 Noguchi Memorial Institute for Medical Research

P-1-15 Typing and Antibiotic Susceptibility of Carbapenem-Resistant Enterobacteriaceae in Taiwan

Chin-Fu Lin, Shu-Chun Hung
Tungs' Taichung MetroHarbor Hospital, Taichung, Taiwan

P-1-16 Impact of MALDI-TOF MS on Respiratory Mold Species Distribution
A Comparison of MALDI-TOF MS and Morphological Identification Methods

Chiahua Chou
Departments of Laboratory Medicine, National Taiwan University Hospital

P-1-17 Serotypes and Antimicrobial Susceptibility of Group B *Streptococcus* in Pregnancy
- A Nationwide Multicenter Study in Japan -

Daiki TANNO[1], Maki KITAGAWA[2], Yasuaki TOMII[3], Yukari NAKATSUKA[4], Kohei UECHI[5], Kazutaka OHASHI[6], Yukio YAMADERA[6], Masahiro TOYOKAWA[1]
1 School of Health Sciences, Fukushima Medical University
2 Kyokuto Pharmaceutical Industrial Co., Ltd.
3 Aiiku Hospital
4 Kitano Hospital
5 University of the Ryukyus Hospital
6 Fukushima Medical University Hospital

P-1-18 Multidrug-resistant Streptococcus agalactiae strain isolated from ascitic fluid in Japan
Whole-genome analysis of antimicrobial resistance and virulence determinants

Saki KANEHIRA, Yusuke OTA, Kazunari SONOBE, Naoya ICHIMURA, Koh OKAMOTO, Yoshiaki GU, Koji SASAKI, Ryoichi SAITO
Department of Clinical Laboratory, Institute of Science Tokyo Hospital, Tokyo, Japan

P-1-19 Dual-Mode uPAD with for Rapid Semi-Quantitative *Staphylococcus aureus* Detection

TSAI, YIN-TAI
Department of Medical Laboratory, Taipei Medical University-Shuang Ho Hospital, Ministry of Health and Welfare, New Taipei City, Taiwan

P-1-20 Evaluation of the DP1R for Antimicrobial Susceptibility Testing of *Nocardia*

Hina Uchikawa[1], Akito Nakajo[1], Riko Isisaki[2], Shiori Sato[2], Mariho Furukawa[2], Daiki Tanno[1], Masahiro Toyokawa[1]
1 Department of Clinical Laboratory Sciences, Graduate School of Health Sciences, Fukushima Medical University
2 Department of Clinical Laboratory Sciences, School of Health Sciences, Fukushima Medical University

P-1-21 Comparison of the Current and the Old CLSI Method
M24-A3 vs M24-A2 for Antimicrobia Susceptibility Testing of Nocardia spp.

Akito Nakajo[1], Riko Isisaki[2], Shiori Sato[2], Mariho Furukawa[2], Hina Uchikawa[1], Daiki TANNO[1], Masahiro TOYOKAWA[1]
1 Graduate School of Health Sciences, Fukushima Medical University
2 Fukushima Medical University

P-1-22 Integrating FilmArray and Codehop RT-snPCR for Enterovirus Genotyping

LI, ROU-TZU, TSAI, YIN-TAI
Department of Medical Laboratory, Taipei Medical University-Shuang Ho Hospital, Ministry of Health and Welfare, New Taipei City, Taiwan

P-1-23 Evaluation of Accelerated Antimicrobial Susceptibility Testing Methods for Enterobacterales

Yuuki HARA, Yukihiro TERAMOTO, Yuusuke NOMURA, Kotone TAKEI, Yui YOGOU, Hiroshi SUGINO

Japanese Red Cross Aichi Medical Center Nagoya Daini Hospital

P-1-24 Rapid Detection Epidemiological Shift of Carbapenemase-Producing Organisms at a medical center in Northern Taiwan.

CHANG, JU-CHUN, TSAI, YIN-TAI

Department of Medical Laboratory, Taipei Medical University-Shuang Ho Hospital, Ministry of Health and Welfare, New Taipei City, Taiwan

P-1-25 Unmasking the Staphylococcus aureus Complex in Clinical Workflow

LIU, PO-YU, TSAI, YIN-TAI, KUNG, LIN

Department of Medical Laboratory, Taipei Medical University-Shuang Ho Hospital, Ministry of Health and Welfare, New Taipei City, Taiwan

P-1-26 Rapid Molecular Testing and Traditional Culture: A Complementary Approach Enhancing Clinical Microbiological Surveillance and Diagnostic Synergy

Kuo Shu Fang, Lee Chih Yi

Department of Laboratory Medicine, Chiayi Chang Gung Memorial Hospital, Chiayi, Taiwan

P-1-27 Conventional Candia Identification Matches MALDI-TOF MS

Toya MAEDA[1], Kazumi TAKEHANA[1], Sanae YAMADA[1], Shiori OIKAWA[1], Yuna KOGA[1], Minori ENAMI[1], Kazunori MIYAKE[2], Taro SIGA[1]

1 Clinical Laboratory Center, Cancer Institute Hospital of JFCR
2 Department of Clinical Laboratory Technology, Juntendo University

P-1-28 Concordance Between Ampicillin/sulbactam and Amoxicillin/clavulanate in *Enterobacterales*

Sayo ADACHI[1], Miyu SATO[1], Soma KAJI[1], Yuka TSUKINO[1], Karin FUJISHA[2], Tatsuya NAKAMURA[2]

1 Graduate School of Health Sciences, Kyoto Tachibana Univ.
2 Faculty of Health Sciences, Kyoto Tachibana Univ.

P-1-29 Comparison of laboratory-developed Cytomegalovirus PCR against Cobas 5800 Cytomegalovirus assay

LiatHui Loo[1], Stephanie Yeo[2], HanYang Soong[1], Matthias Maiwald[1]

1 Microbiology Laboratory, Dept. of Pathology and Laboratory Medicine, KK Women's and Children's Hosp., Singapore.
2 School of Applied Science, Temasek Polytechnic, Singapore.

P-1-30 *floR* as a Marker of Meat-Derived Resistant *E. coli* Whole-Genome Sequencing Analysis of Broad-Spectrum Cephalosporin-Resistant Isolates from Retail Chicken Meat

Yuya HASUNUMA[1], Shota MIKAMI[2]

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P-1-31 Comparing Immunochromatography and Nucleic Acid Amplification Tests for *Clostridioides difficile*
Immunochromatography and Nucleic Acid Amplification Tests Evaluated Against Toxigenic Culture

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P-1-32 Efficacy of a Resistant-Starch-Encapsulated Probiotics Supplement on Gastrointestinal Function
A 4-Week Longitudinal User Experience Study

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P-1-33 ATR-FTIR for Rapid Microbial Identification
A Cost-Effective and Reagent-Free Alternative to MALDI-TOF MS

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P-1-34 Rapid Molecular Diagnosis of CMV-induced Frosted Branch Angiitis
Off-label Multiplex PCR Panel for Aqueous Humor in an Immunocompromised Patient

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P-1-35 Analysis of Misidentification and Carbapenem Resistance in Clinical Serratia Isolates

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P-1-36 Performance Comparison of Panther Fusion and LabTurbo AIO
Evaluation of Diagnostic Accuracy and Efficiency in Respiratory Virus Testing

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P-1-37 Five-Year Blood Culture Trends at Eiju General Hospital
Aiming to Improve the Specific Detection of Pathogenic Microorganisms

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P-1-38 Galactomannan vs. PCR in Aspergillus Diagnosis

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P-1-39 Exploring serum IgG responses to oral commensal bacteria across individuals

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P-1-40 Rapid and Reliable
Emergency Implementation of Molecular Testing

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P-1-41 Bacterial Safety of Street-Vended Ready-to-Eat Fruits and KAP of Vendors
A Correlational Study on Ready-to-Eat Watermelons and Pineapples in Manila

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P-1-42 Evaluation of AI-Assisted IR Biotyper for Hypervirulent Klebsiella pneumoniae

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P-1-43 Imported Brucellosis in a Regional Hospital:
Biosafety and Infection Control Considerations

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P-1-44 ITS rDNA Polymorphisms in Trichophyton verrucosum Complex Strains

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P-1-45 Discrepancy between visual cleanliness and microbiological contamination of ultrasound probes
a cross-sectional point prevalence study across clinical departments

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P-1-46 A Study on Workload Units in Clinical Virology Laboratories, Taiwan

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P-1-47 The 16S rRNA gene nanopore sequencing
Evaluation of background contamination and sequencing depth

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P-1-48 Reconsidering Cerebrospinal Fluid Specimen Storage Practices in Japan

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P-1-49 Genomic Analysis of Resistant K. pneumoniae in Taiwan Retail Food
Evaluating Prevalence, Antimicrobial Resistance, and Genomic Characteristics within a One Health Framework

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P-1-50 Quantification strategy affects Fusobacterium abundance in colorectal cancer

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P-1-51 Microbiological and Clinical Features of Propionimicrobium lymphophilum Infection: Literature Review
Microbiological Findings and Clinical Features of Propionimicrobium lymphophilum Infection: A Literature Review

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P-1-52 Swab-Based Saliva Collection for Reliable EBV PCR Detection
Optimization of Swab-Based Saliva Sampling for Accurate EBV Molecular Diagnosis

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P-1-53 Laboratory Morphological Identification of Ancylostoma ceylanicum from Colonoscopy Specimen
Buccal Capsule Microscopic Evaluation for Definitive Zoonotic Hookworm Identification: A Case Report

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P-1-54 Evaluation of Workflow Efficiency in CMV
Evaluation of Workflow Efficiency in CMV Quantification Using the Fully Automated System

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P-1-55 Uncertainty in the Reproducibility of ESBL-producing *Escherichia albertii*

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P-1-57 FTIR-Based Identification of High-Risk ST316-*bla*$_{NDM}$ Carbapenem-Resistant *Enterobacter hormaechei*

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P-1-58 Mucorales Isolation Enabled by Antibacterial Suppression in Rhino-Orbital Mucormycosis

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P-1-59 Multiplex PCR vs. Culture in Pneumonia Diagnosis
Performance and Clinical Impact on Lower Respiratory Pathogen Detection

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P-1-60 Automated Blood Culture Impact
Workflow Optimization and Processing TAT

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P-1-61 Establishment of a Murine Sepsis Model in Acute Radiation Syndrome
Analysis of Intestinal Barrier Dysfunction After High-Dose Irradiation

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P-1-62 Ceftazidime-Avibactam Susceptibility and Synergy Testing for Carbapenem resistant isolates
Ceftazidime-Avibactam and Aztreonam synergy testing in Carbapenem resistant Enterobacterales and Pseudomonas aeruginosa

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P-1-63 Potential Food-Poisoning Risk of Toxin-Producing *Bacillus cereus* in Common Foods

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P-1-64 Genetic analysis of *Enterococcus faecalis* thymidine-dependent small-colony variants

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P-1-65 Detection of Cefiderocol-Resistant *Escherichia coli* in Wastewater.
Genomic analysis reveals international relatedness of bla_{NDM-5}-producing isolates.

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P-1-66 Evaluating Diverse Specimens for Newborn Congenital Cytomegalovirus Screening
: Diagnostic Performance of Saliva, Urine, and Oral Mucosa by qPCR

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P-1-67 Pulmonary *Mycobacteroides hainanense* infection: The First Case Report from Japan

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P-1-68 Diagnostic Value of Francisella tularensis in a Low-Incidence Setting

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P-1-69 Fungal Skull Base Osteomyelitis
A Three-Case Series of Aspergillus and Candida Infections Highlighting Diagnostic Challenges

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P-1-70 HIV Notifiable Co-infections: Trends and Characteristics
A Laboratory-Based Retrospective Study

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P-1-71 The Association of Soil Factors on the Prevalence of Soil-Borne
Helminths in Organic and Conventional Farms in Selected Areas of Batangas, Philippines

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P-1-72 Clinical Impact of Universal Sputum MTBC DNA Screening
Dual Benefits of Integrating Routine Molecular Diagnostics into Initial Sputum Workups

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P-1-73 Isolation and Antibiotic Susceptibility of *Klebsiella oxytoca* and *Acinetobacter junii* from Well Waters in Selected Barangays of Lubao, Pampanga

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P-1-74 Evaluation of a Multi-step Diagnostic Algorithm for *Clostridioides difficile* Infection Comparison of GDH and Toxin A/B Assays Using RT-PCR and Culture

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P-1-75 NGS-Based Gut Microbiota Modulation by Green Banana Oat Beverage

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P-1-76 Investigation the Clinical Performance of PCR for Detecting Mycoplasma pneumoniae

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P-1-77 Enhancing Blood Culture Specimen Quality
A Regional Hospital QI Project

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P-1-78 The analyzation of Helicobacter pylori Stool Antigen Screening Outcome
Analyzing the Outcome of Helicobacter pylori Antigen Screening at a Medical Center in Taiwan

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P-1-79 Genomic Characterization of Carbapenemase-Producing Klebsiella pneumoniae ST218 Delineating Variants in Putative Phage Resistance-Associated Surface Receptor, Capsule, and CRISPR-Cas Loci

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P-1-80 Does Cardiovascular Health Begin in the Gut?
The Impact of Dysbiosis and Intestinal Barrier Impairment on the Development of Cardiovascular Diseases

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Immunology

P-2-1 Kappa Free Light-Chain Index Predicts Long-Term Outcomes in Multiple Sclerosis

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P-2-2 MLS-ERAS Framework Detects Gastrointestinal-Onset SLE Microperforation
Novel Three-Stage Protocol Overcomes Normal-CRP Pitfalls in High-Risk Case

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P-2-3 Unravelling rAAV-Serotype-Specific Cytokine Profiles in HEK293 cells

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P-2-4 Resolving Immunoglobulin Interference Reveals HLA DQ6 Antibodies in Transplant Rejection
Unmasking Clinically Actionable Donor-Specific Antibodies in Late-Onset Liver Transplant Rejection

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P-2-5 Distinct Senescence States Converge on Sustained PD-L1 in HCC
Temporal uncoupling of PD-L1 mRNA and protein during senescence

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P-2-6 Immunogenic efficacy of mRNA-based influenza vaccines in older adults

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P-2-7 Citrullinated Fibrinogen Suppresses Neutrophil Proinflammatory Functions.

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P-2-9 Efforts and Challenges in HBV Reactivation Prevention

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P-2-10 Seroprevalence to Toxoplasma gondii Antibodies and Cat-Related Risk Factors Among Women of Childbearing Age in Sampaloc, Manila

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P-2-11 Immune Cell Recruitment and Activation Factors as PRP Biomarkers

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P-2-12 ANA Immunofluorescence Patterns in Primary Biliary Cholangitis Clinical Significance in AMA-Positive and AMA-Negative Cohorts

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P-2-13 Reverse Algorithm in Syphilis Testing Evaluation in Routine Clinical Practice

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P-2-15 Clarifying Causes of Optic Neuropathy via Laboratory Data Case Reports

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P-2-16 2025 Allergen Retrospective Analysis, Southern Taiwan Lab Statistical analysis of allergen positivity rates and age distribution

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P-2-17 Anti-rituximab assay formats and analytical interference Comparison of three different in-house bridging immunoassays in rheumatological serum samples

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P-2-18 Diagnostic Utility of Pleural Fluid Mesothelin-Related Peptides in Asbestos-Related Diseases

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P-2-19 Oral mucositis signals acute but not chronic immune complications

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P-2-20 Keratinocyte Injury and Cell Death Pathways in Long COVID Alopecia

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P-2-21 Reducing False-Positives in Fourth-Generation IGRA Screening
Balancing Laboratory Quality and Cost Through Retest Criteria Optimization

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P-2-22 Evaluation of HLA antibodies against recombinant and native HLA
A HLA proficiency testing survey

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P-2-23 Modulation of NLRP3 Inflammasome-related Cytokines by Fatty Acids
Differential Modulation of NLRP3 Inflammasome-related Cytokines by Palmitic Acid and Docosahexaenoic Acid

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P-2-24 POLKESMAS COVID-19 ANTIGEN: Innovative Diagnostic Kit Based Local Indonesian Isolates

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P-2-25 Targeting the NLRP3 Inflammasome for Inflammation Control
Potassium Channels as Targets for Inhibiting NLRP3 Inflammasome Activation

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P-2-26 Laboratory Method Verification of Urit IA-200 Chemiluminescence Immunoassay Anayser
Laboratory Method Verification of Urit IA-200 Analyser at Regional Hospital Bamenda, Cameroon

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Hematology

P-3-1 Vit B12 deficiency among AML patients in Riyadh, retrospective study
Vit B12 deficiency among AML patients in Riyadh, Saudi Arabia; a retrospective study

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P-3-2 Assessing the association between neutrophil-to-lymphocyte ratio and bacteremia
A Case Study of a Teaching Hospital in Hsinchu, Taiwan

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P-3-3 Epigenetic and MYC Signaling Modulation by Vault RNA1-1 in AML

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P-3-4 Smart System Reduces Peak-Hour Blood Draw Waiting Time

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P-3-5 Comparison of Two Cases of T-PLL with Contrasting Clinical Courses

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P-3-6 Andrographolide Induces Ferroptosis and Enhances Bortezomib in Plasma Cell Neoplasms

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P-3-7 AI-Driven Morphological Recognition of Myeloma Cells
Enhancing Efficiency and Accuracy in Bone Marrow Smear Morphological Screening

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P-3-8 Preventing Oversight of Non-Specific Reactions in FDP and D-dimer
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P-3-9 Evaluation of Internal Quality Control Strategy in Peripheral Blood Morphology
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Yuka Aizawa, Yumi Komuro, Keiko Hashimoto, Norihiko Moriyama, Maresuke Takahashi, Eiju Miyamoto, Asami Naito
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P-3-10 Rapid Histiocytic Sarcoma with Hemophagocytosis and Hematoidin Crystals Case
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P-3-11 Alternative Erythrocyte Sedimentation Rate Systems After Tube Discontinuation
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P-3-12 Lymphoma involving cerebrospinal fluid confirmed by flow cytometry
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P-3-13 Dependent Platelet Clumping
A Reversible Pseudothrombocytopenia Case
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P-3-14 Using erythrocyte sedimentation rate as a novel application of biomarker
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P-3-15 Development and evaluation of an automated CLEIA measurement for sCLEC-2
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P-3-16 Impact of permeabilization reagents on CKAP4 detection in myeloma cells
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P-3-17 Evaluation of a Lupus Anticoagulant Sensitive Activated Partial Thromboplastin Reagent Reduced Lot to Lot Variation Using Controlled Synthetic Phospholipid Composition

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P-3-18 p53 Expression by IHC and Cytogenetic-Morphological Findings in MDS

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P-3-19 Iron Intake and Iron Status in Women of Manila, Philippines
Heme and Non-Heme Contributions and Determinants

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P-3-20 PFCT Reference Interval Establishment and Hemostatic Risks in Trauma Patients
A Retrospective Study of Interval Validation, Medication Effects, and Injury Severity

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P-3-21 Alternative D-dimer Cut-offs Corresponding to FDP Thresholds in DIC
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P-3-22 Soluble C-Type Lectin-Like Receptor 2 After Transcatheter Aortic Valve Implantation
Association with Post-Procedural Clinical Status in Cardiovascular Practice

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P-3-23 Deep Learning for Morphological Erythroblast Analysis in MDS
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P-3-24 Verification of Immature Granulocyte and Myeloblast Detection Performance Examination of Operational Workflows Using an Automated Digital Cell Imaging Analyzer(DI-60)

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P-3-25 Flow Cytometry for Erythrodermic Cutaneous T-Cell Lymphoma Diagnosis

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P-3-26 Diagnostic Value of HYPO-He% and MicroR% in Microcytic Anemia Differentiation Utilizing Parameter Ratios to Distinguish Iron Deficiency from Thalassemia and Chronic Disease Anemia

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P-3-27 Extracellular HSP70 Drives Platelet Hyperactivation Under Stress-Associated Thrombotic Disease Conditions
Circulating extracellular HSP70 may provide clinically valuable laboratory information for thrombosis evaluation

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P-3-28 Leukapheresis Variables in CAR-T Cell Therapy
Effects on Cell Yield, Collection Time, and Monocyte Purity

Hsaio Wei Lee, Kuan Der Lee, Hui En Tzeng, Yu Hsuan Shih, Yi Chun Lin, Hsiao Ying Chiu, Sz Ying Yang

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P-3-29 Automated LTA for Antiplatelet Monitoring: Comparison and Throughput Versus Conventional Semi-Automated Aggregometer in Method Performance and Workflow Efficiency

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P-3-30 A Case Report of Disseminated Carcinomatosis of Bone Marrow
DCBM due to carcinoma of unknown primary diagnosed by bone marrow aspiration

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P-3-31 Comparison of Clauss and PT-derived for measuring fibrinogen in hyperbilirubinemia

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P-3-32 CBC-Derived Inflammatory Biomarkers in Diabetic Kidney Disease

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P-3-33 Rotational Thromboelastometry in the Perioperative Management of Cardiac Surgery
Hemostatic Assessment in Cardiac Surgery

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P-3-34 Cold Agglutinin Syndrome as a Paraneoplastic Manifestation of Malignancy

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P-3-35 Cold Agglutinin Effects
Interference in CBC and Rh Typing in an Elderly Patient

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P-3-36 Seeing Before Sequencing: Early AML Treatment
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P-3-37 Evaluating the Platelet Reactivity of Coronary Artery Disease Filipino Patients
Undergoing Aspirin Therapy Using VerifyNow: A Novel One-Shot Case Study

Mary Christie Tan[1], Levi Anna Judea Buccahan[1], Julie Mae Calahi[1], Juliana Dagaas[1], Reyzelle Rodicol[1]
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P-3-38 Reclassification of Gamma W208L and S313I as Hypodysfibrinogenemia
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P-3-39 Nonspecific APTT Prolongation in Cross-Mixing Tests
Effects of Container Air Volume on pH and Coagulation Activity

Shota TSURUZONO, Ryota MASUTANI, Shuichi ASANO, Amu OKADA, Emiko TANAKA, Meri KUBOTA, Akira ASAI
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P-3-40 CWA parameters as surrogate markers for hypercoagulability in warfarin-treated patients

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P-3-41 Early T-Cell Precursor Acute Lymphoblastic Leukemia with DNMT3A Mutation

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P-3-42 Can normalization save Automated Thrombin Generation
Quest for the best normalizator to allow clinical use of Automated Thrombin Generation

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P-3-43 Complete Blood Count Assessment with Health-Related Factors in Navotas City

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P-3-44 Association Between sCLEC-2 and Renal Function in Plasma Samples

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P-3-45 Analysis of FXI Dimerization and Secretion Defects in *F11* Variants

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P-3-46 Atypical Lymphocytes Following Chimeric Antigen Receptor T-Cell Therapy
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P-3-47 Significance of TRBC1/TRBC2 expressions in the diagnosis of T-cell neoplasms
Multicolor flow cytometric analysis

Miku HIGASHIO, Kenji YONEZAWA, Takako TENJIN, Chika KINOSHITA, Takuho YOTSUTANI, Yuriko YAMAUCHI, Toru MURAYAMA, Mitsuhiro ITO

P-3-48 In-House Flow Cytometry Improves Diagnostic Accuracy and Turnaround Time

Moe TANAKA, Yousuke KANAZAWA, Kenshirou TAMAI, Yumi FUJITA, Yukihiro KAI, Aritoshi MIYAZAKI, Eiju MIYAMOTO, Asami NAITOU

P-3-49 Effects of Storage Time and Fixation on Neutrophil Antigens

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P-3-50 Mechanisms of Platelet Activation by *Helicobacter pylori* Lpp20
Potential Involvement of TXA_2- and ADP-Mediated Amplification Pathways

Asako KIMURA, Yuka Arai, Fuka Ishige, Suzuka Watanabe, Aoi Okamoto, Hiroaki Takeuchi
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P-3-51 Delivering Amyloid Precursor Protein 770 to Platelets via Extracellular Vesicles
Secretion of Hypo-O-glycosylated Forms Through a Non-Golgi Dependent Pathway

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P-3-52 Clinical Utility of Ret-He as a Functional Predictor
Targeting Erythrocyte Microcytosis in Maintenance Hemodialysis Patients

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P-3-53 Hematological analysis of captive beluga whales in Westman Islands, Iceland

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P-3-54 Using Principal Components Analysis and Conditional Inference Tree
to Explore CBC Indicators as Predictive Models for Influenza

Sheng Chien Tsai, Li-Ping Tseng, Hsin-Chieh Lin, Po-Chih Chen
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P-3-55 Gut Microbiota Profiling in sCAEBV

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P-3-56 Molecular Characterization of the Fibrinogen A-alpha R491C Variant
Functional and His-Tagged Secretion Analyses of the A-alpha R491C Variant

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P-3-57 Iron Deficiency Anemia Screening using Reticulocyte Hemoglobin Cellular Content (RHCC)
A Real-Time Monitoring Tool of Iron Status in a Previously Malaria-Endemic Area

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P-3-58 Multi-parameter Measurement Using Acridine Orange Fluorescence Staining.
Clinical Utility of Platelet Count and Immature Platelet Fraction Analysis.

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P-3-59 Novel *SERPINC1* c.204dup Frameshift Variant Associated with Inherited Antithrombin Deficiency

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P-3-60 LIS Auto-Verification: Impact on Coagulation Workflow and Reliability
Enhancing PT and aPTT Reporting Efficiency

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P-3-61 Management of Internal Quality Control in complete Blood Count

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P-3-62 Reference Intervals for Immature Platelet Fraction in Healthy Tunisians Including Advanced Platelet Indices

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P-3-63 Method comparison of iMOST-L and Sysmex XN-9100 Analytical agreement and feasibility of home-based monitoring in cancer patients

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P-3-64 Establishing CBC Reference Range Ages 20-29 Filipinos in Metro Manila

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P-3-65 Diagnostic Performance of Immature Platelet Fraction for Differentiating Thrombocytopenia Mechanisms Tunisian Cutt-off Values for Clinical Use

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P-3-66 Characteristics of morphometric parameters of platelets during myeloid neoplasms

MAHJOUB SONIA, Aya Chakroun, Yosr Gnouma,, Mayar Srairi, Nabli Emna, Jannett Eddhib, Sonia Mahjoub
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P-3-67 Bioinspired Nanoliposome Technology for Stabilization of Whole Blood Hematology Control A Novel Preservation Platform for Long-Term Blood Control Stability

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P-3-68 Explainable Machine Learning Score for Thrombocytopenia Mechanism Classification

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P-3-69 Interlaboratory trial of the complete blood count contribution to the estimation of measurement uncertainty of a multiparametric test

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P-4-2 Artificial Intelligence for Clinical Chemistry in Low-Resource Laboratory Settings. Implementing Edge AI for Real-Time Diagnostic Support in Connectivity-Challenged Environments

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P-4-3 Long-term Stability of the Kappa Free Light Chain Index

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P-4-4 The Hidden Danger After Fever Subsides
A Rare Case Report and Laboratory Monitoring of Severe Rhabdomyolysis Complicating Influenza B

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P-4-5 MLS-Led ERAS Framework in Epilepsy-Induced Rhabdomyolysis
Four-Stage Dynamic Laboratory Monitoring with CK/UA Slope Stratification

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P-4-6 Impact of Taiwan's 2026 CKD-EPI Transition on Clinical Reimbursement
Navigating SGLT-2i Eligibility Risks and Staging Reclassification in Laboratory Medicine

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P-4-7 Clinical Use of Beta-D-Glucan Testing in Rheumatology Outpatients
A Single-Center Retrospective Study

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P-4-8 Monitoring Metrological Traceability of Creatinine for Accurate Clinical Decision Making
Enhancing Estimated Glomerular Filtration Rate Reliability through Standardized Accuracy-based Proficiency Testing

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P-4-9 Mind Map Guided Jaundice Analysis in Pancreatic Cancer
Clinical Case Study with Structured Causal Visualization

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P-4-10 Dynamic Changes of Sepsis Biomarkers in Polymorbid Cellulitis
A Collaborative Case Report by a Nurse Specialist and a Medical Laboratory Scientist

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P-4-11 Laboratory-Based Risk Stratification for Complicated Appendicitis
Prognostic Nutritional Index Enhances Risk Stratification in a Large Cohort

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P-4-12 Stability of lactate dehydrogenase activity during storage
-Relationship with its Subunit Structure-

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P-4-13 Pseudo-Low Uric Acid
A Pre-analytical Pitfall in Acute Leukemia

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P-4-14 Correlation Between Plasma Catecholamines and Glycemic Fluctuations via Exercise Intensity
An Empirical Approach Using Heart Rate Reserve to Assess Physical Load

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P-4-15 Association of CK-MB Inter-Reagent Variability with M/B Subunit Reactivity

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P-4-16 Method Bias in CEA Measurement
Clinical Threshold Effects on Classification Discordance

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P-4-17 %CDT and FIB-4 in ALD Diagnosis and Fibrosis Staging
Complementary Roles of %CDT and FIB-4 in Clinical Assessment

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P-4-18 Evaluation of Alternative Centrifugation Settings for Routine Chemistry Samples

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P-4-19 Evaluation of Surfactants added to Automated Clinical Chemistry Reagents

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P-4-20 Short-chain fatty acids bias ion-selective electrode chloride measurements
Evidence from a method comparison with LC-MS/MS

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P-4-21 Combined AFP, PIVKA-II, and GPC3 for Improved HCC Diagnosis.

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P-4-22 Novel ELISA Measuring sPTPRZ Using Glycan Standard for Glioma Diagnosis

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P-4-23 Investigation of Methotrexate-Induced Interference in Urinary NAG Measurement

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P-4-24 Glycan analysis of apoE, a risk factor for Alzheimer's disease.

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P-4-25 Cardiac Biomarker Dynamics in Fabry Disease Myocardial Involvement
Clinical Implications of Biochemical Indicators for Early Detection of Cardiac Injury

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P-4-26 Hypercalcemia Differentiation in Lung Cancer with Concurrent Hyperparathyroidism
Biochemical Markers and Imaging Integration for Accurate Differential Diagnosis

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P-4-27 Severe Hypocalcemia After Thyroidectomy
A Time-Series Laboratory Analysis of Postoperative Hypoparathyroidism

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P-4-28 Fasting Glucose and BMI in the Hong Kong Population
A Retrospective Cohort Study

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P-4-29 BMI and Uric Acid Levels in the Hong Kong Population
A Retrospective Cohort Study

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P-4-30 Analytical Evaluation of Roche Tina-quant Hemoglobin A1c Generation 4 Assay

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P-4-31 Implementing Artificial Intelligence in Clinical Chemistry
Concise Review and Recommendations

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P-4-32 Serum Uric Acid and Fatty Liver Severity
A hospital-based cross-sectional study in Taiwan

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P-4-33 Evaluating the performance of Apexbio Glucosure POC
Apexbio Glucosure POC

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P-4-34 Exploring Multiple Myeloma from a Laboratory Medicine Perspective
A Case Study of Laboratory Analysis in a Patient with Hyperglobulinemia

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P-4-35 RISK FACTORS FOR ABNORMAL BIRTH WEIGHT, A RETROSPECTIVE STUDY
RISK FACTORS FOR ABNORMAL BIRTH WEIGHT, A RETROSPECTIVE STUDY

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P-4-36 Clinical, Biochemical, and Socioeconomic Profiles Correlating with Polycystic Ovary Syndrome

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P-4-37 Unmasking the Pseudo-Stroke
Laboratory Management of Aconitine-Induced Refractory Arrhythmia and Multi-Organ Dysfunction

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P-4-38 The Future of Clinical Chemistry Global Innovations and Healthcare Impact

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P-4-39 Diabetes
DM

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P-4-40 When Low Humidity Disrupts Automated Pipetting, A Real Life Example

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P-4-41 Development of a Highly Linear AST and ALT Activity Assay

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P-4-42 Revisiting the Mediterranean Paradox: Correlation between sun exposure and VitD
Comparative study between populations in the Mediterranean area and Arctic regions

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P-4-43 Biochemical Signature of Academic Stress
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P-4-44 Association Between Fatty Liver Index and Renal Function Indice

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P-4-45 Palmitic Acid-Induced Acinar-to-Ductal Metaplasia in Pancreatic Steatosis
Marine Natural Products as Candidate Inhibitors of Pancreatic Steatosis Progression

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P-4-46 Development of an ELISA Assay for Apolipoprotein C-II Transfer Rate
Toward Assessment of Individual TG Metabolism

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P-4-47 Exosomal Markers Associated with Lipoprotein(a) and Cardiovascular Risk

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P-4-48 Critical Low Glucose Workflow Optimization
Enhancing Pseudo-Hypoglycemia Identification and Laboratory Reporting Efficiency Through Quality Improvement Strategies

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P-4-49 Urine Microalbumin QC Optimization
Improving Analytical Stability Through Open-Vial Calibrator Management

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P-4-50 Integrated NADH Chelate Assay Using a NADH Oxidase

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P-4-51 Measurement method for NAD+ and NADH as an aging biomarker

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P-4-52 Electronic Display Board
the Biochemical Analyzer Track System

chuyin ko

P-4-53 Real-World Verification of CYFRA 21-1 Reference Intervals: Pandemic Partitioning? A 10-Year, 7-Hospital Longitudinal Real-World Evidence Study of 10,046 Asian Health Examinees

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P-4-54 FT4 and FT3 measurement using Equilibrium-Dialysis-LC-MS/MS as a complementary method

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P-4-55 Thyroid Dysfunction in Lithium-Treated Bipolar Patients

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P-4-56 Serum Beta-2 Microglobulin as a Biomarker of Severe Psychoses

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P-4-57 Association Between VPA and Hyperammonemia: A Retrospective Cross-Sectional Study Evaluation of Serum Valproic Acid Concentration, Ammonia Level, Age, and Sex

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P-4-58 Evaluation of True versus suspected pseudohyponatremia in tertiary care setting
Lab based pilot study on pseudohyponatremia reassessment and diagnostic corelation adjusted for patient setting

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P-4-59 Risk-Based Management of Pre-Analytical Non-Conformities In Biochemistry Laboratory According to ISO 15189:2022

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P-4-60 Sigma Metric-Based Internal Quality Control in Clinical Biochemistry

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P-4-61 Comparative Analysis of Semaglutide, Liraglutide, and Tirzepatide Cardiometabolic Outcomes

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P-4-62 Association of hs-CRP and Lipid Profile among Filipino Tobacco Users
Evaluation of Biomarkers for Cardiovascular Disease Risk Among Smokers and Heated Tobacco Users

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P-4-63 Urinary Vanin-1 Improves a Multimarker Diagnostic Model for CKD
Association With Albuminuria and Enhanced Diagnostic Performance

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P-4-64 Verification of venous blood collection tubes with new separating gel

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P-4-65 Coronary Heart Disease Risk Analysis Utilizing Serum Cystatin C
A Quantitative Assessment of Filipino Compliant Type 2 Diabetes Mellitus with Chronic Kidney Disease

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P-4-66 Quality Improvement of Quantitative FIT Screening in Taiwan
A Nationwide Total Quality Management Program for Colorectal Cancer

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P-4-67 Are ovarian reserve hormonal markers always concordant?

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P-4-68 Risks assessment in medical laboratories using Failure Effects Analysis

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P-4-69 Validated UPLC-MS/MS Assay for Monitoring ADHD Medications in Pediatric Urine

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P-4-70 Kidney Injury Molecule-1 Outperforms Conventional Markers for Early Diabetic Nephropathy

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P-4-71 Vitamin D status and thyroid profile in tunisian population

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P-4-72 Preanalytical Practices Among Healthcare Professionals
Knowledge gaps and training needs in blood sampling

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P-4-73 Reproducibility of Routine Chemistry Assays
Internal quality control data from a Tunisian university hospital

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P-4-74 Reference Intervals for Lipid Profile in Healthy Adults
Reference Intervals for Lipid Profile in Healthy Adults in Cameroon

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P-5-1 Emerin, SUN1, and SUN2 Expression Decreased in Poorly-differentiated Lung Adenocarcinoma

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P-5-2 Immunohistochemical Analysis of Hepatocellular Carcinoma After Immunotherapy
Spatial Distribution of Cytotoxic T Cells and Tumor Associated Macrophages

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P-5-3 Digital Control of Formalin Bottles
Barcode-based management using SafeCheck in pathology

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P-5-4 A Novel Formalin Container for Safer Pathology Practice
Development and refinement of exposure source control during tissue fixation

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P-5-5 Insights into Tenascin-C in MAPK inhibitor resistance in melanoma

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P-5-6 Transforming Surgical Pathology Grossing: Digital Frameworks to AI Integration
Leveraging System Success Models for Scalable Training and Future AI Adoption

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P-5-7 Assessment of Fungal Staining with Chromic Acid-Free Methenamine Silver

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P-5-8 Comparative Evaluation of Different Methods of Double Immunohistochemical Staining

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P-5-9 A Study of Rapid Silver Staining Method

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P-5-10 Consistent Membranous Staining of Pancreatic Islets in IGF2BP3/IMP3 Immunohistochemistry:
A Clone Specific and Unexpected Immunoreactivity with Potential Diagnostic Pitfalls

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P-5-11 Digital Pathology Implementation in Remote Canadian Regions
A summary of unique opportunities and challenges

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P-5-12 *Frozen section aids ocular sebaceous gland carcinoma diagnosis & management.*

Neelima Sharma, Seema Sen, Seema Kashyap, Niamul Kabir, Dinesh Kr. Baitha, Neelam Pushker
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P-5-13 Clinicopathological significance of Nectin-4 in urothelial carcinoma
Nectin-4 expression is associated with favorable clinicopathological features

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P-5-14 Evaluation of reaction endpoint in periodic acid methenamine silver staining

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P-5-15 HEQUALYZER: What do you see when you look at H&E?
Empowering Biomedical Laboratory Scientists through an integrated colorimetric and artefact framework

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P-5-16 Analysis of CEACAM6 expression in intrahepatic cholangiocarcinoma
Analysis of CEACAM6 expression in relation to the progression of intrahepatic cholangiocarcinoma

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P-5-17 Implementation of MacroPATH MX SK C-Scan
Image-Based Macroscopic Biopsy Documentation

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P-5-18 Rapid Fresh Pathology for Breast Core Biopsies
A section-free workflow preserving tissue for downstream testing

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P-5-19 ARIA-Like Mouse Model Based on Cerebral Amyloid Angiopathy
Crossing endothelial APP770 mice with a conventional AD model

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P-5-20 Rapid immunohistochemistry using an alternating current electric field
for intraoperative frozen-section diagnosis

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P-5-21 Evaluation of lead-induced ROS *in vitro* and *in vivo*
Implication for molecular mechanisms of heavy metal toxicity and antioxidant intervention
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P-5-22 Anti-Lung Cancer Activities of Curcuminoids via Multi-Target Mechanisms
Insights from Molecular Docking, Cell Culture, and *C. elegans* Models

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P-5-23 Curcumin Enhances Doxorubicin Efficacy in Human Hepatocellular Carcinoma Cells
Synergistic Inhibition of Proliferation, Clonogenicity, and Migration

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P-5-24 Crithmum maritimum L. Suppresses Lung Cancer via p38-MAPK Pathway
Focus on Pro-Apoptotic Effects and Signaling Cascades

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P-5-25 Bioactivity-Guided Isolation of Active Ionone Compound from *Physalis peruviana*
Evaluating Its Anti-Cancer Effects in SKOV3 Ovarian Cancer Cells

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P-5-26 Association Between HPV and Tumor Immunity in Oropharyngeal Carcinoma

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P-5-27 Long-Term Formalin-Ethanol Fixation Affects Nucleic Acid Quality

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P-5-28 Implementation of AT192: automated preparation of paraffin-embedded tissue-blocks
An approach towards integrating more automated work processes in the laboratory

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P-5-29 Analysis of Kaposi's sarcoma-assosiated herpesvirus K1 gene function
The association of K1 gene with invation ability and epithelial mesenchymal transition

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P-5-30 Analysis of ARIA-like pathology in Alzheimer disease model mice
Characterization of Vascular Amyloid-beta in a Novel CAA/ARIA Model Mouse

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P-5-31 GALNT6 Expression and Localization in Luminal A Breast Cancer
Association with epithelial polarity and gland-forming architecture in clinical breast tissues

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P-5-32 Development of a Detection System for PTPRZ-MET Fusion in Glioma

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P-5-33 Rapid Fresh Pathology for Pulmonary Specimens
Whole-mount Gigapixel Imaging of Fresh Lung Surgical Tissue

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P-5-34 KSHV Genotyping in Kaposi Sarcoma: Association with Clinical Subtypes

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P-5-35 11,13-Dehydrolanuginolide Attenuates the Progression of Hepatocellular Carcinoma *In Vitro* Suppression of Long-Term Proliferative Capacity and Tumor Cell Migratory Potential

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P-5-36 Protective Effects of Naringenin Against Hepatic Steatosis and Fibrosis

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P-5-37 Elucidation of microenvironmental changes in precancerous lesions

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P-5-38 Antcin Boosts Cisplatin Efficacy in Non-Small Cell Lung Cancer Suppressing Cell Survival and Migration through Combined Therapy

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P-5-39 Apigenin as a Therapeutic Agent Against Ovarian Cancer
An In Vitro Evaluation of Antitumor Mechanisms in the SKOV3 Cell Line

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P-5-40 FFPE-Compatible RT-PCR for Endometrial Stromal Sarcoma
Detection of *JAZF1::SUZ12* and *YWHAE::NUTM2A/B* Fusion Transcripts

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P-5-41 Trends in Asbestos Body Counting at a Japanese Hospital
A Retrospective Analysis of 305 Cases

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P-5-42 Could Cytokine Profiling Refine Immune Stratification in Colorectal Cancer Patients?

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P-5-43 Improve the processing procedures for frozen sections of breast tissue

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P-5-44 Chromatin Instability by Telomere Dysfunction Promotes Neutrophil Extracellular Trap Formation
Association of TRF2 Downregulation and DNA Damage Response with Neutrophil Extracellular Trap Formation

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P-5-45 Effect of Mumefural on Neutrophil Extracellular Trap Formation
Characterization of NETs Responses to a Japanese Apricot-Derived Bioactive Compound

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Cytology

P-6-1 HPV DNA Genotyping and E6/E7 mRNA for Cervical Precancer Diagnosis

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P-6-2 Immunohistochemical analyses of hydroxylase-immunoreactive amacrine cells in the gerbil retina

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P-6-3 Deep Ocean Water in Cytology Processing
A Preliminary Study of Morphologic Preservation

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P-6-4 Signet-Ring-Like Macrophages in Pleural Effusion
Cytologic Features and Diagnostic Pitfalls: A Case Report

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P-6-5 Validation of Immunocytochemistry Controls in Liquid-Based Cytology
Effects of Fixatives and Storage Conditions

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P-6-6 Atypical Cells in Septic Ascites
Diagnostic Pitfalls in Severe Sepsis with Septic Shock

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P-6-7 Prolongation Factors Among General Applicants in Cytotechnologist Certification Examination

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P-6-8 Imprint Cytology Supports Safer OSNA Practice
A laboratory quality safeguard for discordant sentinel node assessment

Makoto HAMADA, Shogo Baba, Mami Koketsu, Oi Harada, Yasutaka Kato, Hiroyuki Kawami, Hajime Kuroda, #Emmy YANAGITA

P-6-9 A Case of Ependymoma Detected in Pleural Effusion

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P-6-10 Astroblastoma initially suspected as ependymoma on intraoperative cytology a case report with emphasis on differential cytological feature

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P-6-11 Digital Cytology Learning Content Development and AI Applications

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P-6-12 Comparison of ThinPrep UroCyte and Cytospin in Urinary Cytology

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P-6-13 Case Report: Stratified Mucin-Producing Intraepithelial Lesion (SMILE) in Pap Smear

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P-6-14 Analyzing positive cells using CINtec Plus in cervical smears Cytological findings of p16/Ki-67 positivity in high-risk HPV cases

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P-6-15 Calcification and RA cell in Human Osteoarthritis Synovial Fluid

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P-6-16 miRNAs in extracellular vesicles derived from cadmium-exposed hepatocytes inhibit osteogenesis.

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P-6-17 Development of an Eye-Tracking Application for Cytotechnologist Skill Assessment Assessing Diagnostic Expertise Using Machine Learning and Visual Search Features

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P-6-18 A case of neuroendocrine carcinoma of the breast nipple discharge : cytological characteristics

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P-6-19 Cytological Features and Differential Diagnosis of Dermatopathic Lymphadenopathy

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P-6-20 Mollaret cells identified in cerebrospinal fluid cytology. A case of recurrent meningitis underlying Sjogrens syndrome.

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P-6-21 Nested Variant Urothelial Carcinoma in Urine Cytology A Diagnostic Pitfall in The Paris System

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P-6-22 Utility of Cytological Specimens for Molecular Testing in Lung Cancer

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P-6-23 ROSE in Emergency Care: Report of Two Beneficial Cases

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P-6-24 Evaluation of Intraoperative Rapid Cytology in Thoracic Surgery Cases

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P-6-25 Simple Bone Cyst with Spherical Fibrin-like Material in Cyst Fluid A Case Report

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P-6-26 Central Nervous System Involvement in Mantle Cell Lymphoma
The Crucial Role of Cerebrospinal Fluid Laboratory Diagnostics
Mirjana Stupnisek
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P-6-27 Atrophy
Diagnostic Utility of the Estrogen Test in Postmenopausal Cervical Cytology
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P-6-28 Bone Marrow Leishmaniasis in a Patient with HIV Infection:
Lessons from a Relapsed Case
Mirjana Stupnisek, Martina Firic, Katarina Pajtak
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Urinalysis

P-7-1 A case of combined small cell carcinoma and urothelial carcinoma
Bladder cancer in which estimation of histological type was avoided in Urinary Sediment Examination
Taichi ISHIYAMA[1], Mihoko TOMODA[1], Yoshimi KATOUNO[1], Megumi OKUMURA[1], Hitoshi ABE[1], Tomohiro CHIBA[1], Kazunori MIYAKE[2], Taro SHIGA[1]
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P-7-2 Diagnostic Pitfalls and Interpretive Performance in Urinary Cell Identification
Accuracy, Misclassification Patterns, and Predictors of Professional Performance
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P-7-3 Usefulness of Gram staining in continuous ambulatory peritoneal dialysis effluent
Evaluation of characteristics using the fully automated urine particle analyzer UF-5000
Takuya OKAMOTO, Honami MIYASHIGE, Yuka YONEDA, Mayumi YAMADA, Mizuki HARA, Naoki TOKUNAGA, Hiroaki TADA
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P-7-5 Evaluation of Urinary Sediment for Monitoring Fabry Disease Treatment
Longitudinal Changes in Mulberry Cell and Body Counts in Fabry Disease
Noriko KAWAMITSU, Aya UEHARA, Yuuki FUKAGAWA, Ayumi SAKATA
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P-7-6 Quantitative Assessment of Macroscopic Haematuria Using Urinary RBC Counts
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P-7-7 Urinary scattergram parameters predict leukocyte viability and urinary tract infection classification of pyuria by machine learning

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P-7-8 Glomerular Erythrocyte Identification Using LVSEM and 3D-OWFM

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P-7-9 Nuclear long diameter index for identifying HGUC cells
An objective morphological indicator in urinary cytology

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P-7-10 Clinical Significance of Xanthine Crystalluria
A Case of Tumor Lysis Syndrome

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P-7-11 Establish a rapid screen process for bacterial identification from urine
Using Sysmex UF-5000i combined with membrane micro-filtration extraction and MALDI-TOF MS

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P-7-12 UF-5000 Atyp.C for Detecting Atypical Urinary Cells
Impact of identifying intracytoplasmic inclusion-bearing cells

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P-7-13 Macroscopic Brown Urine During Metronidazole and Cefiderocol Therapy

Haruyo MITSUI, Yoko YATABE, Tsuyoshi KOKUZAWA, Akihiko CHIDA, Masaharu YASUI, Tomoko ARAI, Masatoshi WAKUI, Hiromichi MATSUSHITA
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P-7-14 Urinary Nephrin in Early Nephropathy among Hypertensive T2DM Filipino Patients

Allyssa Marie Prado, Andrew Alviar, Leona-Victoria Lapuz, Kattiana Dubongco, Ron Sison, Ruby Meim, Xandro Nieto
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Transfusion Medicine

P-8-1 Utilizing Novel Heat Pipe Thawing Mechanism for Fresh Frozen Plasma
A Pilot Probe on its Hemostatic-Proteometric Viability and a possible Stat Request Algorithm

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Jessa Mae Janoyan, Albena Meilodi Oclarit, Aniska Yonjan, Roscel Iris Vios
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P-8-2 Responses to Depleted Red Blood Cells Transfusion
A Case Study of a Teaching Hospital in Hsinchu, Taiwan

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P-8-3 A Case of Anti-K Alloimmunization After Blood Transfusion
A Rare Case of Anti-K Alloimmunization After Blood Transfusion in a Taiwanese Patient

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P-8-4 Recovering Extracellular Vesicle-Associated Particles from Discarded Cryosupernatant

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P-8-5 Auto-anti-M Mimicking Cold Agglutinin Disease
A Diagnostic Pitfall in Laboratory Interpretation

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P-8-6 AI-Driven Digital Handover in Blood Bank
Improving Efficiency and Transfusion Safety

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P-8-7 When O is Not O: Ael Phenotype Misclassification
A Rare Ael Phenotype Presenting as ABO Discrepancy

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P-8-8 Clinical Significance of Naturally Occurring Anti-Wr^a
IgG Subclass and Functional Analysis

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P-8-9 Dynamic Lewis Antigen Changes During HCV Antiviral Therapy

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P-8-10 Cold Agglutinin Transfusion Management in CAD
A Case Report of High-Titer Autoanti-I Hemolysis

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P-8-11 Establishing Optimal Cut-off Values for Autologous PBSC Collection Using Automated Hematopoietic Progenitor Cell (HPC) Counts

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P-8-12 Incidence and Causal Analysis of Transfusion Incidents at Our Hospital

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P-8-13 Establishing an Emergency Blood Supply Procedure for Resilient Healthcare

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P-8-14 Weak Antigen Reactivity in Acute Myeloid Leukemia

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P-8-15 Analysis of emergency transfusion cases of Fu_Jen Catholic University Hospital

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P-8-16 Strategies and Effectiveness of Improving Management Rh(D)-Negative Blood Components Returns
RhD-Negative Blood Component Return Reduction Strategies

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P-8-17 Meteorological Drivers of Blood Type Specific Transfusion Demand Patterns
A Five Year Retrospective Analysis of Comprehensive Weather Impacts

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P-8-18 Bridging Blood Supply Crisis during COVID-19
Integrating Clinical Decision Support Systems and Dynamic Inventory Management

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P-8-19 Piperacillin/Tazobactam-Induced Drug-Dependent Antibodies Presenting as Autoantibodies: A Case Study

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P-8-20 Managing ABO Discrepancy in a Resource-Limited Laboratory
A Practical Case Experience Suggestive of B3 Subgroup

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P-8-21 Power BI evaluation of prophylactic antihistamines for patient safety

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P-8-22 Unexpected Anti-Jra Antibody Causing Transfusion Delay in Acute Cholangitis
Importance of Rapid Collaboration Between Laboratory, Clinicians, and Blood Center

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P-8-23 Establishing a Quality Control and Appropriate-Use System for In-House Cryoprecipitate

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P-8-24 A Case Report of Suspected Transfusion-Associated Circulatory Overload

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P-8-25 Cold Stored Platelets
Cold and delayed cold storage a promising alternative for the preservation of platelet concentrates

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P-8-26 Generative AI applications in restrictive transfusion strategy
Reducing RBC transfusion overuse

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P-9-1 AI Diagnostic Performance in Medical Laboratory Imaging
Strategic Implementation of AI-Assisted Diagnostic Systems and the Evolving Role of Medical Technologists

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P-9-3 Digitization as a tool for transformation:
Distance learning for acquiring sustainable knowledge of histological morphology

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P-9-4 XR-Assisted Phlebotomy Improving Workflow and Procedural Training in Medical Laboratory

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P-9-5 Escape Room-Based Gamification for Medical Technologists
Impact on Knowledge, Skills and Attitudes

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P-9-6 AI Phlebotomy Training: Enhancing Communication Skills Through Virtual Human Simulation

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P-9-7 Training for Medical Laboratory Interns
Virtual Reality Based Polymerase Chain Reaction Training for Medical Laboratory Interns

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P-9-8 Automated Voice Dialing for Critical Value Reporting: Implementation and Evaluation
An Innovative Automated Voice Dialing and Escalation Framework for Clinical Value Reporting

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P-9-9 Gamification of Learning -"Hospital Escape"
Application of Escape Room Integrated with Live Action Role-Playing in Medical Laboratory Education

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P-9-10 Designing Entrustable Activities for Entry-Level Laboratory Practice
Validation and staged prioritization across three core disciplines

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P-9-11 Development and Implementation of the postgraduate program "histopathology"
A spezialiced 60 - ECTS curriculum for biomedical scientists in Austria

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P-9-12 SIMULATION as a Didactic Concept in Functional Diagnostics

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P-9-13 Academic Program in Functional Diagnostics
Evidence-based specialization for functional laboratory diagnostics in pulmology, sleep medicine, cardiology, and neurology

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P-9-14 Hemoglobin Discrepancy and Sample Inhomogeneity in Syringe Blood Collection
Impact of Pre-analytical Factors and Rapid Sedimentation Triggered by a Critical Incident

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P-9-15 The new era of Biomedical Laboratory Sciences in Portugal
One profession, multiple specializations: A strategic framework for academic progression and professional alliance

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P-9-16 Virtual slide group work enhances understanding in pathology education

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P-9-17 Digital and Flexible Continuing Education for Biomedical Laboratory Scientists

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P-9-18 Career Awareness and Educational Needs among Japanese Medical Laboratory Scientists
Insights from a Survey on Training Gaps and Career Expectations

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P-9-19 Practical Three-Minute Kiken Yochi Training in a Pathology Laboratory

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P-9-20 Designing a Self-Assessment System for Biomedical Laboratory Science Examination Preparation

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P-9-21 Evidence-based competency tools with a next-generation digital system

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P-9-22 Authentic Assessment for Workforce Readiness in Laboratory Medicine
A coherent assessment pathway supporting professional formation and workforce readiness

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P-9-23 Modular Master of Health Studies: Stackable Micro-credentials for Postgraduate Pathways
Flexible master's programme combines lifelong learning with continuous academic development

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Hochschule Campus Wien University of applied sciences

P-9-24 Competency-Based Curriculum Reform in Biomedical Science Education
Early Laboratory Skills Training and Structured Assessment to Enhance Pracitcal Competence

Barbara Kirchknopf, Michaela Hassler
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P-9-25 Curriculum Redesign for Part-Time Biomedical Science Education
Blended delivery, simulation and workload alignment in clinical chemistry

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P-9-26 Shaping the Future: Harmonising Biomedical Laboratory Sciences Education in Portugal
National Council of Biomedical Laboratory Sciences working together for a brighter future!

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P-9-27 Where Standards Meet Practice Educating - Tomorrow's Biomedical Scientists
Curricular Structures and Professional Standards in Portuguese Private Higher Education

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P-9-28 The Importance of Specialized and Standardized Training in Macroscopy
A Proposal for a Competency-Based Educational Model in Biomedical Laboratory Science

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P-9-29 Bridging the Future of Biomedical Laboratory Science Through International Training
Insights from the 2024 TMER Overseas Training Program

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P-9-30 The BLS Academy
An International Academy of Biomedical Laboratory Sciences

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Genetics

P-10-1 Urinary Liquid Biopsy for Nuclear and Mitochondrial Genomics in Practice

Urinary Liquid Biopsy for Nuclear and Mitochondrial Genomics in Practice

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P-10-2 Transcriptomic endotype-dependent mortality risk associated with mitochondrial gene expression

Evidence from a large sepsis whole-blood transcriptomic cohort

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P-10-3 Standardizing RNA Extraction and RNA-Seq Library Prep Using LabDroid MAHOLO

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P-10-4 UGT1A1 Result Documentation and Subsequent Irinotecan Use in Solid Tumors

Insights Into the Real-World Use of UGT1A1 Results

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P-10-5 Detection of Genetic Mosaicism using cfDNA

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P-10-6 Impact of pre-analytical procedures on plasma microRNA expression

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P-10-7 Migraine-Related Autonomic Changes Associated with *ASTN2* Polymorphism

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P-10-8 A NOVEL SLC4A3 VARIANT IDENTIFIED IN DILATED CARDIOMYOPATHY
PREDICTION ASSESSMENT OF SLC4A3 PATHOGENICITY USING A ZEBRAFISH MODEL

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P-10-9 Evaluation of SNaPshot for detecting *BCR*::*ABL1* mutations
Comparison between SNaPshot and Sanger sequencing methods for detecting drug-resistant tyrosine kinase domain mutations

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P-10-10 G-banding decolorization XY FISH in secondary MDS detection: a case

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P-10-11 Simplification and Utility of Urine DNA Extraction Protocol
Aiming for a Lower-cost and Simpler Method

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P-10-12 Standardization and Clinical Evaluation of Circulating microRNAs
Quantitative Assessment of Atrial Remodeling in Atrial Fibrillation

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P-10-13 Cellular Deconvolution Methods for Cell-Free RNA in Liver Cancer
Cellular Deconvolution Methods for Cell-Free RNA in Liver Cancer

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P-10-14 Detection Rate of Trisomy 21 in AMA Pregnancies Undergoing Amniocentesis
A Five-Year Retrospective Study

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P-10-15 Comprehensive Analysis of Genomic Alterations for Precision Oncology
Comparison Across Specimens and Sequencing Platforms

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P-10-16 Evaluation of Exosome Isolation Methods
Comparison Between Serum and Plasma and the Impact of Freeze Storage

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P-10-17 Brushing lavage detects red complex bacteria better than mouth rinse

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P-10-18 Role of Medical Technologists in Comprehensive Genomic Profiling in Japan

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P-10-19 Genetic Variation Analysis of the G6PD
Genetic Variation Analysis of G6PD in Neonate

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P-10-20 Application of Cytogenetic Biodosimetry in Radiation Workers
Enhancing Occupational Safety Tracking in Biomedical Laboratory Science

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P-10-21 Preliminary study of a novel *BRAF* V600E detection method

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P-10-22 Culture-Negative Microsporidial Endophthalmitis Diagnosed by PCR and Electron microscopy

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P-10-23 Molecular analyses of GALNT6 in luminal breast cancer
Subtype-specific transcriptomic association with estrogen receptor-related epithelial programs

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P-10-24 Analytical Validation of a Solid Tumor Comprehensive Genomic Profiling Assay
Analytical Performance of an NGS-Based Comprehensive Genomic Profiling Assay for Solid Tumors

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P-10-25 *BRCA2* LOH Drives Melphalan Sensitivity in Vaginal Clear Cell Carcinoma
A Genomic Case Study on Melphalan Efficacy in Cisplatin-Refractory Clear Cell Carcinoma

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P-10-26 A case of left craniofacial overgrowth with a *PIK3CA* variant localized to the right buccal mucosa

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P-10-27 Implementation of Droplet Digital PCR for Circulating Tumor DNA Detection
Establishing a clinical testing platform for novel cancer markers at Oslo University Hospital

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P-10-28 Quantitative methylation analysis of LINC01869 for colorectal cancer diagnosis

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P-10-30 Haplotype selection improves chimerism quantification accuracy
Wakaba IHA, Shohei SHIGETO
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P-10-32 Relationship Between Mutant Ataxin-3 Protein and Mitophagy in SCA3 Patients
Yu-Chun Lin, Yu-Hsiang Hsiung, Shih-Yun Wei, Hui-Fang Tsai
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P-10-33 The neuroprotective effect of Caffeic acid phenethyl ester on SCA3
Yu-Hsiang Hsiung, Chia-Zong Wu, Shih-Yun Wei, Yu-Chun Lin, Hui-Fang Tsai
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P-10-34 Evaluation of miRNA Enhance Buffer for Improving microRNA Recovery Efficiency
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P-10-35 Polyamine-Based Nucleic Acid Recovery Method
Application to Liquid Biopsy and Methodological Development
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P-10-36 xCT expression in astrocytes on glutamate metabolism under hypoxic environment
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P-10-37 Splicing Analysis of Novel *PROS1* Variant in Protein S Deficiency
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P-10-38 The expression of stress-related mitochondrial non-cording RNA in hair shaft
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P-11-a-1 Developing a Framework for Cognitive Age Estimation.
Using Multidomain Cognitive Scores.
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P-11-a-2 Development of a real-time neurofeedback analysis method using magnetoencephalography.

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P-11-a-3 Motor function assessment using second lumbrical CMAP in CTS

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P-11-a-4 Changes in Body Composition and the Cardio-Ankle Vascular Index
A Longitudinal Study in Children

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P-11-a-5 Ictal Dynamics on Wide-Band Electroencephalography in Childhood Absence Epilepsy
Direct current shifts and high-frequency oscillations as candidate biomarkers of preictal-to-ictal transition

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P-11-a-6 Validity of Smart Ring-Derived Sleep Parameters Compared With Electroencephalography

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P-11-a-7 Development of a New Predictive Index for Carotid Plaque

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P-11-a-8 Segmental beta response evaluation is beneficial for assessing arterial stiffness

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P-11-a-9 EEG Sleep Variability and Depressive Symptoms
Wearable-Based Assessment in Japanese Workers

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P-11-a-10 Association Between Sleep Restfulness and Smart Ring Derived Sleep Parameters

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P-11-a-11 Felt Inversion After Aortic Arch Replacement
A Rare Cause of Mechanical Hemolytic Anemia Diagnosed by Echocardiography

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P-11-a-12 Evaluation of respiratory muscles in patients with Duchenne muscular dystrophy

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P-11-a-13 Telemedicine-Assisted EEG Simulation for Legal Brain Death Determination

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P-11-a-14 Invasive EEG versus Stereo-EEG for Epileptogenic Zone Localization
A Comparative Analysis of Invasive Monitoring Techniques in Presurgical Epilepsy Evaluation

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P-11-a-15 Cross-sectional area of the tibial and fibular nerves using ultrasound
Investigation of reference values and evaluation of reproducibility

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P-11-a-16 Clinical and Sonographic Features Differentiating ICPN from Gallbladder Carcinoma

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P-11-a-17 Wide-Band Scalp Electroencephalography Analysis in Infantile Epileptic Spasms Syndrome
Analysis of ictal direct current shifts during a seizure cluster of spasms

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P-11-a-18 EEG in Neuro emergencies : Role of Biomedical Laboratory Scientists

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P-11-a-19 The relationship between tinnitus pitch and hearing loss.

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P-11-a-20 The reliability of Ultrasound measurements in Knee Tendon Thickness
Effect of Measurement Distance from Tendon Insertion

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P-11-a-21 Exclusion marker of pulmonary embolism on transthoracic echocardiogram.

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P-11-a-22 Maximizing Biomedical Laboratory Scientists' Value
Phase-Free Activities for Preventing Disaster-Related and Sudden Deaths

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P-11-a-23 Home-based sleep EEG assessment of exercise effects in young women
Effects of resistance exercise during the luteal phase

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P-11-a-24 Embolic Events and Clinical Echocardiographic Findings in Cardiac Myxoma Patients

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P-11-a-25 Vascular Function and Subjective Sleep Characteristics in Young Adults
Sex Differences in Sleep-Vascular Associations

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P-11-a-26 Vascular Function and Sleep EEG Architecture in Women
Comparisons Between Young Adult and Menopausal Women

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P-11-b-1 Tableau Monitoring Optimizes Blood Draw for Rehabilitation Bus Patients

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P-11-b-2 Healthcare Needs Assessment in Uzbekistan
Preliminary field survey for future laboratory collaboration

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P-11-b-3 Application of Artificial Intelligence in Preanalytical Phaseof Clinical Laboratory
Promoting Quality Assurance Stewardship

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P-11-b-4 Multidisciplinary CKD Intervention Triggered by Laboratory Data Extraction
Role of Medical Laboratory Technologists in Early Dialysis Prevention

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P-11-b-5 Human Factors Redesign Improves Laboratory Workflow Efficiency
Enhancing Risk Management and Patient Safety in High-Volume Health Screenings

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P-11-b-6 Cerebrovascular Modulation by Spinal Cord Stimulation in Stroke
Insights into Perfusion Dynamics and Recovery in a Mouse Model

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P-11-b-7 Progress of Task Shifting and Sharing Among Medical Technologists
A Multi-Institutional Survey Following the 2024 Work-Style Reform in Tama, Tokyo

Hiroyuki HAYASHI

P-11-b-8 Mitochondrial adaptation mechanisms regulated by caveolin-1 C-terminal region
Toward molecular markers for assessing atherosclerotic plaque vulnerability

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P-11-b-9 Insights into Internal Quality Control in Veterinary Biochemistry Using Chiritrol

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P-11-b-10 Multidimensional Sleep Characteristics and Arterial Stiffness in Older Adults

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P-11-b-11 TLA Improves TAT and Workflow Efficiency
Under High-Demand Emergency Conditions

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P-11-b-12 Automated Reagent Expiry Warning System
Improving management efficiency in clinical biochemistry laboratories

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P-11-b-13 Multilingual Audio Vision Testing System
Enhancing communication in driver license vision examinations

Li Pei Shan, Chang Chih Ning, Sung Yi-Hung, Chen Po-Chih
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P-11-b-14 Meeting Patient Expectations: A Survey for Enhancing Blood Collection Services

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P-11-b-15 AI-Driven Intelligent Document Processing in Laboratory Medicine
Transforming ISO 15189 Documents into Standardized Patient-Readable Information Sheets

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P-11-b-16 Reliable POCT: Risk Defense and Smart Monitoring
A PDCA-Based Model for Enhancing Patient Safety and Clinical Quality

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P-11-b-17 Optimizing Cross-Departmental Administrative Efficiency via Knowledge Management
A SharePoint-based Approach in a Clinical Laboratory

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P-11-b-18 Utility Evaluation of Dedicated On-site Pre-Analytical Laboratory in Clinical Trials
Reducing pre-analytical errors and improving research outcomes by implementing specialized on-site sample handling units

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P-11-b-19 Establishing progastrin-releasing peptide cut-off in lymph node biopsies

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P-11-b-20 Incremental learning framework for adapting shared blood sampling prediction models
A cross-institutional framework for efficient model adaptation and deployment

Rin YOKOYAMA[1], Takahito ARAI[1], Hidekazu ISHIDA[2], Rina ICHIOKA[2], Hiroyuki OKURA[2], Ryosuke KIKUCHI[2], Naoyuki YOSHIKAWA[1], Makoto KURANO[1]

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P-11-b-21 Process-based Analysis of Endoscopy Room Workflow
Impact of Endoscopist Experience, Assistant Competency, and Patient Age

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P-11-b-22 Obesity and Hyperlipidaemia Correlation with Chronic Chlorpyrifos Exposure Workers
Correlation Analysis of Obesity and Hyperlipidaemia with Long-Term Chlorpyrifos Exposure in Pest Control Workers

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P-11-b-23 Impact of Missing Data in Real-World Data Analysis
An Example Using Risk Factors for Anemia

Masato IWAMI, Yoshihiro MIZOGUCHI, Momoka NANRI, Manaki SUKIZAKI, Jun'ichi SATANI, Ryouta FUCHINO, Daisuke UNO
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P-11-b-24 Verifying Third-Party Control Materials for Hormone and Tumor Marker Testing
Comparative evaluation with dedicated controls using patient R-values from the even check method

Masaya TACHIKAWA, Hidekazu ISHIDA, Ayumu KANBE, Yuta YOKOBORI, Akari USHIMARU, Soma YOSHIZAWA, Yohei SHIRAKAMI, Ryosuke KIKUCHI

P-11-b-25 Borrelia burgdorferi detection in Iceland
Detection of Borrelia burgdorferi (s.l.) in Ixodes ricinus ticks collected in Iceland

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P-11-b-26 Avian Influenza screening in Iceland

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P-11-b-27 Vitamin-D status and metabolic risk markers in Icelandic youth
A longitudinal cohort study

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P-11-b-28 Data-driven management of outpatient blood collection crowding
Integrating AI prediction with clinical capability

Rina ICHIOKA[1], Hidekazu ISHIDA[1], Rin YOKOYAMA[2], Takahito ARAI[2], Naoyuki YOSHIKAWA[2], Makoto KURANO[2], Hiroyuki OKURA[1], Ryosuke KIKUCHI[1]
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P-11-b-29 Advancing Efficiency and Safety in RIA via Fully Automated Instruments

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P-11-b-30 MAP-Derived Compounds: Animal Studies to Human Pathological Insights
Translational Pathological Assessment of MAP-Derived Compounds from Animal Models to Human Health

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P-11-b-31 Unmasking Occult CKD via Selective Cystatin C Testing
An Interpretable Routine Data Model for Prioritized Detection Under Resource Constrains

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P-11-b-32 Roles and Duties of medical technologists in the Emergency Department
A Report on Task-Shifting Implementation

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P-11-b-33 ChA induces ROS-mediated apoptosis via HAS in HCC cells
Apoptotic effects of ChA via the ROS/HAS axis in HCC cells

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P-11-b-34 Occupation-specific burnout pathways among Korean healthcare workers
Moderated mediation through job satisfaction using Korea Veterans Health Service data

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P-11-b-35 Enhancing Clinical Laboratory Internship Training Through an Intelligent Learning System
Application to Sperm Counting and Morphological Analysis in Microscopic Examination

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P-11-b-36 The Ethics Game
Exploring Ethical Awareness Through Guided Group Reflection

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P-11-b-37 Menstrual blood stem cells in wound healing
Comparison of regeneration of stem cells derived from women with and without premenstrual syndrome

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P-11-b-38 Antrodia cinnamomea Inhibits Liver Fibrosis
Modulating HIF-1/2-TWIST-BMI1 Signaling and EMT in TGF-beta1 Induced Fibrosis

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P-11-b-39 Antrodia cinnamomea Extract Regulates EMT in Liver Fibrosis
HIF-1/2-TWIST-BMI1 Axis in Liver Fibrosis Reversal Mechanisms

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P-11-b-40 Reusable Strap System Reducing Phlebotomy Waste and Enhancing Safety
A governed reusable strap loan model improving safety and reducing phlebotomy waste

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P-11-b-41 Employer Branding in Generational Change
An Analysis of Expectations in Biomedical Analytics in Austria

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P-11-b-42 Automation of the decantation step in density gradient PBMC isolation
Comparative evaluation of PBMCs isolated by automated and manual decanting

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P-11-b-43 Basic Analytical Performance Evaluation of HISCL HIT IgG Assay Kit
Using Automated Blood Coagulation Analyzer CN-6500

Osamu Shibahara, Toru Mimura, Akiyo Kawamoto, Kiyoko Kohama, Kazuyasu Konko, Tasuku Sakayori, Akiko Hirai, Tatsuya Satomoto
Sysmex corporation

P-11-b-44 Patient Involvement in Research: From Strategy to Practice
Biomedical Laboratory Scientist Bridging Patients and Research Partnerships

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P-11-b-45 Barriers and Motivators for Research among Biomedical Laboratory Scientists
A Mixed-method Study in a Danish Pathology Department

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P-11-b-46 Intelligent A-E Tier Laboratory Inventory Platform: In-House Development

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P-11-b-47 The evolving role of Biomedical Laboratory Scientists in digital transformation
A new framework for competences and practice

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1 Polytechnic Univ. Coimbra, Coimbra Health School (ESTeSC), Coimbra, PT; H&TRC, ESTeSC, Coimbra, PT; iCBR CIMAGO, Univ. Coimbra, Coimbra, PT; CIBB, Univ. Coimbra, Coimbra, PT; EPBS, Brussels, BE; BioMedLab, Calvaria de Cima, PT
2 Pathology Lab, Inst. of Molecular Pathology and Immunology of Univ. Porto (Ipatimup), Porto, PT; Dept. of Pathological, Cytological and Thanatological Anatomy, School of Health, Polytechnic Inst. Porto, Porto, PT; BioMedLab, Calvaria de Cima, PT
3 Dept. of Pathology, Inst. Portugues de Oncologia de Lisboa Francisco Gentil, Lisboa, PT
4 Pathology Lab, Inst. of Molecular Pathology and Immunology of Univ. Porto (Ipatimup), Porto, PT; Dept. of Pathological, Cytological and Thanatological Anatomy, School of Health, Polytechnic Inst. Porto, Porto, PT
5 Dept. of Pathology, Champalimaud Found., Lisboa, PT; BioMedLab, Calvaria de Cima, PT
6 Polytechnic Univ. Coimbra, Coimbra Health School (ESTeSC), Coimbra, PT; H&TRC, ESTeSC, Coimbra, PT; iCBR CIMAGO, Univ. Coimbra, Coimbra, PT; Ctr. for Innovative Biomedicine and Biotechnology, Univ. Coimbra, Coimbra, PT; BioMedLab, Calvaria de Cima, PT

P-11-b-48 Reusable Straps Reduce Phlebotomy Waste and Improve Safety

CHUANCHI CHAN[1], Chih-Pei Lin[2]
1 Dept. of Laboratory Medicine, Taipei Tzu Chi Hosp., Taiwan
2 Taipei Tzu Chi Hospital

P-11-b-49 DENND1A rs2479106 Variant and PCOS Phenotypes in Filipinos

Jason Dominic. Rondina, John Angelo Corales, Sean Kenji Duenas, Princess Allysa Pacubas, Jonell Ponce, Darwin See
Univ. of Santo Tomas, Faculty of Pharmacy, Dept. of Medical Technology

P-11-b-50 Knowledge, Attitudes, and Perceptions of Medical Technologists Toward Laboratory AI
AI Adoption Among Medical Technologists in University-Affiliated Clinical Laboratories in Metro Manila

Janiah Ysabel Yee, Victoria Jane A. Saldua, Precious Gene C. Serna, Carl Yusef J. Tubig, Ayesha Renee A. Villanueva, Canellie P. Canlas-Ocsona, Clarenz Sarit M. Concepcion, Richmon R. Cuatico
University of Santo Tomas - Faculty of Pharmacy

P-11-b-51 An Innovative POCT Integration Strategy for Institution-Level Management

Mei-Hui Lee[1], Shu-Hua Lee[1], Hsueh-Hui Lee[1], Wen-Zhen Wang[2]
1 Department of Laboratory Medicine,Kuang Tien General Hospital,Taichung,Taiwan
2 Department of Information Technology,Kuang Tien General Hospital,Taichung,Taiwan

P-11-b-52 CAR-T Therapy Complication in lymphoma patients in Taiwan
Standardized Monitoring and Clinical Outcomes in 14 DLBCL Cases

SZU YING,YANG, Sz Ying Yang, Kuan Der Lee, Hui En Tzeng, Yu Hsuan Shih, Pi-Hua Chang
Taichung Veterans General Hospital

P-11-b-53 The Performance of Plasma Neurodegenerative Biomarkers in Taiwanese Screening population.
Using the ultrasensitive ImmunoMagnetic Reduction(IMR) method to provides real-world distribution data

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1 Center of Precision Medicine, Chi Mei Medical Center, Tainan City 710402, Taiwan
2 JW Diagnostics Inc. New Taipei City 235029, Taiwan

P-11-b-54 Exploration of Serum miRNA Associated with Early Fibrosis in MASH

Kana MATSUMOTO, Mitsuru CHIBA
Department of Bioscience and Laboratory Medicine, Graduate School of Health Sciences, Hirosaki University

P-11-b-55 From the Blood to the Brain
Development of Novel Human Brain Organoid-on-Chips from PBMCs of Thai Children

Asst.Prof. Tewarit Sarachana[1], Krittaroek Sangsuppamit[2], Timthong Dachkaew[2],
Parames Pensakul[2], Chanikan Bunsupa[2], Chaya Vetiwutajan[2], Salisa Jungvudklang[2]
1 Chulalongkorn Autism Research and Innovation Center of Excellence (ChulaACE), Faculty of Allied Health Science, Chulalongkorn University
2 The Bachelor of Science Program in Medical Technology, Faculty of Allied Health Sciences, Chulalongkorn University

P-11-b-56 Optimizing Outpatient Phlebotomy Through Precision Capacity Management
A data driven laboratory quality improvement project in a tertiary medical center

YUAN, LI-PING, LIU,YU-JIA, LIN,YI-FANG, HUANG,YU-TING, HSIEH,WAN-TING, TSAI, YIN-TAI
Department of Medical Laboratory, Taipei Medical University-Shuang Ho Hospital,Ministry of Health and Welfare, New taipei city, Taiwan

P-11-b-57 Post-Transcriptional Cyclin E Regulation by FIRdExon2 in ESCC

Mayuko Hashimoto[1], Kouichiro Okada[1], Takeshi Toyozumi[1], Sho Hirano[1], Yoshitaka Yamaguchi[2],
Kenji Kawasaki[3], Kazuyuki Matushita[3], Michihiro Maruyama[1]
1 Department of Frontier Surgery, Chiba University Graduate School of Medicine
2 Medical Technology and Sciences, IUHW
3 Division of Clinical Laboratory, Chiba University Hospital

P-11-b-58 Improvement of Laboratory Workflow Efficiency Using the Atellica Sealer

Natsuki UEMATSU, Katsuya HIROOKA, Yui TOYODA, Ayane SODEKAWA, Dai KOYANO,
Keita NISHIGUCHI, Shiori HASEGAWA, Hisanobu KOBATA

P-11-b-59 Two Clocks, one laboratory: Rethinking turnaround time

Anne Hancke
Department of Medical Biochemistry, Oslo University Hospital, Norway

P-11-b-60 AI-Assisted Automated Human Papillomavirus Report Generation System Improving Laboratory Reporting Efficiency Through Automated Workflow Integration

Liu Yu Jia

Department of Medical Laboratory, Taipei Medical University-Shuang Ho Hospital, Ministry of Health and Welfare, New Taipei City, Taiwan

P-11-b-61 Management Analysis of Hyper-Critical Laboratory Values A Patient-Centered Investigation into Clinical Timeliness and Safety Outcomes

Yi-Chang Tsai, Kuan-Chih Wu

Department of Medical Laboratory, Nantou Hospital, Ministry of Health and Welfare, Nantou County 540234, Taiwan

P-11-b-62 Prevalence of Hookworm Infection in Fecal Samples of Stray Dogs from a Public Pound and Selected Private Animal Welfare Organizations in Quezon City, Philippines

Reizhelle Eirsea P. Santos, Vivian G. Villegas, Gregorio Martin

University of Santo Tomas, Manila, Philippines

P-11-b-63 Building High-Reliability Laboratories: ISO 15189 vs CAP Accreditation Strategic Integration of Quality Governance in Multi-Tiered Healthcare Systems

Yu-Ling Huang, Chia-Ni Lin

Department of Laboratory Medicine, Linkou Chang Gung Memorial Hospital, Taoyuan, Taiwan

P-11-b-64 Evaluation of walk-in cool room control measures for auditing: compliance practicalities for the Australian Standard AS ISO 15189:2023 accredited medical laboratory

Dennis Mok[1], Naira Eloyan[2], Sabella Westcott[1], Karlah Norkunas[1], Rana Nabulsi[3], Sharfuddin Chowdhury[4], Mohd Nazil Salleh[5]

1 Faculty of Health, Southern Cross Univ., Australia
2 Armenian Medicinal Products Regulatory Authority, Armenia
3 Dubai Health, United Arab Emirates
4 Mater Misericordiae Univ. Hospital, Ireland
5 Univ. College of MAIWP International, Malaysia

P-11-b-65 Repurposing Furosemide for Acute Myeloid Leukemia Treatment Evidence from Clinical Observations and In Vitro Molecular Mechanisms

Ju-Shan Yu[1], Ming-Chang Hsieh[2], Fang-Hsuan Chang[3], Yu-Wei Chang[3]

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2 Department of Clinical Laboratory, Chung Shan Medical University Hospital
3 Department of Medical Laboratory and Biotechnology, Chung Shan Medical University

P-11-b-66 Misidentification in Leukocyte Differential Counts -Analysis Using Logistic Mixed-Effects Modeling-

Yui NAMIKAWA, Mareki OOTSUJI, Tomomi SHIMIZU, Yo KODERA

Faculty of Biomedical Engineering, Toin University of Yokohama, Kanagawa, Japan

P-11-b-67 Effects of Dietary NaCl Levels on Experimental Ulcerative Colitis Severity

Kaito Yamamoto, Yugo Taoka, Kohki Okada

Kyoto Tachibana University graduate school of health sciences

P-11-b-68 Evaluating a Machine Learning Model for Patient Specimen Mix-ups

Kaede SUGIMURA[1], Shigeharu OKADA[2], Yukinari OOTSUKA[1], Chizuka KUWABARA[1], Kanae KUMAGAI[1]

1 Koshigaya Municipal Hospital
2 Saitama Prefectural University

P-11-b-70 Characterization of a novel factor X variant, c.163dup

Marie Skogstad Le[1], Malu Hestdalen[2], Marit Hellum[1], Marit Sletten[3], Nina Iversen[3], Hilde T. Hilmarsen[4], Geir Tjonnfjord[2], Carola E Henriksson[5]

1 Dept. of Medical Biochemistry, Oslo University Hospital HF, Oslo, Norway
2 Dept. of Hematology, University of Oslo, Oslo, Norway
3 Dept. of Medical Genetics, Oslo University Hospital HF and University of Oslo, Oslo, Norway
4 Dept. of Medical Genetics, Telemark Hospital Trust, Skien, Norway.
5 Institute of Clinical Medicine, University of Oslo, Oslo, Norway

P-11-b-71 Operational Evaluation of Blood Gas Analyzers Using Analytics

Yuki Nouchi, Akinori Nagata, Mina Saito, Kei Sato, Noriyasu Niizeki, Keita Yamashita

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P-11-b-72 Identification of ISO 35001:2019 requirements for medical laboratory internal auditing

Dennis Mok[1], Naira Eloyan[2], Janelle Christoff-Tzazaroff[3], Sabella Westcott[1], Rana Nabulsi[4], Sharfuddin Chowdhury[5], Karlah Norkunas[1]

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P-11-b-73 Evaluation of the Effects of Pin1 Inhibition in ESCC

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P-11-b-74 Identification of ISO 15189:2022 requirements for medical laboratory internal auditing

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2 Armenian Medicinal Products Regulatory Authority, Armenia
3 Dubai Health, United Arab Emirates
4 Mater Misericordiae Univ. Hospital, Ireland
5 Univ. College of MAIWP International, Malaysia

P-11-b-75 Automated LOINC Mapping System Combining LLM and Official API

Szu-Chun Chen, Tz-Jain Ni

An Nan Hospital, China Medical University, Tainan, Taiwan

P-11-b-76 Diagnostic Support System for Pre-Chemotherapy Hematologic Toxicities Automated Detection and Multidisciplinary Notification of Severe Cytopenia

Yousuke SASAKI, Ken SUZUKI, Akira ISHIHARA, Akito IKUMA, Keiko MIYAZAKI, Kentarou NAODA

Department of Clinical Laboratory, Seirei Hamamatsu General Hospital

P-11-b-77 Effect of Water Intake on Venous Dilation with Tourniquet Application

Ibuki Tamura[1], Ibuki Tamura[1], Daisuke SAKONISHI[2], Atsushi SHUKURI[2], Yuriko KURIHARA[1]
1 Graduate School of Clinical Technology ,Tokyo University of Technology
2 School of Health Sciences, Tokyo University of Technology

P-11-b-78 CRP and Leukocyte Correlations After COVID-19 Infection

CHUN KUN LIU, Chuan Po Lee, Yi Yun Chen, Hsiang Ling Ho
Department of Pathology and Laboratory Medicine, Taipei Veterans General Hospital, Taipei City, Taiwan

P-11-b-79 Optimizing Ward Non-Urgent Testing Time via PDCA and ESG

Ching-Mei Cheng, Hsieh Ya-nien, Wei-Chi Tsai, Yi-Ping Chen, Hsiu-hua Huang, Chiung-Ju Chen, Ching-Chao Liang,
Department of Laboratory Medicine Kaohsiung Municipal Siaogang Hospital, Kaohsiung Medical University

P-11-b-80 The Spatiotemporal and Geospatial Evolution of Cholera in the Philippines
A 12-Year Visual Analysis of Endemic Footprints (2014 - 2025)

Nathaniel Magtibay, Antonio Miguel Agtay, Trisha Theryze Gullunan, Lyra Angela Labog, Angel Kristel Anne Palapus, Julius Eleazar Jose
Department of Medical Technology, Faculty of Pharmacy, University of Santo Tomas

P-11-b-81 ISO/IEC 17024 Accreditation for Medical Lab Specialists
Taiwan's Experience in Competence Certification for Medical Technologists

YU YA-YEN[1], Lee Ming-Shih[2], Tsao Kuo-Chein[3], Sung Yu-Ling[4]
1 Taiwan Society of Laboratory Medicine, Changhua Hospital, MOHW
2 Taiwan Society of Laboratory Medicine, Chung Shan Medical University
3 Taiwan Society of Laboratory Medicine, Linkou Chang Gung Memorial Hospital
4 Taiwan Society of Laboratory Medicine

P-11-b-82 Improving TSH Turnaround Time
Implementation of an In-House CMIA System in Critical Care

TSAI YU CHEN
Dept. of Clinical Pathology, Chi Mei Hospital Liouying, Taiwan

P-11-b-83 Expanding the Role of an Independent Clinical Laboratory
Linking Clinical Practice, Research, and Social Implementation

Asami NAITO, Tomokazu NAGAI, Yukihiro KAI, Eiju MIYAMOTO, Aritoshi MIYAZAKI
Tsukuba-i-Laboratory LLP

P-11-b-84 Seasonal Variation in Clinical Laboratory Tests
A Comprehensive Evaluation Using 25 Million Measurements

Kousuke AMANO, Mihana BINGO, Masami INAYOSHI, Wakiko NOGUCHI
Okazaki City Hospital, Department of Clinical Laboratory, Okazaki, Japan

P-11-b-85 Identification of GEN Checklist requirements for medical laboratory internal auditing

Dennis Mok[1], Rana Nabulsi[2], Naira Eloyan[3], Sharfuddin Chowdhury[4], Karlah Norkunas[1], Mohd Nazil Salleh[5]
1 Faculty of Health, Southern Cross Univ., Australia
2 Dubai Health, United Arab Emirates
3 Armenian Medicinal Products Regulatory Authority, Armenia
4 Mater Misericordiae Univ. Hospital, Ireland
5 Univ. College of MAIWP International Malaysia

P-11-b-86 Comparison of the Laboratory Results from Four Missions of JDR
Experience from Water Floods in the Pakistan, Earthquake in Nepal, Turkey , and Myanmar

Chitoshi SATO, Noriko WATANABE, Maiko OOTA, Tomokazu NAJIMA

P-11-b-87 Evaluation of Serum IgG Responses to *Cutibacterium acnes* Phylotypes

Kaoru Furukawa[1], Daisuke Sakonishi[2], Ibuki Tamura[1], Yuriko Kurihara[1]
1 Graduate School of Clinical Technology ,Tokyo University of Technology
2 School of Health Sciences, Tokyo University of Technology

P-11-b-88 Test this si I dont have to test you
A visibility camgaign for biomedical laboratory scientist

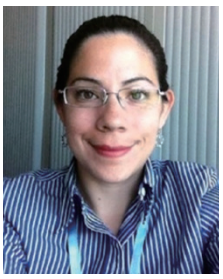
Heidi Andersen, Mari Tjernsmo Melby, Heidi Andersen
The norwegian institute of biomedical science

P-11-b-89 Simplifying On-Call and Standby Rosters with Commercial AI Tools
An operational workflow analysis of automated scheduling and its impact on staff management.

Rika SUZUKI, Saori ABE
South Miyagi Medical Center

P-11-b-90 Evaluation of the OC-SENSOR R70

Yumiko SUZUKI, Kouta OGINASA, Junko NAGAI, Kiyoshi KAMIYAMA
Department of Clinical Laboratory, Medical Diagnostic Center of URAWA Medical Association



Building Bridges: Biomedical Laboratory Science Connecting People, Innovation and Global Health

Ana Aceves Capri

Medical Devices and Assistive Technology team. Department of Medicines and Health Products Policies and Standards. World Health Organization.

This presentation explores how biomedical laboratory science is evolving in response to rapid technological innovation and changing healthcare needs. Traditionally, laboratory professionals have worked behind the scenes, generating reliable diagnostic results through centralized laboratory processes. While this work has been fundamental to diagnosis, treatment decisions and public health responses, the profession is now facing a period of significant transformation.

Key innovation trends reshaping laboratory medicine include decentralized and point-of-care testing, multiplex diagnostics, artificial intelligence (AI)-enabled diagnostics, digital data integration, precision medicine, advanced molecular platforms, automation and global health-oriented diagnostic solutions. These developments are changing both where and how diagnostic services are delivered.

The presentation highlights a strategic risk: adaptation lag. Traditional competencies such as microscopy, instrument operation and routine laboratory procedures are no longer sufficient on their own. Future laboratory professionals will need skills in AI oversight, data analytics, informatics, genomics, bioinformatics, systems thinking and algorithm validation. The greatest challenge is not whether laboratories will continue to need people, but whether the workforce can successfully transition from producing test results to managing, interpreting and governing increasingly automated and decentralized diagnostic systems.

Rather than viewing automation and AI as threats, the presentation frames them as opportunities. While routine tasks may become increasingly automated, healthcare systems will continue to depend on professionals who can ensure quality, patient safety, clinical relevance and responsible use of technology. The future laboratory scientist will act as a manager of diagnostic systems, supervising automated platforms, monitoring AI performance, managing point-of-care testing networks, investigating anomalies, interpreting data and supporting clinical decision-making.

A central message is that the profession's mission remains unchanged despite evolving tools. The future of diagnostics will be determined not only by technological progress but also by the ability to prepare a workforce capable of using these technologies responsibly and equitably. Laboratory professionals are encouraged to embrace continuous learning, digital technologies and leadership roles, while professional societies should modernize education and training to prepare workers for future healthcare demands.

The presentation concludes by emphasizing the global health dimension of diagnostics. For millions of people, particularly those living in rural areas, conflict zones, refugee settings or underserved communities, the primary challenge is not innovation but access. Diagnostic equity is presented as a core responsibility of laboratory professionals. Success should be measured not only by the accuracy of tests but also by whether reliable diagnostic services reach those who need them most. Laboratory professionals are called upon to become advocates for both quality and access, ensuring that diagnostics contribute to treatment, surveillance and health equity for all.

CV

Dr. Ana Aceves Capri is a Technical Officer at the World Health Organization (WHO) in Geneva, Switzerland.

Area of Work:

She focuses on improving access to essential diagnostic tests in resource-limited settings, with the aim of trengthening laboratory capacity and ensuring equitable access to diagnostics worldwide.

Expertise:

Dr. Aceves Capri has a solid background in laboratory medicine and public health.

Her work combines technical expertise with a strong emphasis on quality, safety, and sustainability in health systems.

Other Activities:

In her role at WHO, she has presented and facilitated discussions on topics such as laboratory errors, diagnostic and patient safety, and sustainable laboratory practices. She also has experience managing blood donation centers and infectious disease laboratories, as well as implementing quality management systems – as reflected in her LinkedIn profile.

Affiliation:

Dr. Aceves Capri serves as the IFBLS-designated Technical Officer for WHO.

Regarding emerging infectious diseases such as COVID-19

Shigeru Omi
Chairman, Japan Anti-Tuberculosis Association

Since the Spanish influenza of 1918, which caused unprecedented global devastation, pandemics such as the Asian flu, Hong Kong flu, and SARS have continued to emerge.
This presentation will begin by exploring the background conditions that have contributed to the recurrent occurrence of pandemics.
It will then address how Japan responded to the COVID-19 pandemic, which produced the greatest mortality since the Spanish influenza, and will evaluate the effectiveness of these societal responses.

CV

Nationality: Japanese
Education

1987-1989	PhD in Molecular Biology of Hepatitis B Virus, Division of Immunology, Jichi Medical School, Japan
1972-1978	M.D. Jichi Medical School, Japan
1967-1968	On a scholarship from American Field Service (AFS), graduated from Potsdam Central High School, New York

PROFESSIONAL EXPERIENCE

2022- present	Chairman, Board of Directors Japan Anti-Tuberculosis Association (JATA)
2014-2022	President of JAPAN Community Health care Organization (JCHO)
2013-	WHO Member of Executive Board
2013 May	President, the 66th World Health Assembly
2009-	Regional Director Emeritus for WHO Western Pacific Region
1999-2009	WHO Regional Director for the Western Pacific
1990-1998	Director, Division of Communicable Disease Prevention and Control, WHO Regional Office for the Western Pacific
1987-1989	Researcher, Division of Immunology, Jichi Medical School, Japan

MEMBERSHIPS, AWARDS AND ACHIEVEMENTS

2020	Chairman of Subcommittee on Novel Coronavirus Disease Control Deputy Chair of the New Coronavirus Infectious Disease Control Experts Conference New Coronavirus Infection Control Advisory Board Member
2016	A member of the Global Health Crises Task Force <Request from UN Secretary General Mr.BAN Ki-moon>
2015	A member of the IOG (International Oversight Group) for Multi-Stakeholder Initiative for Creating an Operational Global Health Risk Management Framework for the 21st Century
2013	Chairman of National Advisory Group for Infectious Disease Control in Japan
2009	Polio Eradication Champion Award provided by the Rotary International
2006	Executive Editor, SARS: How a Global Epidemic Was Stopped, a 300-page book on the 2002-2003 outbreak of severe acute respiratory syndrome
2004	Honorary Member of Keio University, Japan
2002	Honorary Fellow, Hong Kong College of Community Medicine
2002	Executive Editor, Polio Eradication in the Western Pacific Region, an account of the successful campaign against poliomyelitis in the Western Pacific
2001	37th Kojima Award, Japan, for outstanding achievement and leadership in the eradication of poliomyelitis in the Western Pacific

Advancing Global Laboratory Practice Through Examination Excellence and Data-Driven Insights: ASCP BOC's Commitment to Professionals and Patients Worldwide

Amy Spiczka
DHSc, MS, HTL(ASCP)^{CM},SCT^{CM},MB^{CM}, CPHQ
Executive Director, Board of Certification, American Society for Clinical Pathology

The American Society for Clinical Pathology Board of Certification (ASCP BOC) advances laboratory medicine, pathology, and adjacent specialties worldwide through rigorous professional credentialing, international collaboration, and data-driven innovation. Guided by its mission to provide excellence in certification on behalf of patients worldwide, the ASCP BOC supports laboratory professionals through globally recognized credentials that validate knowledge and applied skills, strengthen workforce capacity, and contribute to improved patient care.

This presentation highlights how examination excellence and data derivatives are transforming credentialing and workforce advancement globally. ASCP BOC examinations are built on practice analyses, psychometric rigor, continuous content review, and internationally recognized quality standards, ensuring fair, valid, and defensible assessments of professional outcomes. The ASCP BOC further leverages robust data governance, analytics, and publicly available credentialing insights to identify workforce trends, optimize operational performance, and demonstrate the value of ASCP BOC credentialing.

Through engagement with international partners, including IFBLS, JAMT, along with regional advisory boards, the ASCP BOC continues to promote global standards, professional trajectories, and patient-centered outcomes. Together, examination excellence and data-informed insights create a sustainable framework for empowering laboratory professionals and other experts who are partnering with the ASCP BOC to improve patient care worldwide.

CV

● **Professional Experience**
March 2022 – Current
Executive Director, Board of Certification
American Society for Clinical Pathology
2018 – 2022
Senior Director, Quality and Patient Safety
American Society for Clinical Pathology
2010 – 2018
Operations Manager, Division of Anatomic Pathology
Mayo Clinic Arizona
2005 – 2010
Supervisor, Division of Anatomic Pathology
Program Director, Histotechnology Program
Education Coordinator, Cytology Program
Mayo Clinic, Rochester, Minnesota

● **Highest Education and Specialized Field**
Period: (Graduated 2024)
Degree: Doctorate in Health Sciences (DHSc)
School Name: A.T. Still University
Specialized Field: Data Science
Major Field: Leadership and Organizational Behavior
Country: U.S.A.

● **Honor and Awards**
Mayo School of Health Sciences (MSHS)
- Recognition for Outstanding Alumni Award | 1999, 2000
- Outstanding Educator Award | 2005
- Cytotechnology Program, Mentor Award | 2008
- Clinical Educator Award | 2013

American Society for Cytopathology (ASC)
- Future of the Profession Award | 2008
- Cytotechnologist Award for Outstanding Achievement | 2015
- Quality Improvement in Cytology Award | 2020

Journal of Histotechnology Publication
- Editor's Award for "Multimedia Tools- Creating a Connection between Histology and Education" National Society of Histotechnology Symposium | 2010

American Society for Clinical Pathology (ASCP)
- Regional Member Award | 2010
- Best Oral presentation, "Improved Revised Reporting in Anatomic Pathology and Cytopathology" National Meeting | 2013
- Best Healthcare Diversity, Equity, and Inclusion Poster, Opportunities for Promoting ASCPi Credentials in Current & Emerging International Markets | 2023

Mayo School of Continuous Professional Development
- Special Recognition for the Outstanding Quality Improvement Project for the Dermatopathology Specimen Labeling Automation Project | 2013
- Top Honors for Outstanding Quality Improvement Project | 2014

Quality Assurance Framework for Molecular Genetic Testing: International Standards and Risk Management for Laboratory Developed Tests

Hayato Miyachi

Professor, Department of Clinical Laboratory Sciences, Nitobe Bunka College

In FY2022, a research group commissioned by the Ministry of Health, Labour and Welfare (MHLW) conducted a study to establish quality assurance standards for molecular genetic testing in Japan. The study highlighted the increasing importance of advanced diagnostic technologies, including laboratory-developed tests (LDTs), in modern clinical practice. In particular, the research emphasized the need to ensure the quality and reliability of testing services through internationally recognized standards. A key recommendation of the study was the promotion of third-party accreditation for medical laboratories performing molecular genetic testing. Compliance with ISO 15189 (Medical laboratories – Requirements for quality and competence) was recognized as an essential framework for ensuring the competence of laboratories and the reliability of test results. Following the revision of ISO 15189 in December 2022, the Japanese Industrial Standards (JIS) Drafting Committee developed the national standard JIS Q 15189, which was officially issued in 2026. This standard aims to enhance the quality of medical laboratory testing by improving mutual understanding among stakeholders, ensuring the comparability and reliability of laboratory services, and ultimately supporting safe and effective patient care. The revised ISO 15189 places greater emphasis on risk-based thinking in laboratory management. In this context, the application of complementary international standards, such as ISO 22367 (Application of risk management to medical laboratories) and ISO 5649 (Concepts and specifications for the design, development, implementation, and use of laboratory-developed tests), is expected to strengthen risk management practices and improve the overall competence of laboratories performing LDTs. Establishing operational frameworks based on these standards, under governmental leadership, is considered essential for ensuring the quality, efficacy, and safety of LDTs in clinical practice. In 2025, an MHLW research group issued a guidance document outlining requirements for quality assurance when implementing LDTs. In this guidance, LDTs are classified according to their technical complexity into simple and standard LDTs. The recommendations include the appointment of a person responsible for ensuring quality, training of laboratory personnel in quality management and risk management, and the establishment and documentation of standard operating procedures, including disclosure of the assay performance evaluation. The guidance also recommends the regular implementation of appropriate statistical internal quality control and participation in external quality assessment programs or alternative approaches. In addition, third-party accreditation is required for standard LDTs in order to provide an objective evaluation of laboratory quality management systems, while for simple LDTs it is recommended as a best-effort requirement. Risk management practices are expected to include self-conformity assessment based on JIS Q 15189 and ISO 22367, with public disclosure of the results on conformity assessment. Because LDTs often involve highly advanced technologies, some tests would require additional regulatory considerations. In such cases, further requirements would be necessary to objectively evaluate reliability, including the effectiveness and safety of reagents and instruments, as well as the appropriateness of production and quality management systems.

CV

● **Professional Experience**

1981
Resident, Keio Univ. Hospital
1984-1986
Clin and Res Fellow, Hematology, Keio. Univ. Sch. Med
1987-1989
Visting Scientist, Medical Oncology, City of Hope National Medical Center, USA
2004-2022
Professor, Laboratory Med., Tokai. Univ. Sch. Med
2022-Present
Professor, Clib. Lab. Science, Nitobe Bunka Coll.

● **Highest Education and Specialized Field**

Period: 1981, 1990
Degree: MD, PhD
School Name: Keio Univ. School of Medicine
Specialized Field: Molecular Genetics, Hematology and Oncology
Major Field: Laboratory Medicine
Country: Japan

● **Honor and Awards**

Bergmeyer-Kawai Awards (1996)
Nozomu Kosakai Awards (2005)
Roche Infectious Disease Award (2024)

Disaster response supporting system by JAMT

Kentaro Naoda
Seirei Hamamatsu General Hospital (Japan)

Large-scale disasters require coordinated responses in laboratory medicine, including maintaining healthcare services in affected areas, supporting medical activities in evacuation shelters, responding to infectious disease threats, and coordinating with relevant organizations. To address these challenges, the Japanese Association of Medical Technologists (JAMT) has established a disaster response framework within Japan's national disaster medical system. This presentation describes JAMT's role in disaster response, its support activities, collaborative mechanisms with prefectural associations, and current initiatives in workforce development and deployment coordination.

Based on lessons learned from the 2016 Kumamoto Earthquake, JAMT dispatched a total of 554 biomedical laboratory scientists from across Japan following the 2024 Noto Peninsula Earthquake. Their activities included deep vein thrombosis (DVT)-related testing in evacuation shelters, support for maintaining laboratory services at designated disaster hospitals, liaison assignments within prefectural health and welfare coordination headquarters, and assistance with the supply of laboratory equipment and reagents. A notable feature of this response was the simultaneous provision of support to hospitals, evacuation shelters, and disaster coordination headquarters.

Following these experiences, JAMT revised its disaster response regulations and operational manuals and has promoted formal agreements with prefectural governments. JAMT has also introduced video-on-demand (VOD) training programs to standardize the competencies of deployable personnel and established a disaster support registration system through its membership platform. As of March 2026, agreements had been concluded with governmental authorities in 21 prefectures.

Effective laboratory support during disasters requires not only technical expertise but also systems for information sharing, resource management, multidisciplinary collaboration, and operational coordination. This presentation discusses future challenges in strengthening disaster preparedness within the biomedical laboratory profession, including clarifying roles across disaster phases, standardizing collaborative procedures, fostering routine partnerships with governmental and related organizations, and establishing a common framework for workforce development.

CV

● **Professional Experience**
1996–2013
Medical Technologist, Clinical Laboratory
Seirei Mikatahara General Hospital, Japan
2013–2015
Chief Medical Technologist, Clinical Laboratory
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IFBLS-A professional framework towards increased knowledge, advancement and visibility of the profession

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The presentation will give an overview of the International Federation of Biomedical Laboratory Science (IFBLS) initiatives aimed at strengthening the professions advancements and establish a unified professional framework for biomedical laboratory scientists (BLS). The talk will highlight IFBLS structure, governance, and strategic plan for 2024–2028, emphasizing efforts to enhance education, professional development, and international collaboration. Central to these initiatives are the Britta Karlsson Legacy, which facilitate continuous professional development through educational webinars and advancement programs, particularly in low- and middle-income countries. The revision of IFBLS guidelines for core competence and the Code of Ethics underscores the federation's commitment to maintaining professional standards amid evolving scientific and technological contexts, including artificial intelligence and sustainability. Furthermore, IFBLS is actively pursuing the reclassification of BLS within the International Standard Classification of Occupations (ISCO), advocating recognition of biomedical laboratory scientists as health professionals. Collaboration with the World Health Organization (WHO) forms another cornerstone of IFBLS activities, notably in advancing workforce capacity, diagnostic accessibility, and sustainable laboratory practices through engagement with WHO initiatives such as the Essential Diagnostics List (EDL) and the Global Diagnostics Coalition. This presentation concludes by underlining the role of IFBLS congresses—as the ongoing 36th World Congress in Japan—in fostering global exchange, professional visibility, and continuous advancement of biomedical laboratory science.

IFBLS Services to Members International Directory of Biomedical Laboratory Science Education (IDBLSE) and IFBLS Professional Code of Ethics

Marie Nora Roald

Member at Large of IFBLS (Norway)
Laboratory Manager, Department of Medical Biochemistry and Blood Bank, Helse Møre and Romsdal Hospital Trust

International collaboration and shared professional standards are important for Biomedical Laboratory Scientists (BLS). As healthcare systems become more interconnected, there is growing need for tools that support transparency in education, professional mobility, ethical practice, and international cooperation within the profession.

This presentation will introduce two important IFBLS initiatives available to members and the wider international BLS community: the International Directory of Biomedical Laboratory Science Education (IDBLSE) and the IFBLS Professional Code of Ethics.

The IDBLSE was established to provide accessible information about BLS education programs worldwide. By collecting and sharing information about educational pathways, professional qualifications, and national systems, the directory supports international understanding of the profession and may contribute to student exchange, workforce mobility, collaboration between educational institutions, and recognition of qualifications across borders. The directory can be used by educators, students, employers, professional associations, and individual Biomedical Laboratory Scientists.

The IFBLS Professional Code of Ethics represents a shared international framework for professional conduct and responsibility in Biomedical Laboratory Science. The code addresses core principles such as patient safety, professional competence, confidentiality, integrity, equality, and responsibility to society. In a time of rapid technological development, increasing international mobility, and evolving healthcare challenges, common ethical principles may help strengthen professional identity and public trust across different healthcare systems and cultural contexts.

The presentation will also briefly reflect on the collaborative international work behind maintaining and developing these resources, highlighting how contributions from IFBLS members and national associations help ensure that the tools remain relevant and useful for the profession globally.

The aim of the presentation is to demonstrate how shared educational and ethical resources can strengthen the international BLS community, support professional development, and contribute to high-quality laboratory services for patients and society.

ISCO Classification and Biomedical Laboratory Scientists

Marie Culliton
Past-President of IFBLS (Ireland)
MSc, MBA, FACSLM

ISCO is the classification system of the International Labour Office (ILO) to provide labour statistics for countries.
It is a tool for organizing jobs into a clearly defined set of groups according to the tasks and duties undertaken. It aims to be a basis for the international reporting, comparison and exchange of statistical and administrative data about occupations
It consists of 10 major groups, based on their similarity in terms of the skill level and skill specialization required for the jobs with a range of sub major and minor groups.
The latest classification dates back to 2007.

This profession has changed and developed significantly since that time and our current classification does not reflect our current knowledge, skills and competence.

IFBLS is working to achieve recategorization of biomedical laboratory scientists as a Professional Group in the next iteration of this Classification in 2028.
This presentation will update on the progress to date including a meeting with a Senior ILO Statistician to clarify anomalies.

SY01-1
A New Stage in Thrombosis and Hemostasis Testing
The Future of Thrombosis and Hemostasis Testing with Artificial Intelligence

Naoki Tokunaga
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Thrombosis and hemostasis testing is now entering a new era. In recent years, technological innovations utilizing Artificial Intelligence (AI) have also advanced in the field of laboratory medicine.

Although no AI-based applications in thrombosis and hemostasis testing have yet been clinically implemented in Japan, various studies have been conducted at the research level. These include monitoring of patients receiving warfarin therapy, prediction of bleeding and thrombotic events and disseminated intravascular coagulation (DIC), and more recently, disease classification and anticoagulant identification using Clot Waveform Analysis (CWA). Among them, AI-based CWA (CWA-AI) has recently emerged as one of the most promising candidates for clinical implementation.

CWA is a tool that evaluates the rate of fibrin formation as well as quantitative and qualitative information on coagulation by analyzing the optical changes associated with fibrin formation (coagulation reaction waveforms) obtained during automated coagulation assays such as prothrombin time (PT) and activated partial thromboplastin time (APTT). Its usefulness as a comprehensive coagulation function assay has long been recognized, and it has been applied in a variety of clinical settings, including hemophilia, DIC, disease classification, evaluation of anticoagulant effects, and assessment of bleeding and thrombotic tendencies. In recent years, studies of CWA-AI using machine-learning models based on pattern-recognition techniques and neural-network models for disease classification have been reported, and the field of CWA continues to advance rapidly. Although several challenges remain before CWA-AI can be clinically implemented, including evidence generation, standardization, and collaboration among academia, industry, and government, efforts toward standardization and evidence generation are currently being promoted by several academic societies, including the Japanese Society on Thrombosis and Hemostasis.

In this session, I will introduce the clinical utility of CWA and current topics in AI-based thrombosis and hemostasis research, and discuss the future of thrombosis and hemostasis testing.

SY01-2
Seeing Before Sequencing: Early AML Treatment Morphology and flow cytometry as rapid surrogates for AML decision-making

Hui-Ling Chen, Li-Fong Hong, Yi-Chun Kuo, Chia-Yi Hou
Chi Mei Medical Center, Liouying

Background:
Rapid risk stratification in acute myeloid leukemia (AML) is critical for timely therapeutic decisions, yet next-generation sequencing (NGS) often requires several days. Cup-like blast nuclei (CLB) morphology and its associated immunophenotype have been linked to NPM1-mutated AML, but their role in guiding immediate treatment remains underexplored.
Methods:
We describe a 61-year-old female presenting with AML (WBC 29,300/μL; blasts 81.5%). Peripheral blood smear morphology and flow cytometric immunophenotyping were evaluated prior to NGS analysis.
Results:
Morphological examination revealed prominent CLBs with nuclear invaginations. Flow cytometry demonstrated an MPO+/CD33+/CD34–/HLA-DR– immunophenotype, strongly suggestive of NPM1-mutated AML. Based on these early findings, targeted therapy with venetoclax and azacitidine was initiated prior to molecular confirmation. Subsequent NGS identified mutations in NPM1 (VAF 48.78%), FLT3-ITD (VAF 88%), IDH1, and DNMT3A. The patient achieved complete remission within one month, supporting the clinical validity of early morphology-immunophenotype correlation for therapeutic decision-making.
Conclusion:
This case highlights the diagnostic and clinical value of integrating CLB morphology with immunophenotypic findings as a rapid surrogate marker for NPM1-mutated AML. Early recognition enabled prompt treatment initiation several days before NGS confirmation, potentially improving patient outcomes. This approach may help bridge diagnostic delays in settings where immediate molecular testing is unavailable and provides important educational value for laboratory professionals in recognizing morphology–immunophenotype correlations in AML.

SY01-3
The *CALR* mutation in myeloproliferative neoplasms patients: a single institution experience

FRIKHA
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Background: Myeloproliferative neoplasms (MPNs) are hematological disorders characterized by abnormal production of myeloid cells due to genetic mutations. Somatic mutations in the Calreticulin (CALR) gene are one of the most driver mutation, with a relevant heterogeneity in frequency worldwide.
Aims: To assess the prevalence of CALR mutation in Southern Tunisian patients with JAK2 negative myeloproliferative neoplasms (MPN).
Methods: A seven-year retrospective study was carried out at the Hospital University of Sfax, south of Tunisia, including all JAK2 negative MPN patients. The genomic DNA of patients was isolated from peripheral blood samples. A Sanger sequencing was performed using a high-fidelity DNA polymerase to identify the somatic mutations of CALR.
Results: Sixty-eight patients with JAK2 negative MPN were enrolled. The median age was 50 years, and the sex ratio M/F was 0.3. mutational frequencies were 19.2% (13 /68). CALR mutated patients harbor one of only two mutation variants: type 1, a 52-bp deletion (p.L367fs*46) and type 2, a 5-bp TTGTC insertion (p.K385fs*47) in 62% and 38% respectively.
Summary/Conclusion: Our finding highlights that this driver mutation is less common in southern Tunisia unless it is an important marker for the diagnosis of JAK2-negative MPN. A larger study with genetic screening of other mutations is mandatory to elucidate the genetic landscape of this subset of MPN and specific individual disease outcomes.

SY01-4
p53 Expression by IHC and Cytogenetic-Morphological Findings in MDS

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Background: Myelodysplastic neoplasms (MDS) are clonal hematopoietic stem cell disorders characterized by morphological dysplasia in the bone marrow. Morphological evaluation plays a central role in diagnosis and classification. TP53 (tumor protein p53) is a well-known tumor suppressor gene, and its genetic alterations have been reported to be associated with poor prognostic subgroups in MDS. Although detection of TP53 mutations requires molecular genetic analysis, immunohistochemical (IHC) assessment of p53 protein expression is widely used as a surrogate marker. However, the relationship between p53 expression assessed by IHC, cytogenetic abnormalities, and lineage-specific morphological dysplasia remains unclear.
Objectives: This study aimed to evaluate the association of p53 expression patterns assessed by IHC with cytogenetic abnormalities and morphological dysplasia in patients with MDS.
Methods: We retrospectively analyzed 83 patients diagnosed with MDS at our institution between January 2020 and December 2025. Dysplastic features in erythroid, granulocytic, and megakaryocytic lineages were classified based on their specificity for MDS. p53 expression was categorized as strong, moderate, or negative/weak based on the distribution pattern and proportion of p53-positive cells. Associations were analyzed using the chi-square or Fisher's exact test, and ordered trends across the three p53 categories were evaluated using the Jonckheere–Terpstra and Cochran–Armitage trend tests.
Results: Strong p53 expression was significantly associated with a complex karyotype (>3 abnormalities) ($p < 0.01$). Strong p53 expression was more frequent in the poor prognostic group and less frequent in the favorable group ($p < 0.05$). No significant association was observed between strong p53 expression and dysplasia in granulocytic or megakaryocytic lineages. In contrast, strong p53 expression was significantly associated with greater erythroid dysplasia ($p < 0.05$).
Conclusions: Strong p53 expression assessed by IHC is associated with advanced cytogenetic abnormalities and poor prognosis in MDS, and shows a selective association with erythroid dysplasia.

SY01-5
Data-Derived D-dimer Cutoffs Corresponding to FDP Categories in the JAAM-2 DIC Criteria
A Large Real-World Analysis

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【Background】
The Japanese Association for Acute Medicine (JAAM) criteria are widely used for the early diagnosis of disseminated intravascular coagulation (DIC). The recently proposed JAAM-2 criteria retain fibrin-related markers while simplifying the original scoring system. Although either fibrin/fibrinogen degradation products (FDP) or D-dimer (DD) can be used, reagent-specific conversion values are required when DD is used. Because DD results vary among assays and information on the assay or reagent used is often unavailable, practical DD cutoffs corresponding to the established FDP categories are needed.
【Objective】
To derive DD cutoffs corresponding to the JAAM FDP thresholds and evaluate their agreement with FDP-based scoring.
【Methods】
We retrospectively analyzed 35,370 adults admitted to acute-care hospitals between 2014 and 2023 using a database provided by JMDCInc. Patients with concurrent FDP and DD measurements early after admission were included. FDP was categorized as <10, 10–<25, and ≥25 μg/mL. ROC analysis was used to derive DD cutoffs corresponding to FDP thresholds of 10 and 25 μg/mL. The derived cutoffs were compared with the ISTH-proposed DD thresholds of 3/7 μg/mL and with 5/10 μg/mL, rounded values selected for potential clinical implementation.
【Results】
DD cutoffs of 4.5 μg/mL (AUC 0.975) and 9.7 μg/mL (AUC 0.985) were identified for FDP thresholds of 10 and 25 μg/mL, respectively. Complete agreement rates with the FDP categories were 73.2%, 85.5%, and 86.1% using DD cutoffs of 3/7, 4.5/9.7, and 5/10 μg/mL, respectively. The corresponding overclassification rates were 25.6%, 10.3%, and 8.2%, and linear weighted kappa values were 0.680, 0.812, and 0.817. At the FDP threshold of 10 μg/mL, 4.5 μg/mL provided a better balance between sensitivity and specificity than 3 or 5 μg/mL, whereas 9.7 and 10 μg/mL showed similar performance at the FDP threshold of 25 μg/mL.
【Conclusion】
DD cutoffs of 4.5/9.7 μg/mL were derived as candidate values corresponding to the JAAM FDP thresholds and substantially reduced overclassification compared with 3/7 μg/mL. Although 5/10 μg/mL provided slightly higher overall agreement, rounding the lower cutoff from 4.5 to 5 μg/mL reduced sensitivity. Further validation using the complete JAAM-2 score and clinical outcomes is warranted.

SY02-1
Current Career Paths After Studying Biomedical Laboratory Science

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Biomedical laboratory science (BLS) graduates most commonly pursue careers as biomedical laboratory scientists (BLSs) in medical institutions, particularly hospitals. However, career destinations after completion of a BLS curriculum are not limited to clinical practice, and a proportion of graduates choose alternative professional pathways or further academic training. I present the career outcomes of graduates from our Kyoto Tachibana University (KTU) and examine the significance and applicability of BLS education across these diverse career trajectories.

Among KTU graduates, 77.5% entered medical institutions, 15.3% progressed to graduate school, 6.5% obtained employment in companies, and 0.7% pursued other paths. These findings indicate medical institutions remain the primary destination for BLS graduates, reflecting the direct relevance of the curriculum to healthcare practice. A considerable proportion of graduates sought to further develop their academic and professional expertise through postgraduate education, while others pursued careers outside conventional medical settings.

Of those employed in medical institutions, 97.1% worked as BLSs, 2.1% as embryologists, 0.4% as autopsy assistants, and 0.4% as nursing assistants. The BLS curriculum provides not only specialized laboratory knowledge but also practical competencies applicable to related professions. Training in cell handling and culture may facilitate entry into embryology, while foundational knowledge of pathology may support work in forensic or autopsy-related settings. In addition, some KTU graduates pursue more patient-oriented roles within healthcare.

Among KTU graduates employed in companies, 35.0% worked at clinical testing centers, 25.0% at research institutes, 20.0% at medical device manufacturers, 10.0% as clinical research coordinators, and 10.0% in other positions. Knowledge of specimen testing, analytical thinking cultivated through practical education, and the ability to interpret laboratory data represent important strengths in these fields.

These observations suggest BLS education provides a strong foundation not only for professional practice as BLSs, but also for a broad spectrum of academic and occupational opportunities.

SY02-2
BLS Education and Career Paths in Norway

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BLS Education and Career Paths in Norway

Biomedical Laboratory Scientists (BLS) in Norway are educated through a three-year bachelor's degree that qualifies graduates for professional authorization and practice in medical laboratories. In recent years, opportunities for further academic development have expanded considerably, including master's degrees, PhD pathways, and professional specialization programs through our professional association NITO. At the same time, the Norwegian system continues to emphasize practical competence, workplace learning, and professional trust rather than formal hierarchical structures.

This presentation will provide an overview of education and career pathways for Biomedical Laboratory Scientists in Norway. It will describe how the Norwegian educational model combines academic qualifications with a relatively flat organizational culture in healthcare laboratories, where formal postgraduate education is often considered an advantage, but rarely an absolute requirement for advanced professional or leadership positions.

The presentation will discuss the role of bachelor education as the foundation for practice, as well as the increasing availability of master's and doctoral education for Biomedical Laboratory Scientists. It will also introduce the Norwegian specialist approval system, developed to recognize advanced professional competence within laboratory medicine. While specialist recognition and higher academic degrees may support career development, recruitment processes in Norway often place strong emphasis on broad professional experience, leadership abilities, collaboration skills, and practical competence. These traditions are shared across several Nordic countries, where workplace cultures are generally characterized by limited hierarchy, interdisciplinary cooperation, and relatively open pathways between clinical practice, professional development, education, research, and leadership roles.

The aim of the presentation is to provide international colleagues with insight into how Norway approaches BLS education and career development, and to highlight both the opportunities and challenges associated with balancing academic advancement, professional specialization, and flexible career structures in modern medical laboratories.

SY02-3
Closing the Gap
DCLS Practice Model as the Key to Transforming Patient Care from Volume to Value

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1 Texas A&M University-Corpus Christi / IFBLS President-Elect
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4 National Accrediting Agency for Clinical Laboratory Science

The U.S. healthcare system continues its shift from volume-based reimbursement to value-based care centered on outcomes, quality, and cost-effectiveness. Yet a critical disconnect persists: the vast amount of data generated through diagnostic laboratory testing remains significantly underutilized. Despite being foundational to most clinical decisions, laboratory data are rarely fully integrated into patient management, risk stratification, or population health strategies, limiting their potential to improve outcomes and reduce costs.

This presentation examines that gap and introduces a disruptive, practice-based solution: the Diagnostic Health Consultant (DHC), operationalized through graduates of NAACLS-accredited Doctor of Clinical Laboratory Science (DCLS) programs. The DCLS is the terminal practice doctorate for clinical laboratory professionals and the only internationally accredited pathway specifically designed to prepare practitioners for advanced clinical consultative roles, distinct from research-focused PhD programs.

DCLS graduates are uniquely positioned at the intersection of the laboratory, clinical practice, and public health systems. Through doctoral-level preparation, they develop advanced competencies in diagnostic stewardship, clinical consultation, data analytics, risk stratification, and real-time surveillance. In the DHC role, these professionals actively translate diagnostic data into actionable insights that inform clinical decision-making, optimize test utilization, close care gaps, and support population health initiatives.

The session will define the current diagnostic data utilization gap, articulate the DHC practice model, and outline the educational framework that equips laboratory professionals for this expanded consultative function. By strengthening and expanding DCLS education, the profession can evolve from a transactional testing service to an integrated clinical partner, unlocking the full economic and clinical value of diagnostic data and providing a sustainable roadmap for laboratory practice in a value-based healthcare environment.

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SY02-4
The Swedish Biomedical Laboratory Scientist Research School for eXcellence (BioLabX)
A national initiative to increase the amount of university teachers and researchers within biomedical laboratory science

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Biomedical laboratory scientists (BLS) play a critical role in modern healthcare, providing expertise in diagnostics, quality assurance, and interpretation of clinical samples, with ~70% of diagnoses relying on their work. Yet, Sweden faces an urgent shortage of certified BLS and academically trained educators, threatening future faculty recruitment, pedagogical development, research capacity and healthcare quality.
The BLS Research School for eXcellence (BioLabX) is a national initiative uniting seven Swedish universities authorized to award doctoral degrees in BLS. Its objectives are to strengthen faculty competence, integrate research with clinical practice, and advance translation of scientific progress into diagnostics, pedagogy, and healthcare. BioLabX, with its steering board, will admit ~23 doctoral students, many with combined clinical academic positions, ensuring close integration between education, research, and practice. The curriculum includes two new profile-defining courses in pedagogy, leadership, and supervision, complemented by seminars, elective courses, and international collaborations. Partner universities contribute complementary expertise across biomedical and clinical research, supported by global network. By fostering research-trained certified BLS with pedagogical competence, BioLabX addresses workforce shortages, secures future educators, and strengthens
Sweden's position as a leader in precision diagnostics, biomedical innovation and research in BLS.

After a selection of research proposals, the first admissions of PhD students can be registered in the autumn of 2026. The presentation will include an up-to date on the progress of the research school.

SY03-1
Future of Immunoserological Testing Toward the Resolution of Pitfalls

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In laboratory medicine, accurate interpretation of test results requires a clear understanding of their relationship to the underlying pathophysiology. Failure to recognize abnormal results that do not reflect the patient's actual clinical status—commonly referred to as "pitfalls"—may lead to misinterpretation and inappropriate clinical decision-making. Such abnormal results are not always detectable through routine quality control alone and therefore require careful recognition and management.

Pitfalls may arise at any stage of the testing process. In automated laboratory testing, particularly in clinical chemistry and immunoassay, these pitfalls can generally be categorized into specimen-related factors and instrument- or process-related factors. Pre-analytical issues include abnormalities in specimen quality, such as hemolysis, lipemia, fibrin presence, and specimen misidentification. During the analytical phase, potential causes include reagent deterioration, instrument malfunction, contamination of reaction components, and barcode reading errors. In the post-analytical phase, result validation is essential. Key steps include checking for extreme values, such as critical values and values outside the analytical measurement range; assessing consistency among related test items; and comparing current results with previous results with considering the patient's clinical status, sampling site, and possible specimen misidentification. Automated immunoassays enable rapid and precise measurements with smaller sample volumes than conventional manual methods. However, because these assays rely on antigen–antibody reactions, cross-reactivity and non-specific reactions remain significant sources of analytical pitfalls. These factors produce discrepant or misleading results despite acceptable instrument performance indicators.

Currently, identification of pitfalls largely depends on abnormal result patterns, instrument alerts, and the experience of laboratory professionals. In the future,, the integration of artificial intelligence and advanced data analysis is expected to improve the detection of subtle inconsistencies, support root-cause analysis, and enhance the reliability of result validation. Such developments may ultimately strengthen the role of laboratory professionals in ensuring high-quality laboratory data and patient safety.

SY03-2
Transition from intravenous to subcutaneous natalizumab treatment in persons with multiple sclerosis

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Background
In summer 2025, natalizumab treatment for multiple sclerosis (MS) in Norway shifted from intravenous (IV) administration of the biosimilar drug Tyruko® to subcutaneous (SC) administration of the originator Tysabri®. Although the active substance is the same, the transition involves changes in both route of administration and the associated companion John Cunningham virus (JCV) antibody index testing. We present the first experiences with SC natalizumab treatment at Oslo University Hospital.

Methods
All persons with MS at Oslo University Hospital initiating SC natalizumab were followed prospectively with measurements of serum natalizumab trough levels (s-NTZ). Anti-natalizumab antibodies were analysed in samples with s-NTZ <5 mg/L. JCV antibody index was measured using the Immunowell (biosimilar) and Stratify (originator) platforms during the transition from IV to SC administration. Clinical data were retrieved from medical records, including disease duration, Expanded Disability Status Scale (EDSS), and treatment interval. All participants provided written informed consent.

Results
A total of 30 patients were included (73% female, mean age 47 years, mean disease duration 20.9 years, mean treatment duration 11.7 years, median EDSS 2.0). No clinical relapses or new MRI lesions were observed. A significant reduction in s-NTZ was observed from before the first (10.8 mg/L, SD 5.6) to before the second (8.6 mg/L, SD 4.9) SC dose. No anti-NTZ antibodies were detected. Subsequent measurements showed stable s-NTZ levels. At treatment transition, 46% had a positive JCV index with Immunowell compared with 14% using Stratify.

Conclusions
Transition from IV biosimilar to SC originator natalizumab appeared safe and well tolerated, without evidence of increased immunogenicity. The study demonstrated a moderate reduction in s-NTZ following transition to SC treatment. Therapeutic drug monitoring may improve control of s-NTZ, although the clinical relevance of drug levels remains uncertain. Differences in JCV index between testing platforms complicate interpretation of Immunowell results in progressive multifocal leukoencephalopathy risk assessment.

SY04-1
AI in Physiological Functional Diagnostics To What Extent Can We Rely on It?

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[Background] In recent years, AI technologies have been playing an increasingly significant role in improving diagnostic precision and reducing the workload of healthcare professionals. However, the applicability of AI varies depending on the nature of the examination.
[Current Status] In electrocardiography, the most established AI application is the automated detection of atrial fibrillation. In ultrasonography, AI is utilized for the automatic calculation of ejection fraction (EF) from images and for tumor analysis. Furthermore, the latest ultrasound system planned for introduction at our hospital enhances image quality through noise reduction and recognizes the scanning view to automatically set body marks during abdominal examinations. These advancements demonstrate that AI contributes not only to diagnostic precision but also to operational productivity.
[Challenges and Limitations] In contrast, the introduction of AI into pulmonary function testing remains challenging. Unlike the aforementioned imaging diagnostics, these tests rely heavily on the patient's understanding and cooperation to ensure data quality. At this stage, automating the complex interaction required between the technician and the patient is considered difficult.
Furthermore, there is the "black box problem," where the process by which AI arrives at its conclusion is not fully transparent to humans—even to the developers. In ultrasonography, understanding the principles behind artifacts, such as acoustic shadows and multiple reflections, is essential for improving examination quality. Similarly, we believe that technicians will increasingly be required to understand the processes through which AI interprets data. While Explainable AI (XAI) is emerging to clarify AI's decision-making logic, its broad application across the medical fields is strongly desired.
[Conclusion] AI holds the potential to revolutionize clinical workflows and improve both diagnostic accuracy and productivity. However, in physiological diagnostics, while we can rely on AI for data processing, human expertise remains indispensable for examinations dependent on patient cooperation. Until the black box problem is resolved, we should not rely on AI unconditionally. Instead, as medical technicians, we must strive to understand AI with the same depth as we do the fundamental principles of measurement.

SY04-2

Enhancing Clinical Laboratory Internship Training Through an Intelligent Image-Assisted Learning System

Application to Sperm Counting and Morphological Analysis in Microscopic Examination

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Background:
The integration of artificial intelligence (AI) into clinical laboratories presents an opportunity to address key challenges in medical training. Manual semen analysis, while the gold standard in male fertility assessment, is time-consuming and subject to inter-observer variability. Clinical laboratory interns often lack sufficient hands-on training due to limited curricular practice and the high workload of supervising clinicians, leading to inconsistent skills and low confidence. algorithms to develop an AI-assisted platform for sperm analysis training and evaluation. Practical sperm detection was conducted to compare manual examination results with machine-based analysis in order to improve consistency and diagnostic quality in clinical laboratory education. The study protocol was reviewed and approved by the Institutional Review Board (IRB). This research was partially funded by the National Science and Technology Council, Taiwan (NSTC-114-2637-H-161-001).
Method:
This study aims to develop and apply an AI-based computer-aided diagnosis (CAD) system that assists in sperm count and morphology recognition through real-time image analysis, integrating it into a clinical internship teaching platform to optimize students' practical learning experience and clinical testing competency. Our research team has developed an AI-based intelligent medical assistance and teaching system focused on sperm count detection and morphological image recognition. The system simulates the standard clinical workflow by integrating an optical microscope, a high-resolution CMOS camera, and an AI processing unit to analyze directly from the microscope's real-time video feed. The core technology utilizes the advanced YOLO (You Only Look Once) object detection algorithm. Trained on thousands of annotated microscope images, the algorithm can draw bounding boxes around each sperm and assign unique IDs in real-time video frames, enabling rapid, consistent, and objective analysis. This system practice in clinical testing, internship students first perform manual microscopic examination following standard procedures and record their results. They then immediately compare their findings with the intelligent detection report generated by the AI system, which includes sperm count, motility, and preliminary morphology classification.
Results:
Preliminary validation showed promising accuracy (AUC > 0.87). The platform provides immediate, objective feedback and logs student actions for self-review. This "practice-feedback-reflection" cycle significantly improved interns' operational consistency and interpretation confidence. By simulating real workflows, the system helps students accumulate practical experience, directly contributing to future clinical service quality.
Discussion and Conclusion:
The platform effectively reduces inter-observer variability and optimizes teaching resources by shifting instructor focus to complex case guidance. Limitations include the need to expand morphological recognition and conduct long-term outcome studies. In conclusion, this AI-enhanced platform standardizes training, builds intern competency, and supports reliable clinical practice. Future work will extend the algorithm to sperm motility grading and adapt the model for other microscopic analyses, promoting deeper integration of AI in laboratory medicine education.

Keywords: *AI-assisted teaching, Image recognition, Clinical laboratory education, Sperm analysis*

SY04-3
Motor function assessment using second lumbrical CMAP in CTS

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Background:
As clinical neurophysiology enters the digital era, physiological testing is expected not only to detect abnormalities but also to provide quantitative information that better reflects disease mechanisms. Although nerve conduction studies (NCS) remain the gold standard for diagnosing carpal tunnel syndrome (CTS), conventional motor assessment primarily relies on the abductor pollicis brevis (APB). Because the median nerve innervates multiple distal muscles through distinct motor branches, evaluation based on a single muscle may underestimate the complexity of distal motor involvement in CTS.
Objective:
We present second lumbrical (2L) compound muscle action potential (CMAP) assessment as an example of how routine NCS can provide more comprehensive physiological information. We investigated whether 2L CMAP complements conventional APB assessment in patients with CTS, with a particular focus on electrophysiological severity and postoperative functional recovery.
Findings:
2L CMAP amplitudes progressively decreased with increasing electrophysiological severity according to the Bland classification. In patients undergoing carpal tunnel release, postoperative recovery patterns differed between the APB and 2L muscles, supporting non-uniform motor involvement among distal median nerve branches. Furthermore, 2L CMAPs remained recordable in most hands with absent APB responses, demonstrating that clinically meaningful physiological information can still be obtained even in advanced CTS, where APB-based assessment alone may no longer be informative.
Perspective:
These findings suggest that detailed neurophysiological assessment can reveal functional heterogeneity that may not be recognized by conventional evaluation alone. Rather than introducing an entirely new examination, maximizing the information obtained from routine NCS may improve diagnostic precision and deepen our understanding of disease mechanisms. The accumulation of such quantitative physiological data may also facilitate future advances in digital neurophysiology through large-scale data integration, artificial intelligence-assisted interpretation, and more personalized assessment of peripheral nerve disorders.

SY04-4
Invasive EEG versus Stereo-EEG for Epileptogenic Zone Localization A Comparative Analysis of Invasive Monitoring Techniques in Presurgical Epilepsy Evaluation

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Background
Precise localization of the epileptogenic zone is essential for successful surgical treatment in drug-resistant epilepsy. When non-invasive evaluations are inconclusive, invasive electroencephalography (EEG) becomes necessary. Subdural grid/strip-based invasive EEG and stereo-electroencephalography (S-EEG) are the two principal approaches currently in use.
Objective
To compare subdural invasive EEG and S-EEG with respect to clinical utility, safety, spatial resolution, and suitability for presurgical evaluation.
Methods
A comparative analysis was performed focusing on surgical approach, electrode configuration, complication profiles, and effectiveness in identifying epileptogenic networks. Clinical indications favoring each modality were also reviewed.
Results
Subdural invasive EEG provides extensive coverage of cortical surfaces and allows precise functional mapping, particularly in eloquent cortex. However, it requires craniotomy and is associated with higher morbidity. In contrast, S-EEG employs depth electrodes inserted through minimally invasive burr holes, enabling three-dimensional exploration of deep and bilateral brain structures with lower complication rates. S-EEG is particularly advantageous in cases involving deep-seated lesions, multilobar epilepsy, or poorly localized seizure onset zones.
Conclusion
S-EEG offers a less invasive and more versatile approach for evaluating complex epileptogenic networks, especially those involving deep structures. Nevertheless, subdural invasive EEG remains indispensable for detailed cortical mapping. Optimal modality selection should be individualized based on anatomical hypotheses and clinical context.

SY05-1
Toward the implementation of Bacterial WGS to Transform Clinical Practice
Proposing the Concept of Tracking Antimicrobial-Resistant Organisms Timely (TAROT)

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Whole-genome sequencing (WGS) of bacteria is a powerful method for simultaneously revealing comprehensive genomic characteristics. Although benchtop high-throughput short-read sequencers are commonly used, their batch sizes are often unsuitable for routine clinical microbiological testing. Recently, the MinION (Oxford Nanopore Technologies), a real-time, portable, long-read sequencer, has emerged as a valuable tool for facilitating the implementation of bacterial WGS in clinical microbiology laboratories. WGS can precisely determine the genetic relationships between antimicrobial-resistant isolates obtained from patients and their surrounding environments. Previously, nosocomial transmission was primarily investigated retrospectively using batch WGS, yielding results long after an outbreak occurred. To effectively prevent nosocomial transmission, timely, evidence-based reporting using high-resolution methods is essential. To address this, we propose a novel concept called Tracking Antimicrobial Resistant Organisms Timely (TAROT). We have developed an automated bioinformatics pipeline and a remote analysis environment designed to lower technical barriers and training costs associated with integrating bioinformatics into clinical microbiology laboratories. TAROT has been validated using methicillin-resistant Staphylococcus aureus (Aoki K, et al., JAC Antimicrob Resist. 2025 May 7;7(3):dlaf069.). Notably, the turnaround time TAT for the transmission analysis of cultured bacterial isolates is only 6 hours, with an accuracy comparable to that of short-read sequencers. Such rapid reporting can facilitate prompt, actionable infection prevention and control (IPC) interventions. Furthermore, we plan to expand the scope of TAROT to include diagnostics for bloodstream infections (BSIs) and the rapid prediction of antimicrobial resistance. Ultimately, TAROT for BSI will fulfill three primary objectives: effective diagnostics, robust antimicrobial stewardship, and timely IPC interventions.

SY05-2
Enhancing tuberculosis diagnosis and drug resistance detection in Thailand through next-generation sequencing (NGS)

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Thailand remains among the 30 countries globally with the highest tuberculosis (TB) burden, according to the World Health Organization (WHO). Prompt diagnosis and drug susceptibility testing (DST) are critical for initiating appropriate treatment and improving patient outcomes. Conventional diagnostic methods, such as sputum culture and acid-fast bacilli (AFB) staining, are limited by long turnaround times (4–6 weeks) and low sensitivity, respectively. Recently, the WHO has recommended several rapid molecular tests, such as GeneXpert, Loop-mediated isothermal amplification (LAMP), and Real-time PCR, for the clinical diagnosis of TB, providing faster results and detecting primary drug resistance simultaneously.

Over the past decade, Next-Generation Sequencing (NGS) has emerged as a transformative tool in TB management. Unlike traditional molecular techniques, NGS provides comprehensive genomic data, enabling precise identification down to the lineage and sub-lineage levels. This high resolution supports epidemiological investigations, distinguishing between clusters, reinfection, and relapse. Furthermore, NGS allows for the simultaneous detection of resistance markers across the full spectrum of anti-TB drugs, facilitating personalised treatment from the outset, increasing success rates, and reducing further resistance development.

There are two primary NGS approaches are used for TB: whole-genome sequencing (WGS) and targeted next-generation sequencing (tNGS). WGS offers the most comprehensive genetic profile, providing unmatched resolution for outbreak investigation and the discovery of novel resistance markers across the entire genome; however, it often requires a prior culture step. Conversely, tNGS enables rapid, direct-from-specimen testing by focusing on specific high-priority gene regions. This approach significantly reduces turnaround time while providing detailed resistance data for both first-line and second-line drugs, making it a highly practical tool for clinical decision-making in high-burden settings.

Current treatment for new TB cases typically involves the first-line regimen of Rifampicin, Isoniazid, and Pyrazinamide. For multidrug-resistant TB (MDR-TB), defined by resistance to Rifampicin and Isoniazid, the second-line regimens are required. Recently, Bedaquiline and Linezolid have been introduced as core components of the second-line therapy. However, rapid molecular DST for these drugs remains challenging due to the lack of well-defined molecular markers, still necessitating phenotypic DST (pDST).

Because NGS can analyse vast amounts of genetic data simultaneously, it is an invaluable tool for identifying novel mutations associated with drug resistance. In cases involving Bedaquiline and Linezolid, NGS is frequently used alongside pDST to build the genomic databases required to establish definitive molecular markers. This study highlights the application of NGS in 291 TB cases in Thailand, identifying significant mutations potentially linked to Bedaquiline resistance that were initially undetected by phenotypic methods. These findings support the clinical necessity of integrating NGS into laboratory workflows to ensure comprehensive drug susceptibility profiles and enhance TB control in Thailand.

SY05-3
Clinical Determinants of Rapid Influenza Antigen Test Performance Effects of Age and Symptom Duration on Diagnostic Accuracy

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Background / Objective
Rapid influenza antigen assays are commonly used for point-of-care diagnosis, but their performance varies across patient groups and clinical conditions. This study evaluated their diagnostic performance using a rapid molecular influenza assay as the reference standard and examined the effects of age and symptom duration on test sensitivity.

Methods
A prospective diagnostic accuracy study was conducted from June 2020 to January 2023 at a tertiary care hospital. A total of 232 nasopharyngeal swab specimens from patients with influenza-like illness were tested using rapid influenza antigen assays and compared with a rapid molecular influenza assay. Performance was evaluated according to age and time from symptom onset.

Results
Among 232 specimens, 100 (43.1%) were positive for influenza, including 75 influenza A and 25 influenza B. Specificity remained high (99–100%) across all conditions. Overall sensitivity was 75.6% for influenza A and 79.2% for influenza B. Sensitivity was higher within 24 hours of symptom onset (influenza A 80.7%, influenza B 80.0%) than after 24 hours (influenza A 72.3%, influenza B 82.9%). Children showed lower sensitivity (influenza A 68.5%, influenza B 70.0%) than adults (influenza A 79.9%, influenza B 87.7%).

Conclusion
Rapid influenza antigen assay performance is influenced by age and symptom duration. Despite consistently high specificity, sensitivity varied across patient groups and testing conditions. These findings support more appropriate use and interpretation of rapid influenza testing in clinical practice.

Keywords
Influenza, Rapid antigen test, Diagnostic performance

SY05-4
Nomman: automated bacterial nomenclature management in the clinical microbiology laboratory

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Introduction:
Microbial detection and identification constitute the bulk of work performed in the clinical microbiology laboratory. With methods like clinical metagenomics, laboratory reports may be filled with hundreds of microorganism names. The importance of using standard nomenclature is highlighted by the College of American Pathologists (CAP) checklist standard MIC.11375 and Clinical and Laboratory Standards Institute (CLSI) guideline M64. However, this can be very daunting without software support.

Materials and methods:
We identified 3 priority areas of nomenclature management highlighted by the CAP and CLSI requirements: harmonizing names reported by different systems within the laboratory, reviewing current nomenclature with reference to authoritative lists, and verifying the impact of nomenclature revisions on areas such as susceptibility testing. A software workflow was designed to integrate inputs and data sources to automate these tasks.

Results: The software was implemented in Python to enable crossplatform deployment. It summarizes the nomenclature used within the laboratory and identifies inconsistencies. It also performs lookup against nomenclature authorities, namely the List of Prokaryotic names with Standing in Nomenclature (LPSN) and the List of Prokaryotic names with Standing in Nomenclature (LoRN), for reference. Lastly, it supports impact assessment of proposed name revisions on group classifications, e.g. CLSI breakpoint tables. The software is tentatively named NOMMAN, and is made available under an open-source license.

Conclusions:
In summary, NOMMAN is a software system for microbial nomenclature management in the clinical microbiology laboratory, enabling compliance with current CAP and CLSI requirements.

SY06-1
Immunocytochemistry Using the Cell Transfer Method in Cytological Specimens

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In cytological evaluation of body cavity fluids, a wide variety of cells derived from multiple organs may be encountered. Therefore, diagnosis requires not only differentiation between benign and malignant cells but also precise identification of the origin of malignant cells, including carcinoma, mesothelioma, lymphoma, and sarcoma, as well as detailed histological classification with estimation of the primary site. In this context, immunocytochemistry (ICC) provides objective evidence that supports morphological diagnosis and has become an indispensable ancillary technique for improving diagnostic accuracy in modern cytology.

Cell block preparations are generally recommended for ICC because of their superior stability and reproducibility. However, when the specimen volume is extremely limited, preparation of cell blocks may be difficult or even impossible. Furthermore, in cases with only a small number of atypical cells, identification of target cells and interpretation of staining results can be challenging. In such situations, ICC using direct smear or liquid-based cytology specimens is required; however, when the number of available slides is limited, the use of multiple antibodies may not be feasible.

To address this limitation, the cell transfer method provides a useful means of overcoming these constraints. In this technique, cells smeared on a glass slide are peeled off as a thin, membrane-like sheet, divided, and transferred onto multiple slides. This approach enables not only ICC but also the application of histochemical staining, as well as fluorescence in situ hybridization (FISH). In addition, by recording cytomorphological features of Papanicolaou-stained specimens using photomicrographs or whole-slide imaging systems prior to transfer, direct correlation between individual cellular morphology and immunophenotype can be achieved, underscoring its potential as a novel research approach.

In this presentation, we demonstrate that the cell transfer method represents a practical and versatile solution for maximizing limited cytological specimens, thereby enhancing both diagnostic capability and research applicability in cytopathology.

SY06-2
Diagnostic Clues in Pancreatic Cytology
Ancillary Findings Suggestive of Malignancy

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Pancreatic cancer is often detected at an advanced stage and carries a poor prognosis because effective chemotherapy and radiotherapy remain limited. Therefore, early and accurate diagnosis is essential for improving patient outcomes, and cytology plays an important role in this process. Endoscopic ultrasound-guided fine-needle aspiration cytology (EUS-FNAC) and pancreatic juice cytology (PJC) are widely used to evaluate solid and cystic pancreatic lesions. Accurate diagnosis is often challenging because desmoplastic stroma and tumor heterogeneity can contribute to sampling errors. In addition, subtle atypia in well-differentiated adenocarcinoma is another factor leading to false-negative results. Thus, conventional diagnostic criteria alone may have limitations in diagnostic accuracy. To improve the diagnostic accuracy of pancreatic cytology, we have investigated various cytomorphological features. In this symposium, in addition to conventional diagnostic criteria, we will present two ancillary findings that may provide important clues to malignancy in pancreatic cytology.

1. Desmoplastic stroma / cancer-associated fibroblasts

Pancreatic ductal adenocarcinoma is characterized by abundant desmoplastic stroma, and stromal fragments can also be observed in cytological specimens. Desmoplastic stroma is composed of activated fibroblasts or myofibroblasts, also referred to as cancer-associated fibroblasts. Previous studies have defined cancer-associated fibroblasts as “spindle-shaped cells with enlarged nuclei and prominent nucleoli.” We revisited this finding in EUS-FNAC specimens and confirmed that they are a highly specific finding for differentiating pancreatic ductal adenocarcinoma from pancreatitis.

2. Signet-ring cells / signet-ring cell-like cells

Signet-ring cells or signet-ring cell-like cells are characteristic findings observed in various carcinomas and have also been reported in intraductal papillary mucinous neoplasm (IPMN). We previously investigated the diagnostic significance of signet-ring cell-like cells for IPMN based on PJC specimens. We defined the appearance of numerous signet-ring cell-like cells as the “signet-ring cell pattern” and reported that this pattern is a useful finding for the diagnosis of high-grade dysplasia / invasive carcinoma in IPMN.

In this presentation, we will demonstrate the actual cytological features of these findings and discuss their utility as practical diagnostic clues in daily cytology practice. Although advances in automation and artificial intelligence are rapidly transforming cytology, careful microscopic observation and comprehensive interpretation of cytological specimens remain essential skills. We emphasize that careful observation of the entire specimen, including background findings and isolated scattered cells, rather than focusing solely on epithelial atypia, is essential for accurate diagnosis. Through these observations, we hope to highlight the enduring value of morphologic assessment that should be passed on to the next generation of cytotechnologists.

SY06-3
Cytology Beyond Generations: Integrating AI-driven Morphological Recognition with Lean Management in Clinical Practice and Education
Transforming Laboratory Workflows and Morphological Education in The Era of Digital Diagnostics

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Abstract:

Background. Cytology and morphological diagnostics rely heavily on Gestalt perception—an experience-based skill increasingly threatened by the retirement of experts and inter-observer variability. Artificial Intelligence (AI) is widely promoted as a remedy, yet pursuing algorithmic performance without redesigning laboratory workflows risks automation bias and limited clinical utility.

Aim. This symposium presents a first-principles framework that integrates transparent AI with Lean Management and applies it to clinical practice and the educational paradigm for next-generation Medical Technologists (MTs).

Methods. Clinically, we propose a human-in-the-loop triage model built on a Software-as-a-Service (SaaS) platform that uses classical computer vision rather than end-to-end deep learning. The rationale is defensive engineering: a white-box pipeline offers explainable decision boundaries and auditability that black-box models do not readily provide.

Clinical Design. The design maximises Negative Predictive Value (NPV), enabling the AI to serve as a digital filter for routine negative cases and freeing technologists to focus on complex samples. The proportion of cases that are safely clearable remains to be established through prospective pilot evaluation; no clinical performance claims are made at this stage.

Educational Design. Equally critical is intergenerational skill transmission. Continuous exposure to AI-generated Regions of Interest may erode junior staff's competence in microscopic scanning. To counter this, the platform inverts standard pedagogy: AI scaffolds learning, but competency assessment enforces blind testing with adversarial items the algorithm misclassifies (e.g., mucus threads versus cellular casts) to probe independent reasoning. The goal is to cultivate AI validators, not passive microscopists.

Keywords:

Explainable AI; Computer Vision; Cytology; Lean Management; Medical Laboratory Education

SY06-4
Impact of BLS fs Technical Proficiency on Cytologic Diagnosis Focused on Specimen Processing in Central Nervous System Samples

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Introduction

Intraoperative rapid diagnosis of brain tumors is often limited by small specimens and freezing artifacts. Cytology provides detailed morphological information and serves as a valuable adjunct. Although central nervous system (CNS) tumors are infrequently encountered in routine practice, cerebrospinal fluid (CSF) cytology is important for evaluating hematologic malignancies and monitoring.This study highlights the importance of proper specimen handling and the role of BLSs in CNS diagnostics.(A part of this study was presented at the 66th Annual Meeting of the Japanese Society of Clinical Cytology in 2025)

Materials and Methods

Among 339 brain tumor specimens submitted for intraoperative rapid diagnosis over a five-year period (2020–2024), 46 crush preparations performed in conjunction with tissue samples and 1,039 CSF or cyst fluid specimens were analyzed.

Results

Squash smears enabled detailed findings of cellular morphology and the relationship between tumor cells and vasculature, demonstrating high concordance with histopathological diagnosis. In CSF specimens, hematologic malignancies could be inferred from nuclear morphology and cytoplasmic staining characteristics. However, in patients undergoing treatment, degenerative changes complicated interpretation, and cases with very few abnormal cells were frequently classified as suspicious rather than positive.

Discussion

For intraoperative rapid diagnosis of brain tumors, combining frozen sections with crush preparations—less affected by freezing artifacts—proved beneficial. In CSF cytology, Giemsa staining was advantageous because CNS tumor cells tend to detach less easily and can be observed at larger size. Molecular and genetic analyses are now essential for determining the histological type of brain tumors. Cytology provides highly accurate presumptive classification based on cellular morphology and architectural patterns, and its value increases further when integrated with molecular and genetic information. Given the limited specimen volume in CSF, it is important to further refine immunohistochemistry and genetic testing techniques to maximize diagnostic yield.

Conclusion

High-quality specimen preparation for invasive samples is indispensable for accurate diagnosis and greatly contributes to patient care.

SY06-5
Insights into Tenascin-C in MAPK inhibitor resistance in melanoma

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Targeted therapies against the MAPK signaling pathway have improved outcomes for patients with BRAFV600-mutant melanoma. However, rapid resistance to MAPK inhibitors (MAPKi) remains a major challenge driving disease progression. Beyond tumor-intrinsic mechanisms, the tumor microenvironment is increasingly recognized as a key regulator of adaptive resistance. Proteomic profiling identified the extracellular matrix glycoprotein Tenascin-C (TNC) as strongly upregulated in MAPKi-resistant melanoma cells. To investigate its functional relevance, TNC was knocked out in primary BRAFV600-mutant melanoma cells using CRISPR/Cas9. Realtime live-cell imaging showed that TNC deficiency significantly altered proliferation dynamics and migratory behavior, suggesting a role for TNC in regulating cellular programs linked to aggressiveness and adaptation. Phosphoproteomic analyses revealed distinct changes between TNC-knockout and control cells, indicating broad remodeling of intracellular signaling networks. Enrichment analyses linked these changes to, among others, cell adhesion, extracellular matrix organization, and focal adhesion signaling, implicating TNC in both proliferative and microenvironmental adaptation. Kinase-substrate enrichment analysis further showed altered kinase activity, reinforcing the role of TNC in signaling pathways associated with melanoma plasticity and therapeutic adaptation. Ongoing integration with RNA sequencing data aims to identify convergent pathways and refine the mechanistic basis of TNC-mediated resistance. Together, these findings identify TNC as a potential mediator linking extracellular matrix dynamics to intracellular signaling programs that promote therapy resistance, highlighting TNCassociated pathways as potential targets to improve the durability of targeted therapies in BRAFV600-mutant melanoma.

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SY07-1
Navigating Through Standardization, Digital Transformation, and Advanced Quality Control

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Abstract:
Clinical laboratory medicine serves as a fundamental infrastructure for modern healthcare. In Japan, the quality of clinical chemistry has reached a high level of accuracy and precision, evidenced by coefficient of variation (CV) values of 2–3% for major test items. This has been achieved through robust External Quality Assurance (EQA) systems, notably those led by the Japanese Association of Medical Technologists (JAMT) using human serum-based reference materials (MacRM).
However, Japan faces unique challenges amid the rapid globalization of the field. While traditional internal quality control (IQC) remains stable, progress toward next-generation quality assurance has stalled since the early 2000s. To address this, there is an urgent need to transition toward Patient-Based Real-Time Quality Control (PBRTQC). PBRTQC, which utilizes patient data for continuous monitoring, can detect errors that traditional IQC might miss. Furthermore, the integration of Artificial Intelligence (AI) and machine learning models, such as those for early error detection, is becoming essential for automating result verification.
On the digital front, Japan’s Electronic Medical Record (EMR) sharing project, scheduled for full implementation in 2025, aims to standardize clinical test data nationwide using codes like JLAC11. This transformation is vital for improving regional medical cooperation and data interoperability. Additionally, international harmonization activities, such as the standardization of Lipoprotein(a) using mole units, represent Japan's commitment to global standards.
In conclusion, the future of clinical chemistry lies in moving beyond simple statistical precision. By embracing PBRTQC, AI-driven automation, and digital standardization, and by fostering cooperation across East Asia, we can ensure that clinical laboratory medicine remains a reliable pillar of global health.

SY07-2
The development of POCT at Landspítalinn

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Point-of-Care Testing (POCT) refers to laboratory testing conducted in close proximity to the patient. These tests are often simple to perform and typically require only minimal samples, such as a drop of blood, a throat swab, or urine, rather than a full blood draw. Advances in technology have facilitated the development of novel POCT devices and expanded the range of measurable parameters, enabling user-friendly operation and rapid results. Concurrently, accreditation and regulatory requirements have become more stringent. It is essential that POCT adheres to the same standards as those applied in central laboratories. **Biomedical Laboratory Scientists** should take a leading role in managing POCT, developing standard operating procedures, and overseeing education, training and quality management to ensure consistent quality assurance (1).
This study examines the development of POCT at Landspítali and compares the current status with findings from a previous study conducted in 2013. The 2013 study also evaluated the state of POCT in three other hospitals across Scandinavia. The focus of this study is on the current state of POCT management, quality assurance and accreditation, the types of instruments in use, the structure of training programs, and the operation of POCT services.
This investigation demonstrates that substantial progress has been made in the development of POCT at Landspítali, although full implementation and accreditation have not yet been achieved. A management system has been established; instruments are under the supervision of professionals and the responsibility of the laboratory. Daily services, regular monitoring, quality management and organized training are under control. Formal accreditation of POCT remains a future goal.

One of the most significant milestones is the implementation of **electronic data transfer**, enabling measurement results to be sent directly to the patient's medical record. New devices have been acquired, with a primary focus on ensuring automated data transmission. In 2025, new glucose meters will be introduced that fulfill the requirements for logging both the healthcare provider's and the patient's identification at the time of measurement, and for automatically transferring the results to the hospital's Laboratory Information System (LIS).
In conclusion, significant progress has been made in the implementation of POCT at Landspítali. The need for restructuring according to ISO standard 15189 is clear and is currently underway. Knowledge and experience of our neighboring countries were used for this work.

(1) http://www.ifbls.org/index.php/statements/point-of-care-testing-poct

SY07-3
When challenges become opportunities: quality reviews in geographically distributed laboratories in accordance with ISO 15189:2022

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Background
Clinical Chemistry at Karolinska University Hospital operates in six emergency hospitals and in primary care in Stockholm County. In 2025, > 600 full-time employees (55% biomedical laboratory scientists) performed over 1 million phlebotomies and more than 22 million diagnostic tests. Clinical Chemistry functions as a matrix organization in which 19-line managers share production responsibility on-site, while transverse sections are responsible for diagnostic testing methods. Clinical Chemistry has been accredited according to ISO 15189 since 1992. The laboratories within primary care are divided into seven units comprising 42 satellites, which perform sample collection and basic laboratory testing on site. Annual internal audits of all satellite units result in ≥40 reviews per year, which in 2023 generated 96 deviations. Perceived challenges include high resource use and workload for staff and managers, which in turn limit the systematic sharing of improvements. The 2024 implementation of ISO 15189:2022 introduces stricter requirements for patient risk–based work, requiring adaptation of our model for internal audits.

Aim
Develop a patient-risk-based, resource-efficient model for internal audits in compliance with ISO 15189:2022.

Method
The internal audit schedule was redesigned based on a patient-risk model. The satellites were divided into three risk levels based on complaints, operational and personnel changes, changes in diagnostic testing methods, and findings from internal and external audits. A new audit schedule was created with risk levels integrated and each with its own action plan. To ensure that improvements spread beyond the audited laboratory, Quality Assurance (QA) briefed section and unit managers and key personnel on how to handle future deviations.

Results
The new patient-risk-based model enabled a reduction in the number of audits, while still covering all diagnostic method areas. Satellites with greater needs receive more support thanks to the released resources. After implementation in 2024, 15 audits were carried out and 68 deviations were found, compared with 40 audits and 96 deviations in 2023. In 2025, more satellites than expected were rated high risk based on the 2024 results. Based on the results 25 audits were performed instead of 15 and QA incorporated a collaborative self-audit, conducted by the line manager and the section. This resulted in decreased audit-related resource use and increased local engagement in quality improvement. The new approach clarified responsibilities within and between units by defining production responsibilities and diagnostic method responsibilities. This facilitated wider dissemination of successful practices and enabled more systematic management of improvements and deviations. Deviations and observations were directed to the appropriate level of responsibility and disseminated to satellites facing equivalent challenges. Collaboration with QA was strengthened significantly.

Conclusion
This model supports ISO 15189 compliance and increases the dissemination of knowledge within the organization. The model remains in use and is continuously refined in ongoing quality assurance work. Key success factors are a well-known management system, clear roles and responsibilities, mutual trust, and deeper root cause analysis so that corrective actions are taken at the appropriate level.

SY07-4
Falsely Low Total Bilirubin by Elevated Hyaluronic Acid

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A 73-year-old man, diagnosed with pleural mesothelioma (PM) approximately 15 months prior and treated with cisplatin-pemetrexed chemotherapy underwent laboratory testing when follow-up CT showed pleural thickening from the diaphragm, raising suspicion of tumor recurrence. Total bilirubin (T-Bil) measurement was reported as <0.1 mg/dL (below the detection limit) on a BM8040 analyzer (JEOL, Japan), and the analyzer displayed an abnormally low value of –1.1 mg/dL. The reaction time course showed an unexpected absorbance increase, and serial dilutions (2- to 20-fold) lacked linearity. Sia euglobulin precipitation test was negative, with low immunoglobulins (IgG 451 mg/dL, IgA 139 mg/dL, IgM 15 mg/dL) and no paraprotein on electrophoresis. Spike-recovery test showed low recovery of 76.9%. Turbidity appeared after mixing serum with R1 reagent for T-Bil (Total Bilirubin E-HA Test Wako, vanadate oxidation method) and iron (L-type Wako Fe-N, bathophenanthroline method). Alternative methods yielded T-Bil 0.4 mg/dL (Fuji DryChem TBIL-PIII, azo-coupling method) and 0.5 mg/dL (ABL800 FLEX, spectrophotometry). Suspecting hyaluronic acid interference based on our prior experience with turbidity in acidic assays, serum hyaluronic acid was measured and found markedly elevated at 568,000 ng/mL (reference <20 ng/mL). Interference confirmation involved hyaluronidase (FUJIFILM Wako Pure Chemical Corporation): before treatment, T-Bil was <0.1 mg/dL with abnormal absorbance increase on reaction time course and hyaluronic acid 1,700,000 ng/mL; after treatment (1:1 incubation at 37°C overnight), T-Bil was 0.4 mg/dL with reaction time course without abnormal absorbance increase and hyaluronic acid <9 ng/mL. This case suggests profound interference in the T-Bil assay due to markedly elevated serum hyaluronic acid levels. While serum hyaluronic acid elevation can occur in PM due to tumor production, extreme levels as seen here are rare. It may interfere with colorimetric assays using acidic reagents, causing turbidity and falsely low levels. Alternative assays less prone to interference or hyaluronidase treatment are thus warranted.

SY07-5

Artificial Intelligence for Clinical Chemistry in Low-Resource Laboratory Settings

Implementing Edge AI for Real-Time Diagnostic Support in Connectivity-Challenged Environments

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Purpose:

Clinical laboratories in developing regions face substantial diagnostic error rates, largely due to a critical shortage of specialists and unstable infrastructure. This study evaluates "Sudan Lab AI," an offline-capable artificial intelligence model designed to standardize diagnostics and enhance accuracy in limited-resource environments. The primary goal is to provide a resilient solution that overcomes connectivity challenges while maintaining high-quality diagnostic standards and reducing diagnostic delays.

Methods:

We developed a dual-layer AI architecture to ensure continuous operation. The "Edge Layer" utilizes a lightweight, mobile-based image recognition algorithm to process and analyze laboratory data locally, functioning entirely without internet connectivity. This allows for real-time diagnostic support directly at the point of care. The "Cloud Layer" complements this by facilitating periodic, low-bandwidth data synchronization and remote quality control updates whenever a stable connection is established, ensuring the model's long-term accuracy and relevance.

Results:

Preliminary field-testing in simulated low-connectivity settings demonstrated a significant 60% reduction in results turnaround time compared to traditional workflows requiring specialist review. The model maintained over 95% diagnostic accuracy when benchmarked against senior laboratory specialists, effectively mitigating common human interpretive errors. The system proved highly effective in zero-connectivity environments, showcasing its potential for immediate deployment in resource-limited settings.

Conclusion:

Edge AI presents a transformative and resilient solution for biomedical laboratory science. By decentralizing analytical capabilities, it ensures that high-quality, reliable diagnostic standards are accessible even in areas where traditional infrastructure is unreliable or completely non-existent. This approach empowers local healthcare providers and strengthens the overall diagnostic framework in resource-constrained regions, ultimately improving patient outcomes.

SY08-1
Rapid Diagnostic Tests in Malaria Confronting Drug and Diagnostic Resistance

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Malaria poses a significant global threat, disrupting economic development in tropical and subtropical regions. According to the World Health Organization (WHO), there were an estimated 282 million cases and 610,000 deaths in 2024. Most cases are reported in Africa, leading the WHO and academic researchers to concentrate their malaria control initiatives in African countries. However, the emergence of drug and diagnostic resistance presents a substantial challenge to global initiatives. The WHO recommends artemisinin-based combination therapy for malaria treatment; however, partial resistance to artemisinin derivatives has been observed in Southeast Asia and has recently spread to Africa. Drug resistance remains the most critical barrier to controlling malaria. In response, Novartis developed a novel antimalarial drug, GanLum (ganaplacide/lumefantrine), which completed a Phase III trial and is pending official approval. Ganaplacide is a novel compound with a unique mechanism of action that is effective against artemisinin-resistant parasites. For malaria diagnosis in endemic regions, microscopy is the most prevalent method, necessitating skilled laboratory personnel. Rapid diagnostic tests (RDTs) are also available, which detect the parasite antigens Plasmodium falciparum histidine-rich protein 2/3 (HRP2/3); however, the high prevalence of pfhrp2/3 deleted parasites in certain areas is a growing concern. Plasmodium falciparum lactate dehydrogenase (PfLDH) has recently been combined with PfHRP2/3 to develop new RDTs to address this diagnostic challenge. Despite efforts to control malaria, the adaptation of malaria parasites to treatment and diagnostic strategies has hindered progress, resulting in no decline in cases over the past decade. These innovations, including novel drugs and diagnostic methods, have the potential to enhance malaria interventions and improve global health outcomes.

SY08-2
Molecular Detection of *Fasciola* spp. In Farmland Plants and Surrounding Water Samples from Selected *Barangays* in San Jose City, Nueva Ecija: A Corollary for One Health Approach

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Filipinos heavily rely on agricultural products; however, these plants and their surrounding waters can be contaminated with Fasciola spp., a parasite that affects ruminants, farmers, and, subsequently, consumers. The Philippines has a high risk of fasciolosis, yet there are limited studies on plants that serve as secondary intermediate hosts. Furthermore, traditional diagnostic methods, such as microscopy, lack the sensitivity and specificity required for early environmental detection. Addressing this gap, the study aimed to evaluate the presence of Fasciola spp. in farmland plants, including Oryza sativa L., Ipomoea aquatica, and other forage crops within the selected areas, as well as in their surrounding waters, utilizing a sensitive molecular approach to contribute to a One Health framework. A descriptive, quantitative approach was used, involving the collection of fifteen (15) plant samples and fifteen (15) corresponding surrounding water samples from three selected areas in San Jose City: Barangay Villa Joson, Barangay Sibut, and Barangay Culaylay. Sampling sites were selected based on environmental parameters—temperature, pH, and water current—that are known to influence parasite development. Plant species collected included Ipomoea aquatica, Oryza sativa L., and various forage crops such as Citrullus spp., Chromolaena odorata, and Ludwigia hyssopifolia. All samples were initially processed by vacuum filtration through a 2.7 µm microglass fiber filter, followed by preliminary microscopic examination for presumptive metacercariae. All samples were subsequently subjected to DNA extraction and conventional PCR using ribosomal DNA primers (ITS1) and mitochondrial DNA primers (JB3F and JB4.5R). Successful amplicons generated with the ITS1 primers were purified and analyzed by bidirectional capillary sequencing for species identification. Fasciola eDNA was detected in Ipomoea aquatica as well as underrecognized forage crops like Citrullus spp., whereas presumptive Fasciola spp. metacercaria was found in Chromolaena odorata. Throughout the study, molecular analysis with ribosomal ITS1 primers detected Fasciola spp. eDNA in 40.0% of water samples (6 of 15) and 20.0% of plant samples (3 of 15), significantly outperforming traditional microscopy. Statistical analysis demonstrated that the occurrence of Fasciola spp. is significantly influenced by the surrounding water current. Specifically, static water environments were strongly associated with parasite presence—as all positive plant samples were found exclusively in areas with static water—highlighting the critical role of stagnant or slow-moving water in facilitating metacercaria attachment and encystation. Molecular detection of Fasciola spp. in plants and water highlights the need for a One Health Approach to address livestock and human risk. Surveillance using improved molecular methods is recommended to better monitor and control the spread.

SY08-3
Evaluating the Diagnostic Accuracy of the Sysmex XN-31 Automated Malaria Analyzer Against Gold Standard Microscopy: A. cross-sectional study in Kumasi-Ghana

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Introduction
Malaria is a common and life-threatening infection, particularly in Ghana. Hence, a quick and reliable diagnosis is essential for effective malaria control. Although malaria microscopy is the gold standard, it is laborious, requires extensive training, and relies heavily on microscopists' proficiency. Alternative rapid tests, like automated analyzers, provide quick results but have not been thoroughly evaluated in Ghana. This study compared the diagnostic accuracy of the XN-31 Sysmex Malaria automated Analyzer with WHO-expert microscopy at Komfo Anokye Teaching Hospital.
Methods
This cross-sectional study enrolled 118 patients presenting with suspected malaria at the OPD of Komfo Anokye Teaching Hospital, Kumasi, between February and April 2026. Venous blood samples were collected to prepare thick and thin blood smears for microscopy and for concurrent testing with the XN-31 malaria analyser. Microscopy was performed by a WHO-certified microscopist, blinded to the analyser's results. The Wilcoxon rank test was used to compare parasite densities between the two methods, while Spearman correlation and Receiver Operating Characteristic analyses were employed to assess agreement and diagnostic accuracy of the XN-31, respectively. A p-value less than 0.05 was considered statistically significant.
Results
Among OPD cases, about one in ten participants had malaria, with the majority due to P. falciparum (91.7%) and 8.3% due to mixed infection with P. falciparum and P. malariae. Parasite density measured by the XN-31 was higher than that by microscopy, though the difference was not statistically significant [24,085 (9,199-99,789) vs. 22,320 (10,292-69,153), p=0.382], and the two methods showed a strong positive correlation (R=0.995, P<0.001). In terms of diagnostic performance, the XN-31 demonstrated excellent accuracy [98.3% (95% CI: 94.0-99.5)], perfect sensitivity [100% (95% CI: 74.1-100.0)], and high specificity [98.1% (95% CI: 93.4-99.5)], with near-perfect discriminatory ability (AUC=0.991, 95% CI: 0.978-1.000), indicating it is a reliable tool for detecting malaria infection. For species identification, it further achieved perfect accuracy and sensitivity [100% (95% CI: 74.1-100.0)].
Discussion
The XN-31 performed consistently well across all three evaluated domains compared to microscopy. Its strong diagnostic performance, reliable parasite quantification, and accurate species identification suggest it is a viable alternative to microscopy. These findings are particularly relevant in settings like Ghana, where the burden of malaria remains high and access to skilled microscopists is not always guaranteed. The low prevalence of non-falciparum species in this study reflects the known epidemiology of malaria in the region. However, the limited number of positive cases warrants cautious interpretation of some performance estimates, as reflected in the wide confidence intervals observed for sensitivity and positive predictive value. Additionally, the study did not independently evaluate the XN-31's performance in detecting non-falciparum species, given the low frequency of such infections in the sample.
Conclusion
The XN-31 demonstrates high sensitivity and specificity comparable to expert microscopy in detecting, quantifying, and speciating malaria infection. By overcoming the limitations of existing diagnostic methods, it is a promising and practical alternative, particularly in malaria-endemic regions where rapid and accurate diagnosis is critical.

SY08-4
Two Cases of Cryptosporidiosis: Oocysts Initially Detected by Gram Stain

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Cryptosporidium spp. are protozoan parasites known to cause gastroenteritis worldwide, with symptoms ranging from mild diarrhea to severe, life-threatening illness in immunocompromised hosts. Despite its clinical importance, cryptosporidiosis often goes unrecognized, due to diagnostic challenges and the lack of routine testing. We report two cases in which Gram stain findings provided the first clues to diagnosis.

The first case involved a 48-year-old male with a history of syphilis, who presented to a previous hospital with a two-month history of diarrhea, vomiting and 25 kg weight loss. He reported being a man who has sex with men and no recent travel history. His condition worsened with cough, sputum, and dyspnea, leading to a diagnosis of Pneumocystis pneumonia and newly confirmed HIV infection. Due to refractory diarrhea, he was transferred to our hospital. Although the direct stool wet mount was negative for ova and parasites, the Gram stain revealed 4-6 μm unstained, round, halo-like structures, suggestive of *Cryptosporidium* oocysts. The diagnosis was confirmed by modified acid-fast stain and a multiplex PCR using the FilmArray GI panel.

The second case was a 20-year-old male with no significant past medical history, who developed fever and bloody diarrhea while traveling in India. After returning to Japan, he continued to experience persistent watery diarrhea and presented to our hospital. Blood tests showed a mild leukocytosis and slight liver dysfunction. Stool microscopy was negative for ova and parasites, but Gram stain again revealed 4-6 μm unstained halo-like structures similar to the first case, and modified acid-fast stain confirmed *Cryptosporidium* infection.

These cases highlight how Gram stain, a simple and widely available technique, can provide an early indication of cryptosporidiosis, prompting confirmatory staining or molecular tests for timely diagnosis and appropriate management.

SY09-1
Advanced Testing, Built on Strong Foundations Perspectives on Pre-analytical Pathology in the Genomic Era

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Technical pathology practice has undergone a major shift with the introduction of genomic medicine in Japan. Traditionally, the handling of pathological specimens has been optimized for morphological preservation. However, with the adoption of molecular diagnostics in both diagnostic classification and treatment selection, the preservation of nucleic acids has become an equally important concern. Following the widespread implementation of next-generation sequencing-based cancer gene panel testing using formalin-fixed paraffin-embedded specimens, pre-analytical pathology processing has evolved to balance both morphology and nucleic acid quality, and current practices are relatively stable.

Future clinical and research applications of broader genomic analyses, such as whole-genome sequencing, and emerging technologies, such as spatial transcriptomics, will require even higher and more strictly controlled nucleic acid quality. Under these conditions, fundamental pre-analytical steps, such as appropriate fixation, control of ischemic time, and precise tissue handling, remain critically important. Ensuring both a thorough understanding of these principles and their consistent execution is essential for maintaining reliable analytical performance. This perspective ensures that advances in medical care translate into greater benefits for patients.

In this presentation, I will revisit the transition in clinical pathology practice in Japan from a morphology-centered approach to one that places greater emphasis on nucleic acid quality. Additionally, I will outline recent developments in molecular targeted therapies and emerging genomic technologies, highlighting their increasing dependence on high-quality tissue specimens. Drawing on my experience in the analytical phase of genomic testing, I will also discuss how variations in pre-analytical conditions become evident in downstream genomic data and affect data interpretation. From this perspective, I hope to share key considerations in pre-analytical practice that support both reliable analysis and meaningful clinical applications with the pathology and laboratory community.

SY09-2
Integration of Artificial Intelligence (Ai) Technology in Histopathology Curriculum in Medical Technology

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The integration of artificial intelligence (AI) into histopathology is transforming medical technology education. This abstract presents a framework for embedding AI literacy in the histopathology curriculum for medical technology programs, aiming to produce graduates who can effectively utilise AI tools while maintaining essential diagnostic skills. We propose a competency-based model that integrates foundational histology, tissue processing, and digital pathology with core AI concepts, including machine learning, data governance, and algorithm evaluation. The framework consists of five key components: (1) data provenance and ethics, ensuring students understand patient privacy, bias, and responsible AI use; (2) digital pathology skills, including whole-slide imaging, annotation practices, and interoperability with laboratory information systems; (3) AI methods and evaluation, covering model types, performance metrics, validation pipelines, and critical appraisal of automated outputs; (4) practical workflows, integrating AI-assisted decision support into routine laboratory work, quality control, and error analysis; and (5) regulatory and professional considerations, addressing accreditation standards, clinical deployment, and accountability. The curriculum prioritises experiential learning through case-based laboratories, hands-on projects using publicly available datasets, and collaborations with clinical partners to simulate real-world implementation. Assessment strategies include objective structured clinical examinations (OSCEs), project reports, peer reviews, and reflective essays to evaluate technical proficiency, ethical reasoning, and communication skills. The proposed model addresses anticipated challenges, including resource limitations, faculty development, and the need to maintain up-to-date content in a rapidly evolving field. Solutions involve modular course design, cross-disciplinary training with computer science and bioinformatics, open-access curricular resources, and ongoing professional development for educators. By promoting AI fluency alongside traditional pathology skills, the curriculum aims to prepare medical technology graduates to ensure diagnostic accuracy, improve laboratory efficiency, and support responsible innovation in precision medicine. Future research will include longitudinal studies to assess learning outcomes, clinical impact, and the scalability of AI-integrated histopathology education across institutions.

SY09-3
Implementation of MacroPATH MX SK C-Scan Image-Based Macroscopic Biopsy Documentation

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In the laboratory of histology, the MacroPATH MX SK camera with integrated C-scan software has been purchased and implemented for the routine handling of various types of biopsies specimens. The purpose of the C-Scan system is to optimize the process and workflow when handling biopsies by replacing dictated macroscopic description of the histological material with standardized image-based documentation, thereby reducing the workload across different professional groups.
Commissioning of the MacroPATH MX SK C-Scan required an approved acceptance test, for which a set of acceptance criteria was established to ensure that the performance and quality of the equipment met both the laboratory's requirements and the supplier specifications. The criteria included successful QR-code reading on cassettes, image acquisition time, image quality, as well as requirements to the software which included integration with the laboratory information system (LIS), and transfer of image files to the image management system (IMS).
The acceptance test was conducted over a two-week period and included 220 requisition numbers comprising 516 patient samples from gastrointestinal pathology. The process involved continuous evaluation and optimization. System performance and equipment was primarily assessed based on feedback from the pathologists and biomedical laboratory scientists involved.
The MacroPATH MX SK C-Scan fulfilled all predefined acceptance criteria and was therefore approved for routine clinical use.
The implementation of MacroPATH MX SK C-scan resulted in increased uniformity, improved traceability, and more detailed macroscopic descriptions, all of which is beneficial to the diagnostic quality. In addition, the workflow related to handling biopsies has been reassessed to ensure internal quality and traceability which contributes to optimal patient safety.

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SY09-4
Digital Pathology Implementation in Remote Canadian Regions A summary of unique opportunities and challenges

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Background/Objectives: Digital pathology has the potential to revolutionize pathology diagnostics, especially in geographically isolated and underserved regions. By leveraging technology, telepathology, and integration with computer-aided diagnostic tools, digital pathology can improve access to prompt and accurate diagnostics.

Methods: Our key steps to implementing digital pathology and transitioning operations to a digital network are assessing existing infrastructure, identifying gaps in connectivity and resources, and creating a workflow tailored to the needs of the healthcare system.

Results: We present an approach of implementing digital pathology in Timmins, Northern Ontario, Canada, focusing on addressing regional disparities and the improvements that come alongside utilizing digital pathology. Our results show that digital pathology can provide prompt, efficient and better-quality diagnostic services to rural and un-deserved areas, improving patient care and outcomes. It also represents a cost-effective option with savings from eliminating travel costs, courier costs and additional operational efficiencies.

Conclusions: Implementing digital pathology in rural settings presented with challenges related to infrastructure, technical abilities, workforce readiness, cost and other aspects involved in transitioning from traditional microscopy to a fully digital pathway. Digital pathology systems can help ensuring seamless data flow and improving overall healthcare delivery.
Telepathology also allows pathologists to provide diagnostic services from a distance, which is particularly beneficial in areas with a shortage of pathologists.

Keywords: artificial intelligence; digital health; digital pathology; digital pathology implementation; remote diagnosis; telepathology; whole slide imaging.

SY10-1
The Evolving Role of Laboratory Scientists in Genomic Medicine Education and Workforce Development for the Genomic Era in Japan

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Recent advances in next-generation sequencing (NGS) technologies have rapidly expanded the clinical application of genomic medicine and transformed the role of laboratory scientists in molecular diagnostics. Along with the increasing use of cancer genomic profiling and comprehensive molecular testing, laboratory scientists are now expected to possess not only technical expertise but also knowledge of molecular genetics, bioinformatics, quality assurance, and clinical interpretation to support precision medicine.

At our institution, education for future laboratory scientists has been adapted to meet these emerging demands in genomic healthcare. Undergraduate lectures provide foundational training in molecular techniques, including PCR, sequencing, and NGS, together with the principles of genomic medicine, variant interpretation, and quality management. In practical training sessions, students participate in case-based group discussions using cancer genomic profiling cases. Through these exercises, students learn to evaluate genomic alterations, interpret their clinical significance, and understand the role of laboratory scientists within multidisciplinary healthcare teams. In addition, students are encouraged to pursue certifications related to genetic testing and bioinformatics during their undergraduate education to promote early professional development.

From our experience in clinical genomic testing, we recognize that highly automated sequencing technologies alone cannot ensure the quality and reliability of genomic medicine. Laboratory scientists must understand disease biology, testing principles, analytical limitations, and result validation in order to critically assess genomic findings and contribute to appropriate clinical interpretation. These competencies are becoming increasingly important as NGS-based testing continues to expand across diverse clinical settings.

This presentation will discuss the evolving responsibilities of laboratory scientists in genomic medicine and introduce educational initiatives aimed at developing the next generation of professionals capable of supporting high-quality genomic testing in the NGS era.

SY10-2
Current Status of Genome Testing with NGS in Japan and Worldwide. From Companion Diagnostics to CGP: Practical Realities of Cancer Genomic Testing in Japan

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A key feature of Japan's healthcare policy is its universal health insurance system, under which many medical services, including genetic testing, are subject to administrative regulation. Within this system, next-generation sequencing (NGS)–based genomic testing is broadly divided into two categories: multiplex companion diagnostics (CDx), represented by the Oncomine Dx Target Test, and comprehensive genomic profiling (CGP), including the FoundationOne CDx. Since June 2019, CGP testing has been reimbursed to support treatment selection; however, its use remains restricted to designated hospitals and to patients who have completed standard therapy. In contrast, CDx is accessible at all hospitals where cancer treatment is provided.

Although genomic testing in Japan is often outsourced to commercial laboratories, our institution has implemented the Oncomine Dx Target Test in-house and performs approximately 500 tests annually. As a national cancer center, we also analyze pathology specimens prepared at other institutions. Thanks to the nationwide standardization of genomic pathology procedures, differences in specimen quality across facilities have been minimal.

A major advantage of in-house NGS testing is access to BAM files, which enables more detailed analysis. While standard CDx reports are limited to nine driver mutations and gene fusions, additional analyses using BAM files allow detection of single-nucleotide variants (SNVs) and copy-number variations (CNVs) in 46 genes. When necessary, genome browser review is performed to identify alterations not included in the companion diagnostic panel, thereby guiding patients to appropriate additional targeted testing and therapies.

Genomic regions that are challenging to assess by NGS are complemented by immunohistochemistry and fluorescence in situ hybridization (FISH), supported by our extensive antibody and probe resources. For patients who have completed standard therapy, CGP testing is often pursued and reviewed by an Expert Panel (molecular tumor board), with genomic data aggregated nationally by C-CAT.

SY10-3
Advanced Genomic Diagnostics: Current Status and the Vital Role of Medical Laboratory Professionals in the NGS Era
Global Trends and Strategic Adaptations in South Korea fs Healthcare Landscape

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Background: The advent of Next-Generation Sequencing (NGS) has fundamentally revolutionized clinical diagnostics, driving a vital paradigm shift from traditional single-gene testing to comprehensive genomic profiling (CGP). As precision medicine increasingly becomes the standard of care across oncology, rare hereditary disorders, and pharmacogenomics, understanding both global trends and specific regional implementations is critical. This presentation reviews the current clinical utility, regulatory frameworks, and practical challenges of NGS-based genome testing worldwide, highlighting its rapid evolution and the strategic adaptations within South Korea's healthcare landscape.

Global Landscape of NGS: On a global scale, the clinical application of NGS is rapidly expanding. In North America and Europe, large-scale national genomic initiatives and established regulatory pathways have significantly accelerated the adoption of targeted panels and whole-genome sequencing (WGS). Leading institutions are actively refining complex bioinformatics pipelines and standardizing variant interpretation through international guidelines. However, implementation remains heterogeneous; developing regions face substantial barriers, including inadequate laboratory infrastructure and prohibitive costs. Furthermore, achieving global consensus on data privacy and ethical considerations remains an ongoing challenge for the international community.

Current Status in South Korea: South Korea has transitioned from the early adoption phase to a period of technological and structural maturity. Following the landmark 2017 National Health Insurance (NHI) coverage that democratized access to precision medicine, the landscape is currently navigating significant policy shifts. Notably, the 2024 adjustment of patient co-payment rates—rising to 80% for certain cancer types—has introduced complex new variables in laboratory management and clinical decision-making. These changes have necessitated a strategic re-evaluation of diagnostic workflows. In response, Korean medical laboratories are focusing on automating complex procedures and establishing advanced Bioinformatics (BI) pipelines to minimize turnaround times (TAT) and optimize operational efficiency, ensuring that NGS remains a sustainable and essential infrastructure in clinical practice.

The Role of Medical Laboratory Professionals: As the operational backbone of clinical diagnostics, medical laboratory scientists play an indispensable role in this evolving NGS environment. From meticulous library preparation to rigorous sequencing quality control and primary data analysis, the demand for highly skilled technologists is at an all-time high. In an era of shifting reimbursement policies, the ability of laboratory professionals to maintain analytical validity while improving workflow efficiency through automation is essential to sustaining the integrity of advanced genome testing.

Conclusion: NGS has revolutionized diagnostics globally and in South Korea. While policy shifts like adjusted co-payment rates present challenges, they also catalyze laboratory innovation and standardization. Empowering laboratory professionals through continuous education in genetics and bioinformatics is essential for integrating next-generation diagnostics into future personalized care.

SY10-4
Dual luciferase assays for miRNA target investigation in salmonid cells

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MicroRNAs (miRNAs) regulate gene expression post-transcriptionally by binding to miRNA response elements (MREs) in target mRNAs. Previously, we characterized all miRNAs in Atlantic salmon and identified a subset that are pathogen responsive. Using miR-eCLIP, we experimentally identified their target transcripts in vivo. Although identified as targets, the repression efficiency may vary depending on specific miRNA–MRE interactions of the individual miRNA-target pairs. Luciferase reporter assays are widely used for measurements of target repression, but, to our knowledge, such assays have not been established in fish cell lines. Therefore, we aimed to develop a method where the luciferase reporter assay is adapted for use in the salmonid cell line CHH-1.

Different reagents and protocols important for optimal transfection efficiency were tested. Custom-designed miRNA expression vectors containing precursor sequences for miR-462, miR-731 (that are teleost specific miRNAs), and miR-21b were used together with custom-designed dual-reporter constructs expressing Gaussia luciferase (GLuc) and secreted alkaline phosphatase (SEAP). Wild-type or mutated MREs from the target genes IRF1, Lgmn, and CCL19 were inserted into the 3'UTR of GLuc, while the normalization control SEAP was independently expressed.

The results showed optimal co-transfection of vectors using Lipofectamine 2000, and luminescence measurements 7-10 days post transfection showed that GLuc was reduced in all cells with wild-type 3'UTR constructs vs mutant controls. Target activities were reduced by 46–48% ($p < 0.001$) in miR-462 and miR-731 assays, while the miR-21b assay showed ~20% reduction ($p < 0.001$). All three target genes were, thus, confirmed as mediating significant repression of target genes' translation. An advantage of using the CHH-1 cell line instead of the commonly used mammalian HEK293 cell line is that any target repression reflects the activity of teleost-specific miRNA-processing and RISC machinery, thereby providing a more relevant system for assessing miRNA-mediated repression in teleost fish.

SY11-1
Clinical Support by Medical Technologists in Transfusion Medicine Task Shifting and Task Sharing in Japan

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As healthcare systems face increasing demands to reduce physician workload, task shifting and task sharing by medical technologists (MTs) have become important strategies in transfusion medicine. In Japan, a regulatory revision enacted in 2021 expanded the scope of practice for MTs in this field, allowing them to perform a series of procedures related to blood component collection, including venous access, operation of apheresis devices, needle removal, and hemostasis.

To ensure patient safety and professional competence, MTs engaging in these procedures are required to complete standardized national training programs designed to unify knowledge and technical skills. This framework has enabled the safe integration of MTs into clinical settings that were traditionally managed primarily by physicians and nurses.

In addition to these expanded roles, the potential contributions of MTs within the existing regulations are being re-evaluated. These include blood product processing such as washing and splitting, cell processing related to cellular therapies, and clinical support practices such as providing explanations to patients regarding transfusion and participating in the informed consent process.

At our transfusion service, MTs collaborate closely with physicians and nurses to perform all stages of blood component collection. Furthermore, MTs are actively involved in explaining laboratory results and obtaining transfusion consent from patients. These practices have contributed to reducing physician workload while improving the quality, consistency, and accessibility of information provided to patients.

In this symposium, we will present the current status of task shifting and task sharing in transfusion medicine in Japan, together with the implementation strategies and training framework employed in our transfusion service. We will also discuss how these experiences may inform clinical support models in transfusion medicine in other countries, from an international perspective.

SY11-2
Cis-AB Blood Group with Asian-type DEL (c.1227G>A): Serologic and Molecular Characterization of a Rare Case
A rare combination of ABO Cis-AB and RHD*01EL.01 alleles

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The Cis-AB blood group is a rare ABO variant in which both A and B antigen activities are encoded by a single allele inherited from one parent. Unlike the typical AB phenotype, which results from inheritance of A and B alleles from each parent, the Cis-AB allele produces both A and B antigens from a single chromosome. Although it has been reported more frequently in East Asian populations, the Cis-AB phenotype remains uncommon and may lead to discrepancies in routine ABO blood grouping.

Among individuals serologically typed as RhD-negative, approximately 70% have complete deletion of the RHD gene, while the remaining cases carry variant alleles such as weak D or DEL types. The DEL phenotype is characterized by extremely low expression of the D antigen on red blood cells and is usually undetectable by standard serologic testing. In East Asian populations, the most common DEL variant is the Asian-type DEL caused by the c.1227G>A mutation in exon 9 of the RHD gene.

We report a rare case of Cis-AB blood group combined with Asian-type DEL identified through serologic and molecular analyses. A 5-year-old girl was referred to our hospital for blood group testing. In ABO typing, forward typing showed Anti-A (4+) and Anti-B (mixed-field), while reverse typing showed A cells (–) and B cells (1+), suggesting a Cis-AB phenotype. RhD typing was negative, and the weak D test was also negative.

Additional serologic testing showed negative reactivity with Anti-A1 and strong positivity with Anti-H (4+). Rh subgroup testing demonstrated Anti-C (2+), Anti-c (4+), Anti-E (–), and Anti-e (4+). To confirm the ABO blood group, ABO genotyping was performed and revealed the genotype ABO*Cis-AB.01 / ABO*O.01.01, confirming the presence of the Cis-AB allele.

Because RhD serologic testing remained negative, RhD genotyping was additionally performed. DNA sequencing analysis identified the c.1227G>A mutation in exon 9, corresponding to the RHD*01EL.01 allele, known as Asian-type DEL.

The c.1227G>A substitution causes abnormal RNA splicing, resulting in markedly reduced RhD protein expression and extremely low levels of D antigen on the red blood cell surface. Consequently, individuals with Asian-type DEL are usually typed as RhD-negative in routine serologic testing.

In conclusion, we report a rare case of Cis-AB combined with Asian-type DEL (c.1227G>A). This case highlights the importance of molecular genotyping in resolving serologic discrepancies and enabling accurate characterization of rare ABO and RhD variants.

WS01-1
Current Status and Strategic Responses to AMR in Japan Surveillance Systems and Epidemiological Trends of Antimicrobial-Resistant Bacteria

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The increase and spread of antimicrobial resistance (AMR), driven in part by the inappropriate and unnecessary use of antimicrobial agents, has emerged as a critical global health threat and a major priority for healthcare systems. In Japan, comprehensive countermeasures are being implemented under the second National Action Plan on AMR (2023–2027), including the development and dissemination of antimicrobial stewardship guidance, the introduction of a pull incentive scheme aimed at promoting the appropriate use of novel antimicrobials such as cefiderocol and avibactam/ceftazidime by offsetting revenue losses associated with reduced sales, and the revision of the notification criteria under the Infectious Diseases Control Law, effective from April 2025, for major antimicrobial-resistant infections including methicillin-resistant Staphylococcus aureus (MRSA) and carbapenem-resistant Enterobacterales (CRE).

Japan has established a robust, multilayered surveillance system for AMR. This includes the National Epidemiological Surveillance of Infectious Diseases, in operation since 1999; the Japan Nosocomial Infections Surveillance (JANIS), a national hospital-based platform launched in 2000; and antimicrobial use surveillance developed through research-based frameworks such as JSAC/JACS since 2015. These data are integrated annually into the Nippon AMR One Health Report (NAOR), issued by the Ministry of Health, Labour and Welfare. According to the most recent NAOR, MRSA accounts for 32.5% of S. aureus isolates from blood, remaining at a high level despite a long-term decline. Prior to the 2025 revision of the notification criteria, approximately 2,000 CRE cases were reported annually in Japan.

From the perspective of clinical laboratory professionals, this presentation focuses on the current status of AMR surveillance systems and the epidemiological trends of antimicrobial-resistant bacteria in Japan as key components of the nation’s AMR countermeasures.

WS01-2
A glance of carbapenem-resistant situation in Thailand

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Carbapenem-resistant Gram-negative bacilli (CR-GNB) have emerged as a critical public health threat worldwide, with increasing reports from both human and animal sectors. In Thailand, the rise of carbapenem resistance among clinically significant Gram-negative pathogens has become particularly concerning due to its implications for treatment failure, increased healthcare costs, and mortality. This abstract summarizes the current knowledge on the prevalence, molecular characteristics, and transmission dynamics of CR-GNB isolated from humans and animals in Thailand, highlighting the importance of a One Health approach.

In human healthcare settings, carbapenem resistance has been widely documented in pathogens such as *Klebsiella pneumoniae, Escherichia coli, Acinetobacter baumannii, and Pseudomonas aeruginosa*. The primary mechanisms of resistance involve the production of carbapenemase enzymes, notably New Delhi metallo- β -lactamase (NDM), oxacillinase-type enzymes (e.g., OXA-23, OXA-48-like), and *Klebsiella pneumoniae* carbapenemase (KPC), although KPC remains less prevalent in Thailand compared to other regions. These resistance determinants are often associated with mobile genetic elements, including plasmids, transposons, and integrons, facilitating rapid dissemination across bacterial species and healthcare facilities.

In parallel, studies in the animal sector, including livestock, companion animals, and aquaculture, have reported the presence of carbapenem-resistant Enterobacteriaceae and non-fermenting Gram-negative bacilli. Although carbapenems are not approved for routine use in food-producing animals in Thailand, resistance has been detected, suggesting indirect selection pressure through the use of other antimicrobials and environmental contamination. Notably, similar resistance genes, such as *blaNDM* and *blaOXA*, have been identified in isolates from animals and environmental samples, raising concerns about cross-sectoral transmission.

Environmental reservoirs, including wastewater, hospital effluents, and agricultural runoff, play a significant role in the persistence and spread of CR-GNB. The detection of identical or closely related resistance genes and sequence types in isolates from humans, animals, and the environment indicates potential transmission pathways. This interconnectedness underscores the necessity of integrated surveillance systems that encompass human health, veterinary medicine, and environmental monitoring.

Despite increasing awareness, challenges remain in controlling the spread of CR-GNB in Thailand. These include limited routine surveillance in the animal sector, inadequate antimicrobial stewardship, and insufficient infection prevention measures in some settings. Strengthening laboratory capacity for molecular detection, implementing stricter antimicrobial usage policies, and promoting interdisciplinary collaboration are essential steps toward mitigation.

In conclusion, carbapenem-resistant Gram-negative bacilli represent a growing and complex problem in Thailand, affecting both human and animal populations. The convergence of resistance determinants across sectors highlights the urgent need for coordinated One Health strategies to monitor, prevent, and control the spread of these high-risk pathogens.

WS01-3
The Importance of Establishing Testing Strategies Based on Risk Assessment of Drug-Resistant Bacteria -Aligning Local Epidemiology, Facility Resources, and Regional Networks-

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Japanese Red Cross Aichi Medical Center Nagoya Daini Hospital

Antimicrobial resistance (AMR) poses an escalating global public health threat, requiring swift, coordinated, and adaptable countermeasures across clinical settings. In Japan, the current status of drug-resistant bacteria presents unique epidemiological patterns and clinical challenges that demand tailored infection prevention and control practices. Effective AMR mitigation cannot rely on a rigid, one-size-fits-all model; infection control strategies must directly align with local microbial trends. However, healthcare institutions face diverse operational constraints, varying widely in their available financial, human, and diagnostic resources. To address this disparity, establishing diagnostic and testing strategies grounded in facility-specific risk assessments is crucial. Rather than applying uniform protocols, institutions must evaluate their distinct patient populations, local AMR prevalence, and operational capacity to prioritize the most impactful testing methods. Furthermore, establishing collaborative diagnostic networks within regional medical care zones is essential, enabling facilities to share testing capacity, support resource-limited institutions, and achieve regional containment of resistant pathogens. This presentation introduces the contemporary AMR landscape in Japan and illustrates how risk-based testing frameworks enable facilities to maximize their limited resources efficiently. By strategically tailoring diagnostic workflows to individual risk profiles and fostering regional cooperation, healthcare systems can maintain robust surveillance, detect resistant pathogens early, minimize nosocomial transmission, and implement sustainable, community-wide infection control practices suited to their actual clinical needs.

WS02-1
A Multi-Laboratory CSF Workflow for Rapid Hematologic Malignancy Detection

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We describe a practical Japanese workflow for cerebrospinal fluid (CSF) testing in patients with hematologic malignancies, in which Samson staining plays a key role not only in cell counting but also as a rapid trigger for downstream definitive diagnostics. Initial CSF screening is performed in the Urinalysis and body fluid testing laboratory using Samson staining, enabling an immediate assessment of cellularity and early flagging of atypical/suspicious cells under routine clinical practice, including limited sample volume and rapid cell degeneration. When atypical cells are suspected and/or when the clinical context suggests high risk for central nervous system involvement by hematologic malignancy, the screening result is actively used to initiate or request additional testing and to accelerate confirmatory workup through coordinated, parallel escalation. The hematology laboratory performs cytospin preparation with May–Grünwald–Giemsa (MGG) staining for cytomorphologic assessment and flow cytometry (FCM) for sensitive immunophenotypic characterization. When standardized cytologic confirmation and reporting are required, the pathology department performs cytology using Papanicolaou (Pap) staining. Among all CSF examinations performed over a 13-year period, the atypical-cell detection rate flagged at the Samson-based screening step was approximately 2%. Although the proportion is small, these cases represent a clinically high-impact subset in which rapid triage and timely access to complementary modalities (morphology and immunophenotyping, with cytology confirmation as needed) are essential. A central operational challenge is effective communication and coordination across multiple laboratories to ensure that early screening signals reliably activate appropriate downstream testing and that results are integrated into a timely, coherent report supporting clinical decision-making.

WS02-2
Evaluation of Body Fluid Analysis Using an Automated Hematology Analyzer

Kazuho Uchida
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Introduction: There has been an increase in the number of instruments that are able to measure body fluids in recent years. Among these, the Sysmex XR series (hereafter XR) equipped with a body fluid mode (BF mode) enables sensitive detection of various cells appearing in body cavity effusions. In this study, we report the cellular findings and scattergram characteristics of body fluid samples analyzed using the XR BF mode.
Materials and Methods: Histiocytes, mesothelial cells, and malignant cells observed in body cavity effusions were analyzed. Scattergram characteristics of the WBC BF region and the HF BF region (high fluorescence area) obtained by the XR BF mode were evaluated, focusing on their distinctive patterns.
Results: Histiocytes exhibited increased side scatter (SSC), reflecting intracellular phagocytic contents, and tended to spread toward the right within the WBC-BF region. Reactive mesothelial cells showed strong side fluorescence (SFL), extending upward in an arcuate pattern. Leukemic or malignant lymphoma cells displayed a continuous upward extension from the lymphocyte region into the HF-BF region, with moderately increased SFL intensity. Signet-ring cell carcinoma showed a linear upward distribution from the monocyte region into the HF-BF region, often forming clusters. Malignant mesothelioma demonstrated moderately increased SFL intensity, similar to reactive mesothelial cells, including the monocyte region. Small adenocarcinoma cells extended linearly from the monocyte region into the HF-BF region with markedly increased SFL intensity, whereas medium to large adenocarcinoma cells showed an arcuate upward extension. Cells with a high nuclear-to-cytoplasmic ratio tended to exhibit SSC elevation starting slightly left of the usual position.
Discussion: Advances in automated hematology analyzers, the combined capabilities of quantitative measurement and morphological assessment can now be applied effectively to body fluid analysis.

WS02-3
Cerebrospinal Fluid and Body Cavity Fluids Examination: A Hematological Approach
Current Status and Challenges in the Examination of Cerebrospinal Fluid and Body Cavity Fluids

Kei Shimbo
Clinical Laboratory Center, Dokkyo Medical University Hospital

Traditionally, examinations of cerebrospinal fluid (CSF) and body cavity fluids, including pleural, ascitic, pericardial, and synovial fluids, have been performed in general clinical laboratories or cytopathology laboratories. In recent years, automated hematology analyzers have enabled the measurement of cell counts in CSF and body cavity fluids. In addition, there has been an increasing clinical demand for the microscopic examination and differential classification of hematologic malignant cells in CSF and body cavity fluids. Consequently, requests for these examinations to be performed in hematology laboratories have increased.

However, standardized procedures for these examinations have not yet been established in hematology laboratories. As a result, individual institutions have developed their own protocols for specimen preparation, cell classification, and result reporting.

This seminar will introduce practical methods for processing CSF and body cavity fluid specimens in which accurate cell counting is difficult, as well as procedures for preparing May–Grünwald– Giemsa (MG)-stained slides and performing cytomorphological examination. Representative cellular morphologies observed on a MG-stained slides will also be presented.

WS03-1
Quality management in blood transfusion testing

Shunsuke Kojima
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Ensuring reliable results in blood transfusion testing requires appropriate quality management, even though these tests are largely based on qualitative methods. Quality management is supported by two key components: external quality assessment (EQA) and internal quality control (IQC). In Japan, these systems are generally implemented; however, challenges remain in their coverage and standardization.

EQA programs for blood transfusion testing in Japan are mainly organized by professional societies, including the Japanese Association of Medical Technologists (JAMT) and the Japanese Society of Transfusion Medicine and Cell Therapy (JSTMCT). Approximately 2,800 institutions participate in the JAMT program; however, not all testing facilities are enrolled. The JSTMCT program, which uses more specialized samples, has a much lower participation rate—about one-tenth that of JAMT—indicating the need to improve awareness of EQA participation.

Regarding IQC, laboratories using automated systems generally follow standard procedures and maintain adequate control of reagents and instrumentation. In contrast, IQC for manual methods remains insufficient and lacks standardization. In manual testing, quality assurance includes not only the management of reagents and equipment but also the technical competence of laboratory personnel.

Further efforts are needed to improve both the coverage of EQA and the standardization of IQC, as well as to promote a shared understanding of the importance of quality management. This workshop will discuss these challenges and consider approaches toward better standardization in blood transfusion testing.

WS03-2
Strategies and Effectiveness of Improving Management Rh(D)-Negative Blood Components Returns
RhD-Negative Blood Component Return Reduction Strategies

Lin Cheng-Yu, Huang Chen-Tsai
National Taiwan University Hospital Hsin-Chu Branch Laboraory Medicine

Introduction
Rh(D)-negative blood is extremely rare in Taiwan, accounting for approximately 0.3% of the population. As a result, most hospitals do not maintain routine stock. Our hospital experienced a high return rate of unused Rh(D)-negative blood components, primarily due to a lack of clinical consensus on Rh-negative transfusion for Rh-positive recipients. This study aimed to evaluate whether an interdepartmental intervention could reduce return rates and improve blood utilization.
Method
An interdepartmental quality improvement program was implemented, combining process optimization and hospital-wide education. Key interventions included: (1) immediate notification to the blood bank when blood was no longer required; (2) weekly review of patients with reserved blood units; (3) confirmation of utilization or reallocation 10 days prior to expiration; and (4) hospital-level education to unify transfusion decision-making for Rh(D)-negative blood. Return rates before (2020–2022) and after intervention (2023–2025) were compared.
Result
Return rates were calculated as returned units divided by issued units × 100. Before intervention, return rates were 66.67% (40/60), 52.17% (36/69), and 14.81% (8/54), with an overall rate of 45.9% (84/183). After intervention, rates decreased to 16.19% (17/105), 0% (0/88), and 0% (0/201), with an overall rate of 4.31% (17/394), representing a 90.61% reduction.
Discussion
The intervention significantly reduced Rh(D)-negative blood component returns from 45.9% to 4.31%, achieving over 90% improvement. This strategy may serve as a practical model for optimizing the management of rare blood resources and improving patient safety.

WS03-3
Clinical Significance of Naturally Occurring Anti-Wr^a IgG Subclass and Functional Analysis

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Introduction: The Wright antigen (Wr^a) is a low-frequency antigen in the Diego blood group system, and anti-Wra is rarely detected in antibody screening tests. We investigated the clinical significance of anti-Wra in three cases identified incidentally.

Materials and Methods: We evaluated three cases (Case 1: +anti-Wr^a, -E; Case 2: +anti-Wr^a, -E, -Di^a; Case 3: +anti-Wr^a, -E, -Jk^b). Antibody titers were determined by the indirect antiglobulin test (IAT) using the tube technique. Additionally, flow cytometric IgM/IgG subclass analysis and a phagocytosis assay (FCP assay) were performed.

Results: Anti-Wr^a titers were 64, 1, and 2 for Cases 1, 2, and 3, respectively. Subclass analysis identified IgM+IgG1+IgG3 (Case 1), IgG1 (Case 2), and IgG1+IgG3 (Case 3). FCP assay values for anti-Wr^a were 86.79%, 0.87%, and 7.61%, respectively.

Discussion: In all cases, anti-Wr^a was detected in pre-transfusion samples, suggesting it was a naturally occurring antibody. The other coexisting antibodies were detected post-transfusion. Among these, Case 1 anti-E (titer 1, IgG1) showed an FCP assay value of 9.47%; Case 2 anti-E (titer <1, subclass not detected) showed 2.68%, and anti-Di^a (titer 64, IgG1+IgG2+IgG3) showed 91.56%; Case 3 anti-E (titer 256, IgG1+IgG3) showed 60.75%, and anti-Jk^b (titer <1, IgG1) showed 4.51%. All antibodies with low titers exhibited low FCP assay values (<10%) regardless of subclass. In contrast, FCP assay values were high (≥60%) in samples with IgG1+IgG3 antibody titers of ≥64. These findings suggest that even naturally occurring anti-Wr^a can be of IgG1 or IgG3 origin. When titers are high, they require the same clinical vigilance as immune antibodies, such as anti-E and anti-Di^a.

Conclusion: Anti-Wr^a has the potential to cause hemolytic transfusion reactions, even when it is naturally occurring.

WS04-1
Understanding technical limitations of genetic testing by short read NGS
Toward improving diagnostic accuracy

Takayuki Ishige
Department of Applied Genomics, Kazusa DNA Research Institute

Next-generation sequencing (NGS) is a powerful technique in modern clinical genetics laboratories due to its scalability, high resolution, and cost-effectiveness. It is widely used for viral epidemiology, detection of somatic mutations in cancer, and genetic testing of rare diseases. In this workshop, I will discuss limitations in NGS-based genetic testing that can affect diagnostic accuracy, using three representative examples.

First, the choice of variant caller can influence the results. Multiple nucleotide variants, which consist of adjacent variants on the same strand, may be incorrectly detected as separate single nucleotide variants depending on the variant caller used. This can lead to inaccurate functional interpretation. Therefore, careful method validation is essential to ensure diagnostic accuracy.

Second, the analysis of genes with highly homologous pseudogenes remains a major challenge for short-read NGS. Reads derived from functional genes and their pseudogenes are often misaligned, resulting in false-positive or false-negative variant calls. To overcome this limitations, additional approaches such as long-range PCR-based target enrichment or complementary long-read sequencing technologies are often required.

Third, the detection of large genomic variants, including structural variants and copy number variations, is also technically challenging. Standard small-variant callers are not designed to identify these alterations, and their detection typically relies on indirect signals such as read depth and split reads. However, these signals can be affected by coverage bias, GC content, and repetitive genomic regions, leading to reduced sensitivity and specificity. Orthogonal validation methods are therefore necessary.

Overall, diagnostic accuracy is influenced not only by laboratory processes but also by genomic context. Because diverse types of variants contribute to disease onset, appropriate methodologies must be selected to detect clinically relevant variants that may not be captured by standard NGS approaches. Understanding these technical limitations and genomic complexities is essential to ensure accurate and reliable results.

WS04-2

How Biobanking enables Precision Oncology in the IMPRESS-Norway study

From Bench to Clinic: The importance of biobanking perspectives in the IMPRESS-Norway study

Britina Kjuul Danielsen*, Solveig Kokkvoll*, Ingrid Dyvik, Aaslaug Helland, Hege G. Russnes, Kajsa A, M. Johansson, Mona Otrebeski Nilsson, Gry A. Gjeitvik *Co-first authors.

Department of Cancer Genetics, Institute for Cancer research, Oslo University Hospital, Oslo, Norway

IMPRESS-Norway is the largest national, pan-cancer clinical research study offering patients with advanced, incurable cancer off-label treatment based on molecular genetic alterations, funded on precision medicine principles. We highlight the role of integrated biobanking and diagnostics in enabling precision medicine through molecular analyses and clinical data.

At screening, plasma samples were analyzed for circulating tumor DNA (ctDNA). In parallel, the primary tumor was analyzed using the TSO500 panel. To evaluate ctDNA as a minimally invasive approach for longitudinal monitoring and early identification of resistance, 648 patients were included. 118 patients had multiple actionable biomarkers and were eligible for IMPRESS-Norway. Of those, 50% presented concordant biomarkers between tissue and blood. Notably, 8% of patients presented actionable biomarkers only on plasma, underscoring the clinical utility of blood-based approaches. Whole-genome sequencing (WGS) was performed on fresh frozen biopsies to identify targeted therapies that could provide clinical benefit when started treatment. Results from genomic profiling of approximately 4000 patients identified 498 patients who met criteria to be included in the study. Importantly, 20% of the patients were offered new treatment, providing a clinical benefit of 45%. The biobank material enables future precision medicine research through molecular and clinical data analyses. Liquid biopsy can be a valuable complement to tissue profiling, showing promising concordance. Thanks to our approach we have been able to identify new targeted therapies that have provided long lasting benefits for patients within the IMPRESS-Norway study.

WS05-1
Fostering a Culture of Safety in Healthcare: A Japanese Perspective on Communication, Checklists, and Continuous Improvement

Shota Miyao
Department of Pathology Laboratory, Osaka Saiseikai Nakatsu Hospital, Osaka, Japan

Ensuring patient safety remains a global priority, and fostering a strong safety culture is essential for reducing preventable harm. This presentation focuses on three key components of safety culture—effective communication, standardized checklists, and ongoing quality improvement—from the perspective of the Japanese healthcare system.

In Japan, a high level of standardization and strict adherence to standard operating procedures (SOPs) contribute to a highly reliable healthcare environment. The widespread use of checklists and double-check systems plays a significant role in minimizing variability and preventing human error. These strengths are supported by established quality management frameworks, such as ISO 15189, which emphasize documentation, traceability, and compliance.

In addition, systems for incident reporting and continuous quality improvement, including the PDCA cycle, are widely implemented. Further enhancement of safety culture can be achieved by optimizing the use of these systems and integrating them more effectively into daily practice. Promoting open communication and psychological safety facilitates organizational learning from errors.

The concept of a “Just Culture” provides an important foundation for efforts to improve patient safety. By viewing errors as opportunities for learning rather than individual blame, healthcare organizations can encourage reporting while maintaining appropriate accountability, thereby creating a positive cycle of improvement in patient safety.

In conclusion, Japan has a strong foundation in standardization and quality management. By further strengthening communication and the practical implementation of continuous improvement, a more resilient safety culture can be achieved.

WS05-2
Championing a safety culture
Good professional practice for the ISO 15189:2022 accredited medical laboratory

Dennis MOK
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The management of medical laboratories has become more competitive, complex, and dynamic, even before the implementation of ISO 15189:2022. In addition, laboratory personnel management has become increasingly sophisticated due to the recognition of variations in human behaviour in diverse and multicultural contexts. Laboratory management may wonder whether it is possible to manage safety performance whilst consider managing quality culture effectively using a one-size-fits-all solution. Measures taken may require laboratory management to take reasonable steps to ensure safety management will not become an area of vulnerability in routine operations. It is difficult to appreciate how culture influences one's own behaviour, and one may even ask, when faced with practices from different cultures, how current cultural assumptions can be comptaible with safety management. It is important to note that laboratory personnel should have knowledge of their behaviours and cultures in their areas of operations because culture exerts significant influence on medical laboratory structures and processes. Analysis of culture helps to understand how laboratory personnel interact and justify their relationships under standard operating conditions. This has the potential to deliver a competitive advantage through the maintenance of safety practices at a higher level in the medical laboratory. At the same time, laboratory personnel can support laboratory management to conduct analysis of situations and develop influences to improve measures and practices. This workshop will provide a utilitarian perspective on different cultural variables that have significant influence on safety management. The following cultural variables that will be discussed include communication, motivation, negotiation, structure, and change. Implications for laboratory management to consider will be provided for each cultural variable to encourage effective managerial action to improve the medical laboratory management system. In sum, understanding culture can equip the attendees to deal with risks and operational challenges of contemporary safety management more effectively.

WS05-3
From Reactive to Predictive Data-Driven Risk Management Across the Clinical Laboratory Testing Process

Hidekazu Ishida
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Clinical laboratories operate under persistent constraints on human resources, while risk is distributed across the testing process, from pre-examination activities to post-examination interpretation. Conventional management often responds after workload pressure, competence gaps, or clinically important abnormalities have become apparent. In contrast, ISO 15189:2022 emphasizes risk-based thinking throughout laboratory activities. This creates a practical question: when staffing cannot simply be increased, where and when should professional attention be directed?

We present three data-driven approaches that use information already generated through routine laboratory practice to support more proactive allocation of human attention.

In the pre-examination phase, XGBoost models were developed at Gifu University Hospital using outpatient phlebotomy logs to predict daily patient volume, 30-minute reception counts, queue length, and waiting time. To examine transferability across institutions, the Gifu models were adapted through incremental training using data from the University of Tokyo Hospital. In prospective validation at the University of Tokyo Hospital using 522 time slots, the adapted model achieved an R^2 of 0.884 and RMSE of 3.6 patients for queue-length prediction, and an R^2 of 0.888 and RMSE of 1.2 minutes for waiting-time prediction. These forecasts can support advance staffing and operational planning around anticipated congestion.

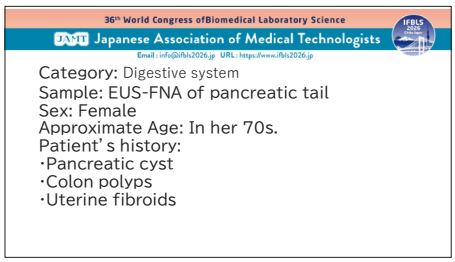
For personnel competence management, a conventional skill map was transformed into a cloud-based Microsoft 365/Power Apps system linking staff, skill, and evaluation databases. The system enables competence records to be updated and retrieved in real time and can generate lists of personnel qualified for specific activities. By replacing fragmented records and individual recollection with a shared and continuously updated view of competence, the approach supports more systematic supervisory oversight, assignment, and follow-up.

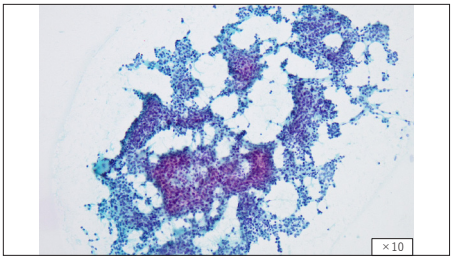
In the post-examination phase, an interpretable decision-tree model was developed to stratify the risk of elevated NT-proBNP (> 300 pg/mL) using routinely available laboratory parameters. The model was developed from 19,889 encounters and integrated into diagnostic support middleware. In an independent temporal validation cohort of 14,903 encounters, it achieved an AUROC of 0.806, sensitivity of 0.882, and negative predictive value of 0.852. Its transparent rule-based structure enables higher-risk cases to be prioritized for confirmatory testing or professional review while maintaining auditable decision logic.

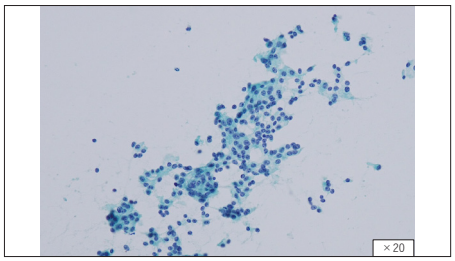
Although these approaches differ in target, scale, and technology, they share a common management principle: data can help determine which risks warrant professional attention first. The objective is not to replace laboratory professionals with algorithms, but to use routinely generated information to allocate limited expertise more deliberately and efficiently. The three approaches were evaluated using different operational and model-performance measures, and each requires local validation and continued evaluation in real-world practice. Together, they illustrate a practical shift from reactive management toward proactive, risk-directed laboratory operations. Routinely generated laboratory data can therefore provide a scalable basis for directing professional attention earlier, before operational or clinical risk becomes apparent.

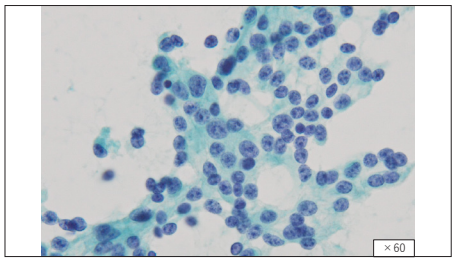
WS06-1
Global Cytology Case Conference: Sharing Diagnostic Perspectives Across Borders

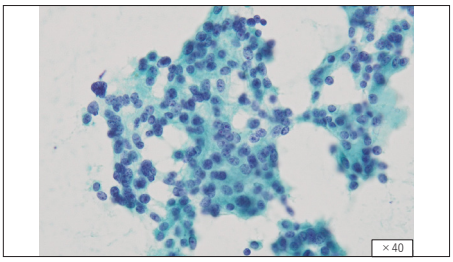
Kazuyo Yoshida
Nihon University Itabashi Hospital

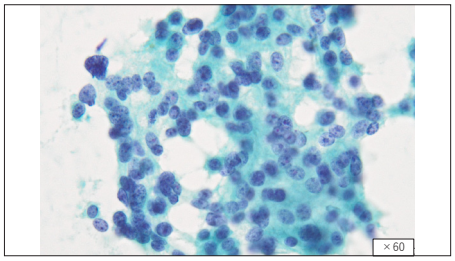


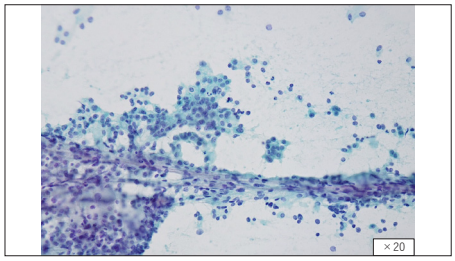


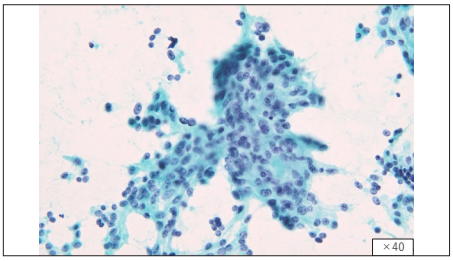


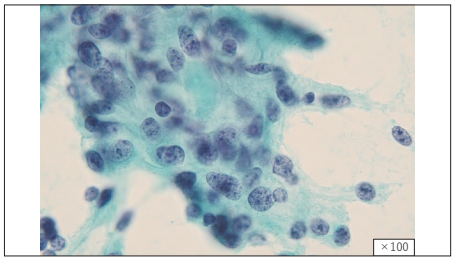


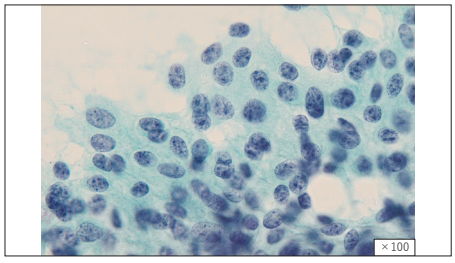












Multiple Choice

A. Intraductal papillary mucinous neoplasm (IPMN)
B. Neuroendocrine tumor (NET)
C. Solid pseudopapillary neoplasm (SPN)
D. Invasive ductal carcinoma
E. Acinar cell carcinoma

WS06-2-1
Global Cytology Case Conference: Sharing Diagnostic Perspectives Across Borders

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IFBLS Case Conference

Prof. dr. sc. Mirjana Stupnisek, MSc.BLS, PhD, FIFBLS

University Hospital for Infectious Diseases, Zagreb, Croatia
Faculty of Dental Medicine and Health, J. J. Strossmayer University of Osijek, Croatia

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Category: Cytological Diagnostics in Infectious Pathology (1st Case)

Sample: Cerebrospinal Fluid
Sex: Male
Age: 71-year
Patient' s history: Transferred from Department of Neurology (UHC Sestre Milosrdnice) to the UHID due to suspected meningitis, presenting with progressive confusion, disorientation, and psychomotor slowing.

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CSF findings (at Neurology):
- turbid
- cell count 3,640×10^6/L (H)
- protein 2.78 g/L (H)
- glucose <0.28 mmol/L (L)
- lactate 11.2 mmol/L (H)

Acute therapy:
- Ceftriaxone 2 g i.v.
- Ampicillin 2 g i.v.

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Brain CT revealed a right temporoparietal corticosubcortical hyperdensity with intense gyral and meningeal enhancement, without ischemia or hemorrhage.

Despite empirical antimicrobial therapy, patient consciousness deteriorated to stupor.

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Past Medical History:
- Mantle cell lymphoma, stage IV, treated with the R-CHOP (3 cycles) and R-DHAP (2 cycles) regimens
- Arterial Hypertension

Chronic therapy: Pantoprazole, Acyclovir, Sulfamethoxazole/Trimethoprim, Allopurinol, Amlodipine/Perindopril, Atorvastatin

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Anamnesis upon admission at UHID (Clinical Presentation):

- The patient was unaccompanied and, although capable of verbal contact, was an **inadequate source of history** due to speech impairment and psychomotor slowing; consequently, the **medical history was obtained from available medical documentation**.
- A CD containing a brain CT scan was provided.
- According to the discharge summary from neurology department, the patient had reportedly been **confused and disoriented for the past 3 weeks**.
- Twelve days prior to admission, he was evaluated at another institution, where a brain CT scan indicated a **hygroma**, and a follow-up CT scan was recommended.
- **The exact duration of the illness and the primary presenting complaints remain unclear**.

Upon admission at UHID (1st day):
- **Lumbar puncture was performed**

CSF Findings:
- Appearance: slightly turbid
- Cell count (in Fuchs-Rosenthal chamber): **2,827** x 10^6/L (H)
- RBC count (FR): 352 x 10^6/L (H)
- protein **2.69** g/L (H)
- glucose 2.7 mmol/L
- lactate **12.56** mmol/L (H)

CSF Findings (at Neurology):
- turbid
- cell count 3,640×10^6/L (H)
- protein 2.78 g/L (H)
- glucose <0.28 mmol/L (L)
- lactate 11.2 mmol/L (H)

Complete Blood Count (CBC) and Differential:
- **WBC:** 5.3 × 10⁹/L
- **RBC:** 4.25 × 10¹²/L (L)
- **Hemoglobin (Hb):** 138 g/L
- **Hematocrit (Hct):** 0.427 L/L
- **MCV:** 100.4 fL (H)
- **MCH:** 32.6 pg
- **MCHC:** 324 g/L
- **RDW-CV:** 15.8% (H)
- **Platelets (PLT):** 94 × 10⁹/L (L)
- **MPV:** 9.8 fL

Absolute Differential:
- Absolute Neutrophils: 3.5 × 10⁹/L
- Absolute Lymphocytes: 0.8 × 10⁹/L (L)
- Absolute Monocytes: 0.8 × 10⁹/L
- Absolute Eosinophils: 0.0 × 10⁹/L
- Absolute Basophils: 0.0 × 10⁹/L

Relative Differential:
- Neutrophils: 67.0%
- Lymphocytes: 16.1% (L)
- Monocytes: 15.8% (H)
- Eosinophils: 0.6%
- Basophils: 0.5%

Serum Electrolytes, Metabolites, and Substrates:
- **Sodium (Na):** 148 mmol/L (H) *(Result confirmed upon retesting)*
- **Potassium (K):** 3.9 mmol/L
- **Chloride (Cl):** 108 mmol/L
- **Blood Glucose:** 5.9 mmol/L
- **Urea:** 10.4 mmol/L (H)
- **Creatinine (Cr):** 82 µmol/L
- **Total Bilirubin (T-Bil):** 14 µmol/L
- **Total Protein:** 66 g/L
- **Albumin:** 44.9 g/L

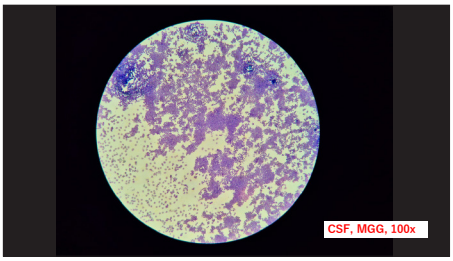
Enzymes and Cardiac Biomarkers:
- **AST:** 23 U/L
- **ALT:** 17 U/L
- **GGT:** 22 U/L
- **Alkaline Phosphatase (ALP):** 111 U/L
- **Lactate Dehydrogenase (LDH):** 170 U/L
- **Creatine Kinase (CK):** 222 U/L (H)
- **CK-MB:** 18 U/L
- **hs-TnT (High-sensitivity Troponin T):** 0.019 µg/L
- **NT-proBNP:** 48 pg/mL

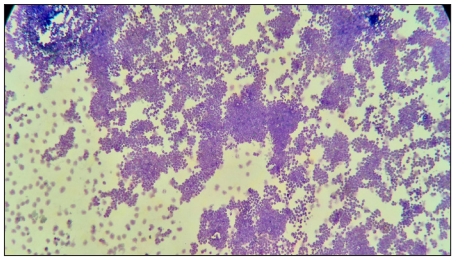
Inflammatory Markers and Coagulation Panel:
- **CRP:** 20.8 mg/L (H)
- **Procalcitonin (PCT):** 0.053 µg/L
- **Prothrombin Time (PT):** 1.08
- **INR:** 0.98
- **aPTT:** 19.6 s (L)
- **aPTT Ratio:** 0.7 (L)
- **Thrombin Time (TT):** 16.6 s
- **Fibrinogen:** 5.3 g/L (H)
- **D-Dimer:** > 4.23 mg/L (H)

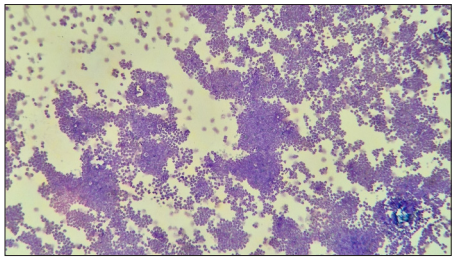
Blood-CSF barrier function:
- IgG, Serum: 4.83 (L)
- IgG, CSF: 82.20 (H)
- Q IgG (IgG quotient): 17.02
- limQ-Ig (Limiting IgG quotient): 44.86
- Albumin, Serum: 38.8 (L)
- Albumin, CSF: 1940 (H)
- Q alb (Albumin quotient): 50.0
- limQ-alb (Limiting albumin quotient): 8.7

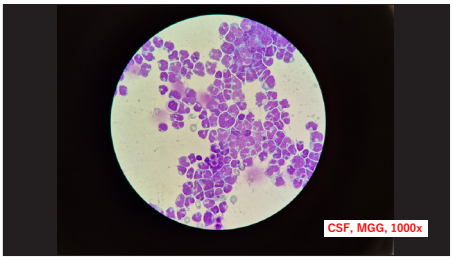
- ZONE 2 - Dysfunction of the blood-CSF barrier.

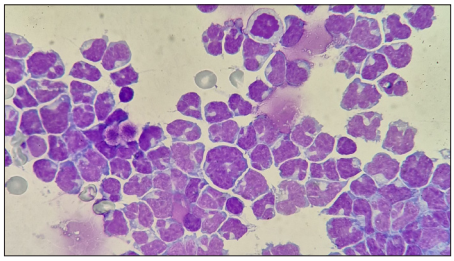
CSF Microbiology:
Multiplex PCR meningitis/encephalitis panel test: NEGATIVE
includes:
- **bacteria** – *Escherichia coli* K1, Haemophilus influenzae, *Listeria monocytogenes, Neisseria meningitidis, Streptococcus agalactiae, Streptococcus pneumoniae,*
- **viruses** – cytomegalovirus (CMV), enterovirus, herpes simplex virus 1 (HSV-1), herpes simplex virus 2 (HSV-2), human herpesvirus 6 (HHV-6), human parechovirus, varicella zoster virus (VZV);
- **yeasts** – *Cryptococcus neoformans/gattii*

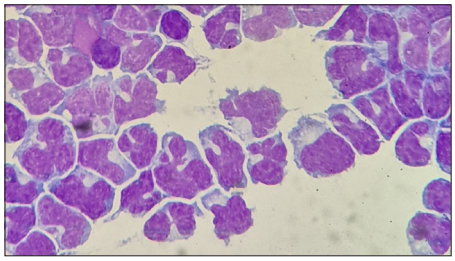












Based on the turbid appearance of the CSF and the markedly high pleocytosis (2,827 × 10⁶/L) in an immunocompromised patient with clinical features of meningitis, what is the most likely diagnosis (upon admission to the UHID)?

A. Viral meningoencephalitis
B. Reactive pleocytosis caused by an occult fungal infection
C. Toxic encephalopathy induced by prior chemotherapy (R-DHAP)
D. Central nervous system infiltration by mantle cell lymphoma(MCL)
E. B-cell acute lymphoblastic leukemia (B-ALL)

WS06-2-2
Global Cytology Case Conference: Sharing Diagnostic Perspectives Across Borders

Mirjana Stupnisek

University Hospital for Infectious Diseases, Zagreb, Croatia

36th World Congress ofBiomedical Laboratory Science
JAMT Japanese Association of Medical Technologists
Email : info@ifbls2026.jp URL : https://www.ifbls2026.jp

IFBLS Case Conference

Prof. dr. sc. Mirjana Stupnisek, MSc.BLS, PhD, FIFBLS
Martina Firic, Katarina Pajtak

University Hospital for Infectious Diseases, Zagreb, Croatia

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Email : info@ifbls2026.jp URL : https://www.ifbls2026.jp

Category: Cytological Diagnostics in Infectious Pathology (2nd Case)

Sample: Bone Marrow
Sex: Male
Age: 57
Patient's history: HIV-positive, who exhibited a weight loss of over 20 kilograms, intermittent fever, and pancytopenia

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Past Medical History (during a one-year period):

- patient was hospitalized multiple times across various institutions due to urticaria, exudative pleuritis (suspected tuberculosis), an anal fissure, and aphthous stomatitis, as well as suspected pulmonary eosinophilic granuloma and angioedema
- following a positive anti-HIV screening test, the patient was transferred to the University Hospital for Infectious Diseases

Upon admission at UHID

Complete Blood Count (CBC) and Differential:

- **WBC:** 2.2 × 10⁹/L
- **RBC:** 3.86 × 10¹²/L
- **Hemoglobin (Hb):** 120 g/L
- **Hematocrit (Hct):** 0.36 L/L
- **MCV:** 93.3 fL
- **Platelets (PLT):** 121 × 10⁹/L

Relative Differential:

- Neutrophils: 48%
- Bands: 3%
- Lymphocytes: 33%
- Monocytes: 13%
- Eosinophils: 3%

Upon admission at UHID

Serum Electrolytes, Metabolites, and Substrates:

- **Sodium (Na):** 139 mmol/L
- **Potassium (K):** 3.2 mmol/L
- **Chloride (Cl):** 100 mmol/L
- **Blood Glucose:** 5.2 mmol/L
- **Urea:** 2,6 mmol/L
- **Creatinine (Cr):** 73 µmol/L
- **Total Bilirubin (T-Bil):** 11.2 µmol/L
- **Total Protein:** 67 g/L
- **Albumin:** 32 g/L

Enzymes:

- **AST:** 34U/L
- **ALT:** 33 U/L
- **GGT:** 84 U/L
- **Alkaline Phosphatase (ALP):** 84 U/L
- **Lactate Dehydrogenase (LDH):** 328 U/L

- **anti-HIV: ELISA & Western blot: positive**
- **antiHBs: positive**
- **antiHBc: positive**
- **CMV IgG: positive**
- **PPD: neg**
- **RTG lung: b.o.**
- **PCR HIV1 RNA: 299,082 copy/mL**

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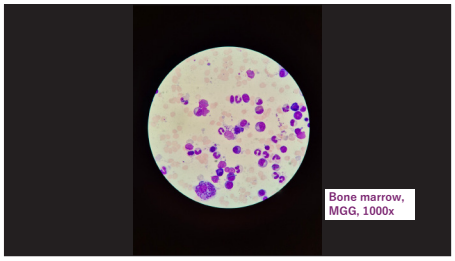
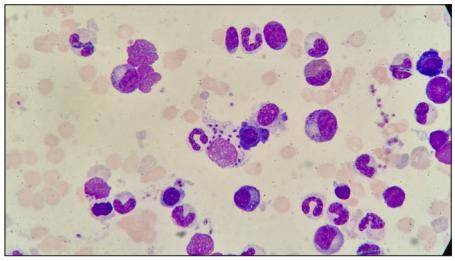
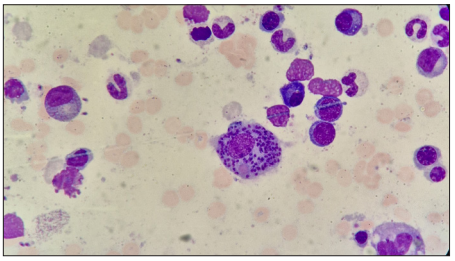
During a five-month hospitalization at UHID (Clinical Presentation):

- his disease course was characterized by febrile episodes, with occasional occurrences of oropharyngeal candidiasis and an episode of CMV viremia
- anemia and leukopenia progressively worsened
- ultrasound detection of hepatosplenomegaly
- a bone marrow aspiration was performed







Upon examination of a Giemsa-stained bone marrow smear, numerous bodies are microscopically observed.
What do we find?

A. Cryptococcus neoformans
B. Histoplasma capsulatum
C. Mycobacterium avium complex (MAC)
D. Leishmania spp.
E. Pneumocystis jirovecii
F. Toxoplasma gondii

WS06-3
Global Cytology Case Conference: Sharing Diagnostic Perspectives Across Borders

Mei-Ling Wu
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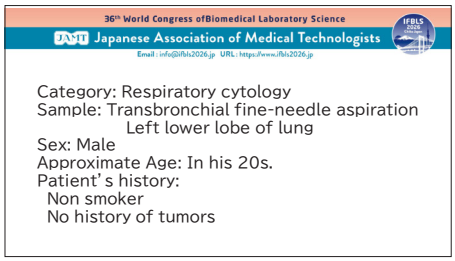
Background:
Cytologic evaluation plays a critical role in the diagnosis of a wide range of diseases. Accurate cytologic diagnosis is essential for timely patient management, particularly in uncommon or diagnostically challenging lesions.

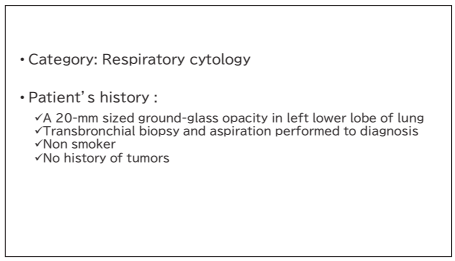
Case Presentation:
A 58 year old female presented with hypothyroidism and right thyroid lesion 13 mm. She also diagnosed left breast cancer post operation and chemotherapy 9 years ago. Cytologic FNA specimens form right thyroid were obtained with 2 conventional slides and one liquid-based bottle. Cytologic features include some clusters of epithelial cells with hyperchmatism, enlarged nuclei, prominent nucleoli and glandular formation. Few clusters of bland-looking follicular cells with focal atypia also noted. Because of overlapping morphologic findings, additional investigations including cell block preparation, and immunocytotochemistry stains were performed to further characterize the lesion.

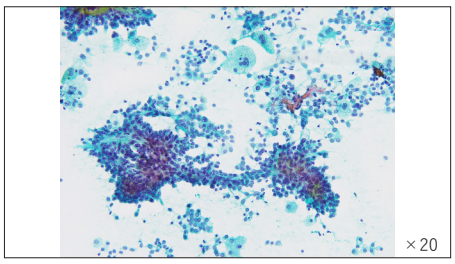
Conclusion:
This case highlights the diagnostic challenges encountered during cytologic evaluation and emphasizes the importance of correlating cytomorphology with ancillary techniques. It also demonstrates the essential contribution of medical laboratory scientists in specimen preparation, interpretation, and multidisciplinary collaboration. Awareness of these diagnostic features may improve recognition of similar cases and facilitate appropriate patient management.

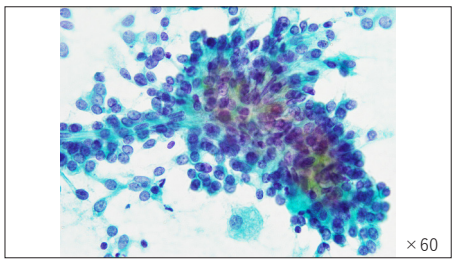
WS06-4
Global Cytology Case Conference: Sharing Diagnostic Perspectives Across Borders

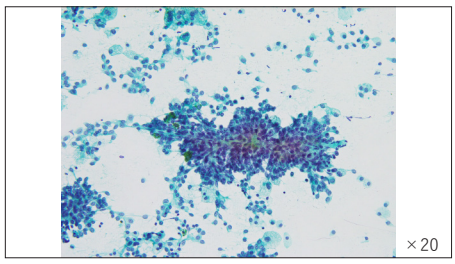
Kumi Nakatani
National Cancer Center Japan

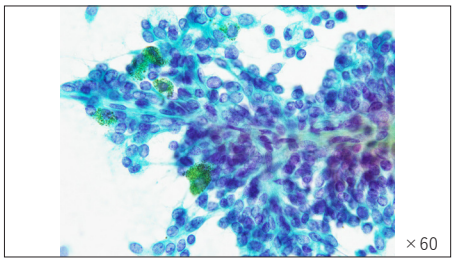


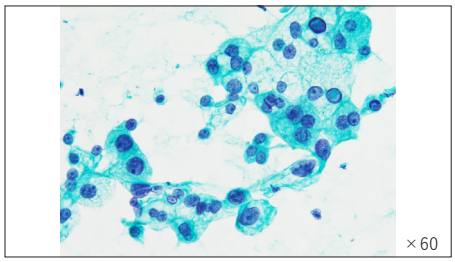


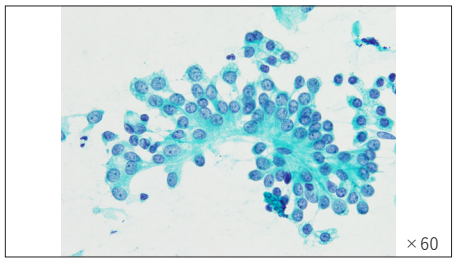


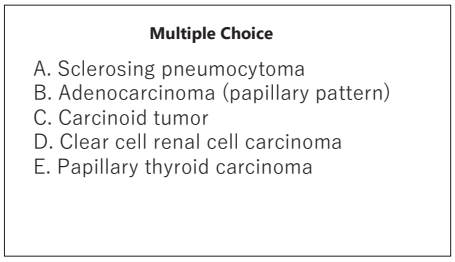


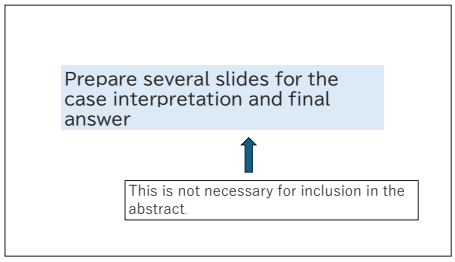












WS06-5
Global Cytology Case Conference: Sharing Diagnostic Perspectives Across Borders

Hitomi Kanno
Kyorin University Hospital

36th World Congress of Biomedical Laboratory Science
JAMT Japanese Association of Medical Technologists

IFBLS Case Conference

Hitomi Kanno, CT
Department of Hospital Pathology, Kyorin University Hospital, Mitaka, Tokyo, Japan

36th World Congress of Biomedical Laboratory Science
JAMT Japanese Association of Medical Technologists

Category: Respiratory & Mediastinum

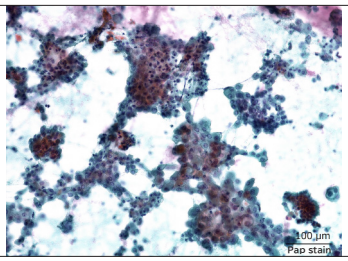
Sample: Endobronchial ultrasound-guided transbronchial needle aspiration(EBUS-TBNA), Smear of needle wash solution

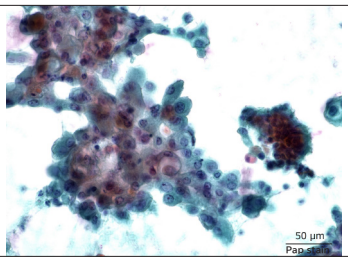
Sex: Male

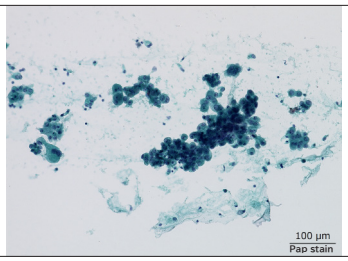
Approximate Age: In his 60s.

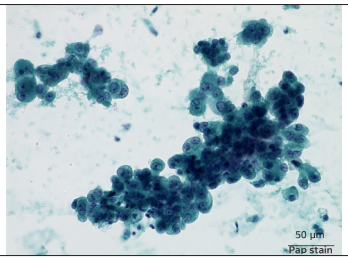
- Category: Respiratory & Mediastinum
- Patient's history:
  - ·First visited our hospital one month ago due to right chest pain.
  - ·Chest CT revealed right pleural effusion and pleural thickening.

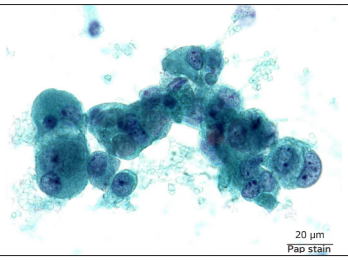
◦Further Workup:
- ·Enlargement of the #7 lymph node was detected, raising suspicion of metastatic lung cancer.
- ·EBUS-TBNA of the #7 lymph node was performed.

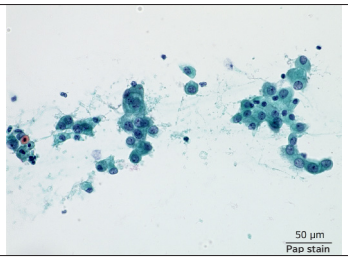












Multiple Choice

A. Thymoma

B. Squamous cell carcinoma

C. Adenocarcinoma

D. Renal cell carcinoma

E. Mesothelioma

WS07-1
Adenovirus-Infected Cells Distinguishable in Urinary Sediment

Noriko Kawamitsu
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We report a case in which adenovirus (ADV) infection was suspected based on cytomorphological findings in urinary sediment, leading to a rapid diagnosis through the combined use of a pharyngeal rapid immunochromatographic test. The patient was a teenage male diagnosed with aplastic anemia, who presented with urinary frequency two months after undergoing hematopoietic stem cell transplantation. Urinary sediment examination revealed atypical cells resembling urothelial carcinoma cells; however, these cells showed nuclear enlargement, a high nuclear-to-cytoplasmic (N/C) ratio, indistinct nuclear borders, and a uniformly smudged, degenerative nuclear appearance. Based on these findings and previous reports, ADV-infected cells were suspected, and a pharyngeal rapid diagnostic test yielded a positive result. Subsequently, a high urinary ADV-PCR viral load was confirmed.

ADV-associated hemorrhagic cystitis is a serious complication that can occur after hematopoietic stem cell or kidney transplantation. It may result in urinary retention due to blood clots or progress to systemic dissemination, leading to potentially fatal outcomes; therefore, rapid diagnosis is essential. In kidney transplant recipients, elevated serum creatinine levels may also be observed, necessitating differentiation from acute rejection, in which urinary sediment findings provide valuable diagnostic clues. Importantly, ADV-infected cells may be detected in urinary sediment prior to the onset of gross hematuria, enabling recognition even before clinical suspicion arises and contributing to early diagnosis. Furthermore, even in cases where differentiation from urothelial carcinoma is challenging, the combined use of morphological assessment and rapid diagnostic testing allows prompt reporting of suspected ADV infection to clinicians.

WS07-2

The Impact of Acute Caffeine Consumption on Routine Urinalysis Parameters in Healthy Adults: A Cross-Sectional Observational Study Clinical Implications of Caffeine as a Pre-Analytical Confounder in Spot Urine Testing

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Background: Caffeine is widely consumed and exerts mild diuretic effects, yet routine urinalysis is typically interpreted without considering a patient's caffeine intake. Prior research has focused on renal clearance and urine flow rate using timed or 24-hour collections, leaving the practical implications of caffeine consumption for routine urinalysis parameters unknown. Furthermore, spot urine samples are the standard specimen type in outpatient clinics, emergency departments, and general practice. This study aimed to determine whether acute caffeine consumption significantly alters key urinalysis parameters in spot urine samples.

Methods: A cross-sectional observational study was conducted involving 40 healthy adults aged 18–50 years. Participants were divided based on habitual caffeine intake: Group A (habitual/moderate consumers, >25 mg/day, n=20) and Group B (infrequent/non-consumers, <25 mg/day, n=20). Spot urine samples were collected from all participants, reflecting real-world clinical conditions. Samples were analyzed for osmolality, specific gravity, and pH using standard laboratory equipment. Independent t-tests compared mean values between groups.

Results: Habitual caffeine consumers demonstrated significantly higher urine osmolality (509.60 vs. 183.30 mOsm/kg, $t(26.06)=5.86$, $p<0.001$) and specific gravity (1.009 vs. 1.002, $t(24.21)=6.17$, $p<0.001$) in spot urine samples compared to infrequent/non-consumers. These differences cross clinically meaningful thresholds: Group B values fell within the dilute range suggestive of polydipsia or early diabetes insipidus, while Group A values approached the normal concentrating range. No significant difference was observed for urine pH (6.13 vs. 5.92, $t(38)=1.29$, $p=0.203$).

Conclusion: Habitual caffeine consumption significantly elevates spot urine osmolality and specific gravity, which may confound clinical interpretation of hydration status and screening for renal concentrating ability. Since spot urine samples are sufficient to detect these differences, the findings are immediately relevant to routine practice. This study supports two clinical recommendations: (1) patient caffeine history should be documented prior to urinalysis interpretation, and (2) caffeine abstinence for 4–6 hours before spot urine collection may improve diagnostic accuracy.

Keywords: Caffeine, urinalysis, spot urine, specific gravity, osmolality, pre-analytical variable, hydration assessment

WS07-3
Quantitative Assessment of Macroscopic Haematuria Using Urinary RBC Counts

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Introduction
The Japanese Evidence-based Clinical Practice Guidelines for Hematuria 2023 define macroscopic hematuria as “urine that appears red to brownish-red and can be visually confirmed as hematuria.” However, despite its clinical importance in urothelial carcinoma risk stratification, the diagnosis of macroscopic hematuria still relies largely on subjective visual assessment. Consequently, no objective standard for urine color evaluation currently exists. Therefore, this study examined the validity of using quantitative urinary red blood cell (RBC) counts measured by flow cytometry (FCM) as an alternative approach to visual assessment for the diagnosis of macroscopic hematuria.

Methods: ① Participants: Forty first-year undergraduate students from the Department of Medical Technology, Hokuriku University. All participants had no prior knowledge or technical experience related to hematuria assessment. ② Samples: Forty simulated hematuria samples of varying concentrations were prepared by adding quantified volumes of self-collected capillary blood obtained via fingerstick into 10 mL of phosphate-buffered saline. ③ Quantitative Measurement: Urinary RBC counts in uncentrifuged urine were measured using flow cytometry (FCM) with the UF-5000 fully automated urine particle analyzer (Sysmex Corporation). ④ Visual Assessment Experiment: The 40 participants evaluated the presence or absence of macroscopic hematuria in the 40 prepared simulated samples in a blinded manner.

Results and : Conclusion: The urinary RBC count in samples successfully identified as positive for macroscopic hematuria (n=28) was 3,024.9 ± 1,792.9 /μL (M±SD). The urinary RBC count in samples not identified as macroscopic hematuria (n=12) was 427.8 ± 349.6 /μL. Based on these results, the borderline zone where distinguishing macroscopic hematuria becomes difficult was estimated to be 800 to 1,200 /μL . The objective determination of macroscopic hematuria using the urinary RBC count is possible and useful.

WS08-1
Evaluation of Immunofluorescence in Renal Biopsy and the Critical Role of Biomedical Laboratory Scientists

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2 Shonan Fujisawa Tokushukai Hospital, Japan

Introduction

Renal biopsy is essential for the diagnosis of kidney diseases and typically requires hematoxylin–eosin (HE) staining, immunohistochemistry (IHC), immunofluorescence (IF), and electron microscopy. Because renal pathology demands specialized expertise and biopsy tissue is limited, the role of Biomedical Laboratory Scientists (BLS) in specimen preparation and ensuring diagnostic accuracy is critical.

IF requires advanced technical skills and careful handling, whereas IHC procedures are more standardized and automated.

This study aimed to evaluate whether IHC could serve as an alternative to IF in renal biopsy diagnostics and to clarify the evolving role of BLS in this context.

Methods

We examined 10 cases of membranous nephropathy. IHC for IgG and IgG4 was performed, and staining patterns were compared with IF findings. Two BLSs with more than 10 years of experience independently evaluated the specimens. Feasibility was also assessed based on turnaround time (TAT), reagent availability, and cost.

Results and Discussion

Both IF and IHC demonstrated granular IgG deposition along the glomerular capillary walls. IF provided clearer visualization of fine deposits and their distribution. IgG4 deposition was detected in all cases by IF; however, IHC showed weak positivity in one case and negative results in the remaining nine cases.

TAT was shorter for IF, allowing same-day evaluation, whereas IHC required four days to complete. No major differences were observed in reagent availability or cost.

Although partial replacement of IF by IHC may be feasible, complete replacement remains difficult because of sensitivity and TAT.

Conclusion

Despite the widespread use of IHC, IF using a 13-antibody panel remains indispensable in renal biopsy diagnostics. Standardized workflows are provided by the manufacture; however, as with IHC, the final diagnostic value still depends heavily on specimen quality. Because renal biopsy is invasive and re-biopsy should be avoided, BLS competency directly influences specimen quality and ultimately contributes to patient care. Continuous education and skill development for BLS are essential.

WS08-2
Implementation of AT192: automated preparation of paraffin-embedded tissue-blocks
An approach towards integrating more automated work processes in the laboratory

Hoerdum, Jill Moeller
Department of Pathology, Odense University Hospital

The implementation of the automated trimming machine AT192 for block preparation prior to automated sectioning represents a significant step toward improving standardization, efficiency, and reproducibility in the histopathology laboratory. The AT192 is designed to precisely trim paraffin-embedded tissue-blocks before microtomy, thereby optimizing downstream automated sectioning workflows and reducing manual handling variability.
Trimming of paraffin-embedded tissue-blocks for automated sectioning has until now been done manually which requires the time of two biomedical laboratory scientists to ensure completion of the daily production volume. By implementing an automated trimmer, preparation time could be reduced. The implementation process included technical installation, calibration, and validation of trimming accuracy, section surface quality, and block alignment consistency. By using one hundred paraffin-embedded test blocks, eight different programs were established to ensure quality requirements. Standard operating procedures were developed to define workflow integration, maintenance routines, cleaning protocols, and troubleshooting procedures. Emphasis was placed on operator training to ensure safe handling, correct block positioning, and optimal parameter selection for different tissue types. Risk assessment addressed mechanical safety and blade handling. After implementation, the laboratory observed enhanced workflow efficiency, reduced and improved consistency in block preparation, contributing to more stable automated sectioning performance. Comparative analyses between manual trimming and AT192-assisted preparation demonstrated improved uniformity of block surfaces and reduced preparation time per paraffin-embedded tissue-block. In conclusion, the integration of the AT192 supports improved standardization, productivity, and quality assurance in histological sample preparation, strengthening the overall robustness of the laboratory’s automated sectioning processes.

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WS08-3
Rapid Fresh Pathology for Pulmonary Specimens Whole-mount Gigapixel Imaging of Fresh Lung Surgical Tissue

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Purpose

Rapid evaluation of fresh pulmonary specimens remains challenging in routine pathology workflows. Conventional frozen section examination may introduce tissue artifacts and requires labor-intensive preparation, while formalin-fixed paraffin-embedded (FFPE) processing prolongs diagnostic turnaround time. This study investigated the feasibility of rapid fresh pathology (RFP) imaging for whole-mount visualization of fresh lung specimens.

Methods

Fresh pulmonary surgical specimens were processed using rapid whole-mount hematoxylin and eosin staining followed by nonlinear optical mesoscale imaging. Histology-like gigapixel virtual H&E images were generated without tissue sectioning or freezing. Imaging performance was evaluated for preservation of pulmonary architecture and large-area visualization capability.

Results

RFP enabled rapid generation of large-area histological images from fresh lung specimens within minutes. Pulmonary structures including alveolar architecture, stromal distribution, necrotic regions, and tumor-associated morphologic patterns were identifiable on whole-mount H&E-contrast images. The section-free workflow preserved tissue integrity while allowing visualization across centimeter-scale specimen areas. Rapid gigapixel imaging also demonstrated potential utility for fresh tissue mapping and rapid specimen assessment during pathology workflows.

Conclusion

RFP provides a rapid whole-mount imaging approach for fresh pulmonary specimens with preservation of large-scale tissue architecture. This workflow may support future applications in rapid pathology assessment and fresh tissue specimen management.

WS08-4
The Role of Biomedical Laboratory Scientists in Diagnostic Pathology and Medical Research
Supporting Diverse Research Needs through High-Quality and Reproducible Tissue Preparation

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Biomedical laboratory scientists play an essential role not only in diagnostic pathology but also in medical research. In tissue-based research, the quality of specimens and sections directly affects the accuracy and reproducibility of subsequent analyses. Therefore, technical expertise in fixation, embedding, sectioning, equipment maintenance, reagent management, and quality assurance is indispensable.

Biomedical laboratory scientists prepare various types of specimens for research, including paraffin-embedded tissues, frozen tissues, and specialized cellular samples. Depending on the purpose of each study, they adjust fixation methods, embedding orientation, section thickness, and sectioning conditions. For RNA analysis, consistent section thickness and the prevention of cross-contamination are particularly important for obtaining stable and reproducible results. Frozen tissues and technically difficult specimens also require careful orientation and appropriate preparation conditions to ensure that the target area is included and preserved.

These responsibilities extend beyond the production of individual tissue sections. Biomedical laboratory scientists maintain equipment and reagents, evaluate technical problems, and establish standardized procedures. They also share specialized techniques among staff members so that the quality of specimen preparation does not depend solely on the experience or skills of one individual.
Through close communication with pathologists and researchers, biomedical laboratory scientists translate diverse scientific questions into appropriate specimen preparation strategies. Their professional knowledge, technical judgment, and quality management support trustworthy research data. These contributions are essential not only to current pathological diagnosis but also to biomarker development, new diagnostic methods, and advances in future medical care.

WS09-1
Empowering the Next Generation: A Competency-Based Model for Lifelong Learning and Professionalism - Insights from Japan
Bridging Clinical Laboratory Excellence and Professional Leadership through Competency Development

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Background
As medicine shifts toward personalized and regenerative therapies, medical laboratory scientists (MLSs) must evolve beyond traditional generalist roles toward competency-driven professionals. While a strong foundation of broad knowledge remains essential, the integration of advanced, specialized expertise is increasingly critical to ensure high-quality and safe clinical practice.

Competency Development through Specialized Certification
At the Center for Advanced Cell Therapy, this model is applied to integrate laboratory expertise with clinical practice. Specialized certifications—including Certified Manager of Cell Therapy and Certified Blood Transfusion Technologist—serve as structured frameworks for competency development in complex clinical settings. In addition, advanced roles in cell processing, such as Clinical Cultivator (Certified Cell Processing Specialist), further reinforce competencies in quality control and the clinical implementation of therapies such as CAR-T cell therapy and platelet-rich plasma (PRP) therapy.

Integration into Clinical Practice and Multidisciplinary Collaboration
This competency-based approach extends beyond laboratory practice into active participation in apheresis and multidisciplinary care. By integrating transfusion medicine with cell processing expertise, MLSs contribute to the collection, manufacturing, and clinical application of cellular products. This integrated model supports both the safety and the quality of regenerative medicine.

Scaling through Professional Leadership and Education
To ensure sustainability and scalability, this model is extended through professional leadership within a regional medical technologists' association. Structured educational initiatives targeting early-career MLSs promote horizontal knowledge sharing and competency development across institutions. This approach prevents the fragmentation of specialized expertise while maintaining a strong foundation of general competencies across the workforce.

Conclusion
Leveraging specialized certifications to enhance professional competency enables the delivery of safe and high-quality medical care.

This continuous model of individual skill development, grounded in both broad foundational knowledge and advanced expertise, not only strengthens clinical practice but also promotes mindset transformation and supports the advancement of the next generation of healthcare professionals.

WS09-2
Using an Ethics Board Game in Biomedical Science Education Experiences and Insights

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Professional ethics is a core component of both Biomedical Science education and professional practice. In line with this responsibility, The Norwegian Association of Engineers and Technologists (NITO) and The Norwegian Institute of Biomedical Science (NITO BFI) have established ethics councils and developed resources to strengthen ethical awareness, reflection, and professional responsibility among members and students. These initiatives are rooted in NITO BFI's mission to advance professional and ethical standards in education and practice.

One such resource is the Ethics Board Game, developed in collaboration with an external agency and used both in teaching sessions with Biomedical Science students and in activities involving Biomedical Scientists and other members of NITO. Through visits to educational institutions, representatives from the ethics councils and NITO staff have used the game to facilitate dialogue, ethical reflection and discussions of dilemmas relevant to the professional role of the Biomedical Scientist.

This presentation explores experiences with the game, the types of tasks it includes and the reflective frameworks that underpin it. Some tasks are straightforward, whereas others require more explanation and discussion, making the game a flexible pedagogical tool in ethics education. The presentation examines how structured ethical reflection can support students' professional awareness, role understanding and professional identity.

The presentation is situated within the broader ethical framework of the profession, including NITO BFI's professional ethical guidelines and complementary materials designed to prepare students and Biomedical Scientists for ethical challenges in working life. Professional ethics also forms part of the national learning outcomes for Biomedical Science students, underscoring the relevance of introducing such reflective tools during education.

WS09-3
Global Harmonization of Medical Laboratory Science Education: Bridging Education, Competencies, and Emerging Career Opportunities -Preparing a Future-Ready Medical Laboratory Workforce for Global Healthcare

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Medical Laboratory Science (MLS) is undergoing a profound transformation driven by rapid technological advancements, including precision medicine, artificial intelligence, molecular diagnostics, genomics, digital health, automation, and an increasing emphasis on quality assurance and patient safety. Although the fundamental job roles, professional responsibilities, and core competencies of Medical Laboratory Professionals are largely consistent worldwide, and laboratory quality management systems are increasingly guided by international standards such as ISO 15189, but considerable variation exists in educational structures, programme duration, curriculum content, competency frameworks, professional registration requirements, regulatory systems, and career pathways across countries. These disparities create barriers to workforce mobility, mutual recognition of qualifications, career progression, and the consistent delivery of high-quality laboratory services within an increasingly interconnected global healthcare environment.

This presentation examines the need for global harmonization of Medical Laboratory Science education through competency-based curricula aligned with internationally accepted standards while retaining the flexibility to address national healthcare priorities and regulatory requirements. It advocates the development of globally comparable educational outcomes and competency frameworks that prepare graduates not only with strong technical expertise but also with leadership, quality management, research methodology, evidence-based practice, digital health, communication, ethics, professionalism, interprofessional collaboration, and lifelong learning skills. Harmonized education will facilitate curriculum benchmarking, competency mapping, academic credit transfer, and mutual recognition of professional qualifications, thereby strengthening international workforce mobility and collaboration.

The presentation also highlights the expanding scope of Medical Laboratory Science beyond traditional hospital and diagnostic laboratories. Medical Laboratory Scientists are increasingly contributing to molecular diagnostics, genomics, precision medicine, public health, epidemiology, clinical research, regulatory authorities, health informatics, artificial intelligence, academia, quality assurance, laboratory management, healthcare policy, and national health programmes. Preparing graduates and post graduate for these evolving career opportunities requires educational systems that foster innovation, critical thinking, entrepreneurship, multidisciplinary collaboration, digital competencies, and continuous professional development. Drawing upon international experiences and recent developments in healthcare education and professional regulation, this presentation proposes a collaborative framework involving professional associations, educational institutions, accreditation agencies, regulatory authorities, employers, and international organizations. Such collaboration can promote curriculum modernization, competency-based assessment, faculty and student exchange, collaborative research, and the establishment of globally accepted minimum educational standards while respecting national priorities and cultural contexts.

Global harmonization should not imply educational uniformity but rather the development of internationally accepted competency standards that ensure quality, facilitate professional mobility, and strengthen healthcare systems worldwide. This concludes with strategic recommendations for enhanced international collaboration under the leadership of the IFBLS and similar bodies to advance excellence in MLS education, promote global recognition of qualifications, and prepare a future-ready workforce capable of addressing emerging healthcare challenges.

WS09-4
Comparative Analysis of Cytotechnology Training Systems in East Asia Current Status in Japan, Taiwan, and Korea.

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Background: Training pathways and certification systems for cytotechnologists (CTs) vary considerably globally. While the United States and Europe are shifting toward standardized master's level or post-baccalaureate education, Asian systems remain diverse. Understanding these regional differences is essential for workforce development and international harmonization. This study compares current systems in Japan, Taiwan, and Korea.

Methods: A structured 20-item questionnaire addressing national certification mechanisms, educational pathways, and training requirements was distributed to national cytotechnology societies in Japan, Taiwan, and Korea in May 2025. Descriptive analysis was performed to compare system characteristics and workforce indicators.

Results: The number of registered CTs was approximately 8,100 in Japan, 860 in Korea, and 630 in Taiwan. Notably, the proportion holding International Academy of Cytology (IAC) certification was highest in Korea (74%), followed by Taiwan (47%) and Japan (43%). In all three countries, the Biomedical Laboratory Scientist (BLS) license is a mandatory national qualification, whereas the CT credential is issued by professional societies. Education involves 6 months to 2 years of specialized training post-BLS licensure; however, Japan uniquely offers a 4-year university program enabling dual qualification. Examination pass rates differed markedly: around 30% in Japan versus 70–95% in Korea and Taiwan. Annual new certifications were 250–300 in Japan, about 20 in Korea, and 10–15 in Taiwan. Japan and Korea mandate certification renewal every five years, while Taiwan utilizes continuing education credits.

Conclusions: Substantial differences exist in CT education and certification across East Asia. With cervical cancer screening shifts toward HPV testing and vaccination, the CT role must evolve. Asian frameworks require ongoing adaptation and greater standardization to align with global trends.

WS10-1
Disaster Field Hospital Overseas Clinical: Laboratory Activities, The Use of POCT, Challenges
Is it possible to conduct clinical laboratory during a disaster?This question is simply silly.

Chitoshi Sato
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Can Clinical Laboratory Work on Disaster Medical Teams?
The presenter is a member of the Japan Disaster Relief (JDR) Medical Team of Japan's goverment, and has worked as a clinical laboratory in Pakistan, Nepal, (the Philippines), Turkey, and Myanmar. This medical team is composed of medical professionals, and while clinical laboratory scientists are registered under the "logistician" category. However, in recent deployments they have increasingly been conducting clinical laboratory on-site as clinical laboratory scientists. To the best of my knowledge, a dedicated clinical laboratory department has been established since the 2000s.
POCT is a powerful ally for clinical laboratory scientists due to its high convenience and portability, which allow it to be used even in the laboratories of field hospitals set up at disaster sites overseas. However, in disaster medical settings, the POCT principles of "anyone can do it," "it's always accurate no matter who performs it," and "it can be used anywhere" do not always hold true. To ensure the reliability of testing in such settings, clinical laboratory scientists must not only adhere to standard principles regarding equipment, personnel, procedures, and record-keeping but also adapt flexibly to the specific situation and team, tailoring their approach to the mission at hand.
On the other hand, as an International EMT and a government organization, JDR encounters situations that require diplomatic consideration. Specifically, useful information obtained through clinical testing is not always officially disclosed. It becomes necessary to consider whether the clinical test results could pose a problem for the Department of Health (DOH) of the affected country.
At this conference, I will present a comprehensive report on the JDR, the details of deployments, test results (primarily POCT), and the challenges.

If you are interested in JDR Medical Team,
please scan this QR code.

WS10-2
POCT related personnel certification systems in Japan Roles of the POC Coordinator and Operator in POCT

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Introduction: Point-of-Care Testing (POCT) has become increasingly popular worldwide since the late twentieth century. Two key points are essential for effective POCT management in the hospital. The first is maintaining quality control of POCT instruments and reagents; the second is training. However, in most cases, POCT users, such as nurses and physicians, are not laboratory professionals and are unfamiliar with the importance of analytical quality management. Therefore, improving their knowledge and skills through training and education is critical to maintaining effective POCT management. To address these issues, two major POCT certifications are issued by two different bodies in Japan. Both certifications must be renewed every 5 years. Personnel who wish to renew must earn the required credits within the 5-year period to meet the qualification review criteria for renewal.

POC Coordinator: Certified by the Clinical Laboratory Science (JCLS) POC Technology Committee (formerly the Japan Society for Clinical Laboratory Automation (JSCLA) POC Promotion Committee). The main task of the POC Coordinator (POCC) is to manage POCT devices and to train POCT users at his/her institution. To become a certified POCC, candidates must meet two requirements. First, candidates must be members of the JCLS. Second, candidates must attend training sessions and seminars approved by the JCLS POC Technology Committee. The applicant must complete at least one credit in each of the following four curricula. The POCC is key personnel responsible for the effective management of POCT in accordance with the hospital's POCT policy.

Operator in POCT: Certified by the College of Laboratory Medicine of Japan (CLMJ) to assess the accuracy and precision of knowledge and techniques appropriate for POCT measurements. To become an Operator in POCT, candidates must pass an examination consisting of a written exam followed by practical and oral exams to evaluate practical skills. The certification examination is administered once a year, based on the Operator in POCT Qualification Examination Curriculum published on the CLMJ website. The examination consists of a written test featuring multiple-choice questions, as well as a practical skills test comprising a hands-on measurement technique examination and a video-based examination. An Operator in POCT who has passed the examinations covering knowledge and practical skills related to POCT is thereby guaranteed to have attained a certain standard of fundamental knowledge and technical proficiency in POCT measurement.

Conclusion: POCC provides training for POCT users and oversees POCT equipment and reagent management to improve laboratory operations. If there is no POCC in the hospital, staff members with POCT Operator certification can effectively manage POCT. These two certifications can improve laboratory management through POCT. Based on my experience launching both certifications as a founding member, I will explain what they are and outline their respective roles.

P-1-1

一般演題 Microbiology

Comparing Autof MS and VITEK MS for Microbial Identification

Routine Clinical Isolates and Stored Isolates

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Objective: To evaluate the agreement between microbial identifications obtained by Autof ms1600 (Medical & Biological Laboratories Co., Ltd. [MBL]) and VITEK MS (bioMérieux) using routine clinical isolates and stored isolates.

Methods: We analyzed 743 isolates, including 434 routine clinical isolates and 309 stored isolates. VITEK MS-reported identifications included 86 groups among routine clinical isolates and 248 groups among stored isolates. Autof ms results were compared with VITEK MS results and classified as species-level agreement, genus-level agreement, or discordance. Categorical distributions were compared using the chi-square test, and genus-level-or-better agreement rates using Fisher's exact test. Statistical analyses were performed using EZR (version 1.70).

Results: Among routine clinical isolates, species-level agreement was observed in 412/434 (94.9%) and genus-level agreement in 21/434 (4.8%), with 1/434 (0.2%) discordant result. Among stored isolates, species-level agreement was observed in 245/309 (79.3%), genus-level agreement in 58/309 (18.8%), and discordance in 6/309 (1.9%). Overall, species-level agreement was 88.4% (657/743), and genus-level-or-better agreement was 99.1% (736/743). The categorical distribution differed significantly between the two groups ($p<0.001$). Genus-level-or-better agreement remained high in both groups, although it was slightly lower in stored isolates than in routine clinical isolates (98.1% vs 99.8%, $p=0.023$). Genus-level agreement was frequently observed in *Enterobacter*, *Aeromonas*, *Bacteroides*, *Citrobacter*, *Pseudomonas*, and *Neisseria*. Discordant isolates were mainly associated with fungi and gram-positive bacilli.

Conclusion: Autof ms showed excellent agreement with VITEK MS for routine clinical isolates. The wide variation in species identified among stored isolates may have contributed to the lower species-level agreement observed in this group. The discordant identification of fungi and gram-positive bacilli suggests that these organisms may be more prone to inter-platform discrepancies under the conditions of this study.

P-1-3

一般演題 Microbiology

Integrating Genotypic and Phenotypic Data to Strengthen MRSA Resistance Surveillance

Evaluation of Emerging Resistance Patterns in MRSA Bloodstream Infections Using Integrated Diagnostics

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The presence of methicillin-resistant *Staphylococcus aureus* (MRSA) continues to be a significant health threat due to its dynamic resistance mechanisms and clinical impact on bloodstream infections. Traditional phenotypic methods are routinely used in diagnostic laboratories but will frequently fail to accurately identify emerging resistance patterns. There is a need for investigations that enable the exploration of the integrative advantages of utilizing genotypic and phenotypic data in laboratory surveillance, to optimize diagnostic accuracy and antimicrobial resistance reporting. Across global studies, the mecA gene remains consistently prevalent, with frequent co-occurrence of accessory resistance determinants including erm, tet, and fos genes associated with antimicrobial-modifying enzymes. Research highlights notable clonal transitions, including the shift from hospital-associated sequence type ST239 to community-associated ST59 in parts of Asia, the increasing presence of livestock-associated clonal complex CC398, and the continuing circulation of CC1, CC5, and CC8 related lineages in various regions. Integrating genotypic findings with routine phenotypic testing enhances early recognition of atypical resistance to beta lactams, macrolides, lincosamides, tetracyclines, aminoglycosides, and fluoroquinolones allowing for improved interpretation of discordant results and more targeted therapeutic decisions. Studies also underscore the role of combined approaches in strengthening antimicrobial stewardship, supporting outbreak detection, clarifying phylogenetic relationships, and informing infection control interventions. However, challenges to implementation persist, including variability in molecular infrastructure, the need for bioinformatics expertise, and the lack of standardized reporting frameworks across institutions and regions. The integration of genotypic and phenotypic data offers a more effective MRSA surveillance framework, improving diagnostic precision, advancing early resistance detection, and informing stronger clinical and public health interventions.

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P-1-4

一般演題 Microbiology

Two Cases of Cryptosporidiosis: Oocysts Initially Detected by Gram Stain

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Cryptosporidium spp. are protozoan parasites known to cause gastroenteritis worldwide, with symptoms ranging from mild diarrhea to severe, life-threatening illness in immunocompromised hosts. Despite its clinical importance, cryptosporidiosis often goes unrecognized, due to diagnostic challenges and the lack of routine testing. We report two cases in which Gram stain findings provided the first clues to diagnosis.

The first case involved a 48-year-old male with a history of syphilis, who presented to a previous hospital with a two-month history of diarrhea, vomiting and 25 kg weight loss. He reported being a man who has sex with men and no recent travel history. His condition worsened with cough, sputum, and dyspnea, leading to a diagnosis of Pneumocystis pneumonia and newly confirmed HIV infection. Due to refractory diarrhea, he was transferred to our hospital. Although the direct stool wet mount was negative for ova and parasites, the Gram stain revealed 4-6 μm unstained, round, halo-like structures, suggestive of *Cryptosporidium* oocysts. The diagnosis was confirmed by modified acid-fast stain and a multiplex PCR using the FilmArray GI panel.

The second case was a 20-year-old male with no significant past medical history, who developed fever and bloody diarrhea while traveling in India. After returning to Japan, he continued to experience persistent watery diarrhea and presented to our hospital. Blood tests showed a mild leukocytosis and slight liver dysfunction. Stool microscopy was negative for ova and parasites, but Gram stain again revealed 4-6 μm unstained halo-like structures similar to the first case, and modified acid-fast stain confirmed *Cryptosporidium* infection.

These cases highlight how Gram stain, a simple and widely available technique, can provide an early indication of cryptosporidiosis, prompting confirmatory staining or molecular tests for timely diagnosis and appropriate management.

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P-1-5

一般演題 Microbiology

Vertical Transmission of Candida albicans

A Microbiological Perspective on Maternal Chorioamnionitis and Early-Onset Neonatal Candidemia

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Introduction: *Candida albicans* commonly colonizes the female reproductive tract and increases during pregnancy. Ascending infection such as vulvovaginal candidiasis (VVC) may cause intrauterine inflammation and preterm birth.

Case Presentation: A 30-year-old pregnant woman with gestational diabetes mellitus presented at 27+6 weeks with preterm labor, vaginal bleeding, and “cottage cheese–like” discharge. After delivery of a 1245 g neonate, placental culture and pathology confirmed Candida albicans chorioamnionitis with funisitis. Neonatal skin KOH stain, gastric (OG) culture, and blood culture were positive for *C. albicans*, confirming vertical transmission.

Result and Discussion: Vertical transmission occurs in about 33% of preterm infants born to mothers with VVC. In this case, GDM and pregnancy-related hormonal and immune changes favored fungal overgrowth and reduced cell-mediated immunity. Although many pregnant women remain asymptomatic, ascending infection may trigger inflammatory cascades, cervical maturation, and preterm labor. In Taiwan, neonatal candidemia in very-low-birth-weight infants has a mortality rate of about 17.1%. The neonate was treated with intravenous fluconazole (12 mg/kg) according to IDSA recommendations.

Conclusion: Careful monitoring of maternal fungal colonization in high-risk pregnancies is essential to prevent severe neonatal systemic infection.

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P-1-6

一般演題 Microbiology

Hungatella effluvii Bacteremia in a Hemodialysis Patient

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Background: *Hungatella effluvii* is a strictly anaerobic, spore-forming bacterium that is rarely reported as a human pathogen. Conventional biochemical identification systems may misidentify this organism as *Clostridium* spp., making accurate identification challenging. Because only a limited number of clinical cases have been described, the clinical characteristics and antimicrobial susceptibility profiles of *H. effluvii* infections remain poorly understood.

Case Presentation: A 77-year-old man undergoing maintenance hemodialysis for end-stage renal disease was admitted with fever, hypotension, and hypoxemia. Blood cultures yielded an anaerobic gram-variable rod that was initially identified as *Clostridium* spp. by an automated biochemical identification system. MALDI-TOF MS suggested *Hungatella effluvii* or *H. hathewayi* with similar confidence scores. Definitive identification was achieved by 16S rRNA gene sequencing, confirming *H. effluvii* with 99.86% sequence identity. Antimicrobial susceptibility testing demonstrated resistance to benzylpenicillin and moxifloxacin, whereas susceptibility to piperacillin/tazobactam, meropenem, clindamycin, and metronidazole was observed. Despite antimicrobial therapy, the patient's condition deteriorated and he died, possibly due to catheter-related bacteremia.

Discussion: Previous reports indicate that infections caused by *Hungatella* species are frequently associated with severe clinical conditions such as sepsis and necrotizing infections. In addition, gram staining may show a gram-negative appearance despite phylogenetic classification as gram-positive bacilli, which can lead to diagnostic confusion.

Conclusion: Although rare, *H. effluvii* can cause life-threatening bacteremia in immunocompromised patients. Molecular identification methods, particularly 16S rRNA gene sequencing, are important for accurate diagnosis and appropriate antimicrobial therapy.

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P-1-7

一般演題 Microbiology

Environmental Detection of *Balamuthia mandrillaris* in Bangladesh

Molecular Analysis of Soil and Water Samples to Assess Infection Risk

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Purpose

Balamuthia mandrillaris is a free-living amoeba that causes granulomatous amoebic encephalitis (GAE), a rare but often fatal human infection. Although it is thought to inhabit soil environments, its environmental distribution and associated infection risks remain unclear. In South Asia, reports of both clinical cases and environmental detection are extremely limited. This study aimed to investigate the environmental distribution of *B. mandrillaris* in Bangladesh and assess the potential risk of infection using molecular analysis of soil and water samples.

Methods

Environmental samples were collected in September 2018 from areas surrounding the Turag River near Dhaka, Bangladesh. A total of 14 soil samples and 13 water samples were analyzed. DNA was extracted from each sample and stored at −80 °C until analysis. Nested PCR targeting the 16S rRNA gene region (approximately 230 bp) was performed using *Balamuthia*-specific primers. PCR products were confirmed by agarose gel electrophoresis, and amplified fragments were subjected to sequence and phylogenetic analyses.

Results

B. mandrillaris–specific gene sequences were detected in 5 of 14 soil samples (35.7%), whereas no positive results were obtained from water samples. Sequence analysis demonstrated that the detected sequences shared 97.8–100% identity with previously reported *B. mandrillaris* sequences. Phylogenetic analysis using the neighbor-joining method demonstrated that the Bangladesh-derived sequences clustered with previously reported strains from California (USA), Peru, and Hirosaki (Japan).

Discussion

These findings suggest the presence of *B. mandrillaris* in soil environments in Bangladesh. Detection of this amoeba indicates a potential infection risk for local populations. Further environmental surveys and epidemiological studies are needed to clarify its distribution and public health significance.

P-1-8

一般演題 Microbiology

Validation of PCR for H. pylori and Clarithromycin Resistance Detection

Enhancing Precision Therapy by Detecting Heteroresistance and Overcoming Culture Limitations in Clinical Practice

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Background
Helicobacter pylori is a primary risk factor for gastric cancer and peptic ulcers. Rising resistance to Clarithromycin and Levofloxacin has significantly compromised empirical treatment efficacy. Traditional culture-based antimicrobial susceptibility testing is limited by prolonged turnaround times of 2–3 weeks, fastidious growth requirements, and potential sampling bias that often misses low-frequency resistant sub-populations.

Methods
We developed a molecular diagnostic platform utilizing a two-round PCR strategy (pre-amplification followed by Real-time PCR). The assay targets the *ureA* gene for species identification and the *23S rDNA* gene for Clarithromycin resistance-associated mutations, specifically A2142G and A2143G. System validation involved 75 clinical isolates and participation in international INSTAND EQA schemes. Metrological traceability was established using *H. pylori* ATCC 26695 genomic DNA and custom pUC57-based plasmid standards.

Results
The platform demonstrated 100% concordance with Sanger sequencing for both species identification and *23S rDNA*-based Clarithromycin resistance typing. The Analytical Measurement Range (AMR) spanned 10^3 to 10^{10} copies, with a Limit of Detection (LoD) of 10^3 copies. Precision tests showed a CV <3.3%, and the system remained stable across multiple freeze-thaw cycles and long-term storage. Notably, in gastric biopsy samples, the assay identified heteroresistance cases overlooked by traditional culture, providing a more comprehensive resistance profile.

Discussion
This platform reduces turnaround times from weeks to 4–6 hours, enabling same-day targeted therapy. Detecting heteroresistance is a critical advantage; unlike culture, which may select only dominant colonies, our molecular approach captures minority resistant populations, reducing treatment failure risks. Regarding Levofloxacin, high *gyrA* gene polymorphism presents technical challenges for probe-based PCR, including probe competition. Consequently, we propose a strategic workflow: utilizing this PCR platform for first-line Clarithromycin screening while reserving sequencing for Levofloxacin resistance, optimizing cost-effectiveness and clinical accuracy.

P-1-9

一般演題 Microbiology

Nomman: automated bacterial nomenclature management in the clinical microbiology laboratory

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Introduction:
Microbial detection and identification constitute the bulk of work performed in the clinical microbiology laboratory. With methods like clinical metagenomics, laboratory reports may be filled with hundreds of microorganism names. The importance of using standard nomenclature is highlighted by the College of American Pathologists (CAP) checklist standard MIC.11375 and Clinical and Laboratory Standards Institute (CLSI) guideline M64. However, this can be very daunting without software support.

Materials and methods:
We identified 3 priority areas of nomenclature management highlighted by the CAP and CLSI requirements: harmonizing names reported by different systems within the laboratory, reviewing current nomenclature with reference to authoritative lists, and verifying the impact of nomenclature revisions on areas such as susceptibility testing. A software workflow was designed to integrate inputs and data sources to automate these tasks.

Results:
The software was implemented in Python to enable cross-platform deployment. It summarizes the nomenclature used within the laboratory and identifies inconsistencies. It also performs lookup against nomenclature authorities, namely the List of Prokaryotic names with Standing in Nomenclature (LPSN) and the List of Prokaryotic names with Standing in Nomenclature (LoRN), for reference. Lastly, it supports impact assessment of proposed name revisions on group classifications, e.g. CLSI breakpoint tables. The software is tentatively named NOMMAN, and is made available under an open-source license.

Conclusions:
In summary, NOMMAN is a software system for microbial nomenclature management in the clinical microbiology laboratory, enabling compliance with current CAP and CLSI requirements.

P-1-10

一般演題 Microbiology

Rapid Bloodstream Pathogen Identification and Resistance Screening via FilmArray BCID

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Background: Bloodstream infections (BSIs) are associated with significant morbidity and high fatality rates. Rapid pathogen identification is essential to improve clinical outcomes and optimize antimicrobial therapy.

Objective: We evaluated the FilmArray blood culture identification (BCID) panel for the rapid detection of pathogens from positive blood cultures compared to conventional phenotypic methods.

Methods: Forty-six positive blood culture samples collected between 2023 and 2026 were prospectively analyzed. Results from the FilmArray BCID assay were compared to standard culture workups using the BD Phoenix system for pathogen identification and antimicrobial susceptibility testing.

Results: Conventional culture recovered 59 unique pathogens. The BCID assay identified 52 (88.1%) isolates overall. Five recovered organisms (including Morganella morganii, Aeromonas sobria, Bacteroides caccae, Acinetobacter lwoffii and Vibrio fluvialis) were not included in the assay design. Excluding these off-panel isolates, the adjusted recovery rate was 96.3% (52/54). The assay correctly identified 100% (42/42) of targeted Gram-negative bacteria, 80.0% (8/10) of Gram-positive bacteria, and 100% (2/2) of Candida species. Furthermore, the panel successfully detected critical resistance determinants, including CTX-M, NDM, OXA-48-like, KPC, vanA/B and mcr-1.

Conclusion: The FilmArray BCID panel provides highly accurate and rapid identification of common BSI pathogens. Compared to standard phenotypic methods, the assay reduced the time to pathogen identification by 1 to 2 days. These results support the routine integration of rapid molecular testing to enhance antimicrobial stewardship and patient management.

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P-1-11

一般演題 Microbiology

Identification of *Taenia* spp. in a Regional Hospital

From Proglottids to Morphological Confirmation

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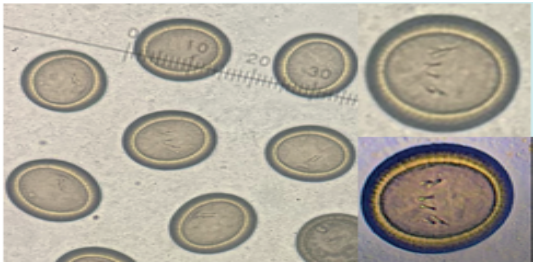
Abstract

Human *Taeniasis* is a parasitic infection caused by intestinal infestation with cestodes of the genus *Taenia*, typically acquired through ingestion of raw or undercooked beef or pork containing infective cysticerci. Although the prevalence of *Taeniasis* has declined in many regions, sporadic cases may still be encountered in routine clinical practice and require accurate laboratory identification.

A 25-year-old male patient presented to the emergency department with gastrointestinal discomfort and reported passage of visible worm segments from the anus for one day. The patient collected nine yellowish, flat proglottids, with a total length of 7.0–9.0 cm, which were submitted to the clinical laboratory for examination. Eggs were obtained by manual compression of the proglottids and examined microscopically (400×). The eggs measured approximately 30–40 μm and showed spherical morphology, a thick embryophore with radial striations, and a hexacanth embryo with visible hooklets, consistent with *Taenia* spp.



Following laboratory identification, the patient was referred to a tertiary care center for further management. This case highlights the diagnostic value of morphological examination and underscores the essential role of clinical laboratories in both detection and post-treatment evaluation of *Taeniasis* through follow-up parasitological examinations.

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P-1-12

一般演題 Microbiology

In vitro activity of macrolides against *Mycobacterium avium* complex

Implications for macrolides resistance risk in long-term prophylactic therapy

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Low-dose, long-term macrolide therapy is widely used in Japan for chronic inflammatory airway diseases such as diffuse panbronchiolitis and bronchiectasis. The safety of this approach relies on erythromycin (EM) lacking antimicrobial activity against *Mycobacterium avium* complex (MAC), thereby minimizing macrolide resistance risk. Recent EM supply disruptions have prompted interest in roxithromycin (RXM) as an alternative, but its in vitro activity against MAC has not been evaluated. We compared MIC distributions of 54 clinical isolates (28 of *M. avium* and 24 of *M. intracellulare*), MIC50, and MIC90 of five macrolides—RXM, EM, clarithromycin (CAM), azithromycin (AZM), and midecamycin (MDM) by broth microdilution method conforming to CLSI M24-A2.

Against *M. avium*, the rank order of activity (MIC50) was: CAM (1 μg/mL) > RXM (2 μg/mL) > AZM (16 μg/mL) > EM and MDM (both >32 μg/mL); similar rankings were observed for *M. intracellulare* with higher MIC values overall. RXM MICs correlated with CAM MICs (Spearman rho = 0.571, $p < 0.001$) across all isolates, consistent with shared 14-membered ring macrolide pharmacology. In contrast, no significant correlation was observed between RXM and EM MICs (rho = 0.299, p = 0.097); isolates with EM MICs >32 μg/mL frequently showed low RXM MICs, confirming distinct activity profiles.

These findings suggest that RXM, unlike EM, exerts meaningful antimicrobial activity against MAC and shares cross-susceptibility with CAM, and that MDM—with negligible activity (MIC50 and MIC90 >32 μg/mL for both species) analogous to EM—may carry lower macrolide resistance risk during long-term use. Given RXM's prolonged tissue half-life and high pulmonary penetration, long-term prophylactic RXM in patients with coexisting MAC infection may risk inducing macrolide resistance—including cross-resistance to CAM and AZM—and warrants careful clinical evaluation before replacing EM.

P-1-13

一般演題 Microbiology

Hospital Wastewater Biofilms as Antimicrobial Resistance Reservoirs

In situ evidence for prevalence, expression, and spread of carbapenemases

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Antimicrobial resistance (AMR), particularly in carbapenemase-producing organisms, represents a global health threat driven by multidrug resistance and dissemination within close-contact microbial communities. Hospital wastewater is widely recognized as a hotspot for AMR, but its functional role in shaping AMR dynamics remains unclear across environmental microbial communities. We developed *in situ* biofilms in hospital wastewater and analyzed community structure and functional gene expression using integrated metagenomic, metatranscriptomic, and culture-based approaches. Biofilms showed substantial biomass and higher contamination by extended-spectrum β-lactamase-producing *Escherichia coli* than planktonic wastewater. Biofilms were enriched in surface-adapted *Flavobacteriaceae*, and a broader repertoire of carbapenemase determinants, whereas wastewater showed a higher abundance of gut-associated *Bacteroidaceae* and virulence genes. Co-occurrence networks were dominated by Tn*3* family transposons and insertion sequences linking multiple AMR genes. Transcriptomic analyses indicated increased expression of insertion sequences and bla_{IMP}-family carbapenemase genes in biofilms. Culture-based methods detected bla_{IMP} in four biofilm isolates spanning the genera *Citrobacter*, *Pseudomonas*, and *Aeromonas*, but in one *Aeromonas* isolate from wastewater. The *Aeromonas* biofilm isolate was closely related to the hospital-wastewater isolate but carried an additional bla_{IMP-1}-containing contig, consistent with its reduced susceptibility to meropenem. All bla_{IMP-1} genes were located adjacent to Tn*3* family transposons. Phylogenetic analysis indicated that a *Citrobacter* isolate was closely related to a bla_{KPC-2}–harboring strain previously isolated from an upstream hospital environment, while additionally carrying bla_{IMP-1}. Hospital-wastewater biofilms act as stable reservoirs that facilitate the persistence and dissemination of clinically relevant carbapenem resistance, supporting the value of biofilm-focused environmental AMR assessment within a One Health framework.

P-1-14

一般演題 Microbiology

Pathogenic *Bacillus cereus* Group from Hospital Wastewater in Ghana

Genomic and phenotypic evidence of environmental adaptation and virulence traits

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Bacillus cereus group includes spore-forming bacteria with notable environmental adaptability and pathogenic potential; hospital wastewater constitutes an important but insufficiently characterized reservoir for these organisms, particularly in resource-limited settings, where wastewater treatment and monitoring infrastructure remain limited. This study aimed to characterize the genetic, phenotypic, and virulence-related attributes of *B. cereus* group isolates for the first time from Effia Nkwanta Regional hospital wastewater in Ghana. *Bacillus cereus* group strains were screened using selective agar from six sampling points of wastewater; these isolates were evaluated for whole-genome analysis, antimicrobial susceptibility, growth kinetics, biofilm formation, spore resistance, cytotoxicity, and silkworm virulence. One *B. cereus* and two *Bacillus bombysepticus* strains were recovered, all harboring major virulence genes, including those encoding cereulide, cytolysin, cytotoxin, hemolysin, and enterotoxin. Phylogenetic analysis revealed close relationships with globally distributed strains from food and environmental sources. The *B. cereus* group isolates were resistant to β-lactams, which is consistent with those from Ghana. Phenotypic profiling showed strain-specific features in growth kinetics, biofilm formation, and spore resistance. Cytotoxicity assays using human Caco-2 cells showed lactate dehydrogenase release by cell-free supernatants of *B. cereus* and *B. bombysepticus*. In the silkworm infection model, both isolates caused complete larval mortality within 24 h. Genomic and phenotypic analyses of *B. cereus* isolates from hospital wastewater in Ghana revealed varied stress adaptation capabilities and cytotoxic properties, reflecting their ecological diversity and pathogenic potential. These findings underscore the public health risks of untreated hospital wastewaters and support the need for integrated surveillance and wastewater management under a One Health approach.

P-1-15

一般演題 Microbiology

Typing and Antibiotic Susceptibility of Carbapenem-Resistant Enterobacteriaceae in Taiwan

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Background
The global spread of Carbapenem-Resistant Enterobacteriaceae (CRE) is extensive, and the clinical use of new antibiotics is closely linked to specific carbapenemase types. Understanding the distribution of these types and comparing their carbapenem susceptibility results is essential for informing infection control measures and making treatment decisions.
Methods
A total of 259 CRE strains were collected from sterile sites between 2022 and 2025 in Tungs' Hospital. Species identification was performed using MALDI-TOF (Bruker), and antibiotic susceptibility was confirmed as CRE using the BD Phoenix system. The NG-Test CARBA 5 (NG-Biotech) was utilized to detect KPC, NDM, VIM, IMP, and OXA-48.
Results
Among the 237 categorized strains, Klebsiella pneumoniae was the most prevalent species (66.6%), followed by Escherichia coli (16.4%) and the Enterobacter cloacae complex (11.8%). The results identified KPC as the dominant carbapenemase type (83 strains), followed by OXA-48 (38), NDM (15), and various combinations such as OXA-48/NDM and KPC/NDM. Susceptibility testing revealed that strains harboring Class A (KPC), Class D (OXA-48), and all combination genotypes exhibited high resistance to Imipenem (IPM), with the vast majority reaching an MIC > 4. In contrast, the 99 untyped strains demonstrated significantly higher susceptibility, with approximately 50% maintaining an MIC ≤1.
Conclusion
The study highlights significant correlations between bacterial species, carbapenemase types, and antibiotic MIC values. These findings emphasize the importance of molecular typing in guiding effective clinical interventions and infection management.

P-1-16

一般演題 Microbiology

Impact of MALDI-TOF MS on Respiratory Mold Species Distribution

A Comparison of MALDI-TOF MS and Morphological Identification Methods

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While traditional morphological identification is time-consuming and expertise-dependent, MALDI-TOF MS provides a rapid alternative, though its performance can be constrained by database limitations. This rationale underpins our evaluation of shifts in identified species distribution following the implementation of MALDI-TOF MS for respiratory mold isolates. This retrospective study analyzed respiratory filamentous fungi recovered during August 2023 to October 2025. Following the implementation of MALDI-TOF MS as the primary tool, a dual-workflow was utilized: isolates failing to yield high-confidence scores were subsequently identified via traditional morphological methods. Data were compared against a baseline period (January–July 2023) to assess diagnostic resolution.

During the baseline period (January–July 2023, n=172), *Aspergillus fumigatus* (22.7%) and unspecified *Penicillium* species (18.0%) predominated. In the post-implementation phase (Aug 2023–Oct 2025), a total of 712 respiratory isolates were processed. MALDI-TOF MS successfully identified 440 isolates (61.8%), with *Aspergillus fumigatus* (22.5%), *Penicillium citrinum* (10.5%), and *Aspergillus versicolor* (9.1%) being the most prevalent. Conversely, 272 isolates (38.2%) required traditional methods due to MALDI-TOF MS limitations. In this subgroup, unspecified *Penicillium* species (27.2%) and *Aspergillus fumigatus* (12.5%) predominated. Compared to the baseline, the integration of MALDI-TOF MS significantly improved species-level resolution within the *Aspergillus* and *Penicillium* genera, although traditional methods remained essential for identifying complex or underrepresented species in the MALDI-TOF MS database.

MALDI-TOF MS significantly improves the speed and precision of respiratory mold identification. However, the 38.2% reliance on morphology highlights that it cannot yet fully replace microscopy; therefore, a hybrid workflow remains essential for comprehensive diagnostic accuracy and mycological surveillance.

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P-1-17

一般演題 Microbiology

Serotypes and Antimicrobial Susceptibility of Group B *Streptococcus* in Pregnancy

- A Nationwide Multicenter Study in Japan -

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Introduction: Group B *Streptococcus* (GBS) causes severe infections in neonates via vertical transmission. Preventive strategies for early-onset GBS infection include intrapartum antibiotic prophylaxis and vaccine development, both of which require continuous surveillance of antimicrobial resistance and capsular serotypes. In this study, we conducted a multicenter collaborative survey across four regions in Japan to clarify the current capsular serotype distribution and antimicrobial susceptibility patterns of GBS isolated from pregnant women.

Materials and Methods: A total of 430 GBS strains were collected from pregnant women at 35–37 weeks of gestation between March and August 2020 at four institutions: Aiiku Hospital (Tokyo), Kitano Hospital (Osaka), Fukushima Medical University Hospital (Fukushima), and University of the Ryukyus Hospital (Okinawa). Capsular serotypes were classified into types Ia through IX using both the slide agglutination method and a multiplex PCR assay. Antimicrobial susceptibility for 13 antimicrobial agents was analyzed using the broth microdilution method. Susceptibility results were determined according to CLSI breakpoints.

Results: The most frequently observed capsular serotypes were type V (23.5%), followed by type III (23.3%), type Ib (18.4%), type Ia (18.1%), and type II (9.3%). The nonsusceptible rates to erythromycin (EM), clindamycin (CLDM), levofloxacin (LVFX), and tetracycline (TC) were 57.2%, 30.5%, 29.5%, and 75.8%, respectively. Additionally, the D-zone test was performed on 106 isolates (EM ≥ 1 μg/mL, CLDM ≤ 0.5 μg/mL), of which 55 (51.9%) were positive. Including inducible resistance, the overall nonsusceptible rate to CLDM was 43.3%. No strains resistant to penicillin, vancomycin, or meropenem were detected.

Conclusion: These results indicate that the predominant capsular serotypes and the high nonsusceptible rates to EM and CLDM in Japan are comparable to those reported in Europe and North America. In addition, our findings suggest regional differences in capsular serotype distribution, as well as serotype-specific antimicrobial resistance; thus, further investigation is required.

P-1-18

一般演題 Microbiology

Multidrug-resistant Streptococcus agalactiae strain isolated from ascitic fluid in Japan

Whole-genome analysis of antimicrobial resistance and virulence determinants

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Streptococcus agalactiae can cause severe infections in immunocompromised individuals, with growing concern regarding antimicrobial resistance (AMR). Herein, a multidrug-resistant *S. agalactiae* isolate was recovered from the ascitic fluid of a hospitalized patient at the Institute of Science Tokyo Hospital in Japan. Antimicrobial susceptibility testing was performed using the broth microdilution method, and capsular serotyping was conducted by PCR. Whole-genome short-read sequencing was performed using the Illumina NovaSeq 6000 system, followed by genomic analyses for phylogenetic classification, AMR, and virulence profiles. The isolate revealed nonsusceptibility to penicillin G and ampicillin and resistance to erythromycin, azithromycin, minocycline, and levofloxacin. The strain was classified as serotype Ib. The isolate was identified as ST1665 and belonged to clonal complex 1, which has been associated with invasive infections in Japan. Resistome analysis revealed the presence of AMR genes against macrolides (*mreA*) and tetracyclines (*tetM*). Mutations associated with reduced susceptibility to penicillin were identified in PBP2X (V405A, Q557E), whereas those linked to quinolone resistance were found in GyrA (S81L). Several other mutations of unknown relevance to AMR (PBP2X: G398A; GyrA: V486I) were detected. The isolate carried virulence genes for adherence (*hylB*, *lmb*, *pilC*, *scpB*, and *srtC*), hemolysis (*cyl* operon), and defense (*cps* operon), suggesting the potential to colonize host tissues and cause infection. Our data provide a basis for understanding AMR mechanisms and the pathogenic potential of a *S. agalactiae* isolate recovered from a clinical specimen and highlight the clinical relevance of genomic characterization for infection control strategies.

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P-1-19

一般演題 Microbiology

Dual-Mode uPAD with for Rapid Semi-Quantitative *Staphylococcus aureus* Detection

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Introduction:
Staphylococcus aureus is a major cause of severe infections and antimicrobial resistance (AMR), yet conventional culture-based diagnostics require 24–72 hours, delaying targeted therapy and promoting empirical antibiotic use. Rapid, accessible diagnostic tools are urgently needed to support early clinical decision-making.
Methods:
We developed an AI-enabled dual-mode paper-based microfluidic device (μPAD) integrating colorimetric immunoassay with digital image analysis. A sandwich immunoassay using HRP–TMB generates a blue color signal on paper. Images captured under standardized conditions were analyzed using a Python/OpenCV pipeline. Quantitative features from the RGB blue channel were extracted, and an exponential regression model was constructed to estimate bacterial concentration.
Results:
The platform demonstrated a strong correlation between color intensity and bacterial load ($R^2 = 0.96$), with a limit of detection of approximately 10^6 CFU/mL. Diagnostic evaluation showed 80% accuracy and 86% specificity compared with the gold-standard culture method. The total assay time was reduced to 30 minutes, enabling near real-time preliminary screening.
Conclusion:
This AI-assisted μPAD platform enables rapid, low-cost, and semi-quantitative detection of *Staphylococcus aureus* within 30 minutes, significantly shortening diagnostic turnaround time. By converting colorimetric signals into objective digital data, it improves reproducibility and reduces operator dependency. The platform demonstrates strong potential for point-of-care testing and early infection screening, supporting timely clinical decisions and antimicrobial stewardship. Future optimization to enhance sensitivity and expand to multiplex pathogen detection may further strengthen its role in next-generation decentralized diagnostic systems.

P-1-20

一般演題 Microbiology

Evaluation of the DP1R for Antimicrobial Susceptibility Testing of *Nocardia*

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Objectives: *Nocardia* species are aerobic, weakly acid-fast, Gram-positive bacilli. The microdilution method published by the Clinical and Laboratory Standards Institute (CLSI) is the only standardized susceptibility test for these bacteria. Although CLSI recommends frozen plates, their requirement for -80°C storage poses logistical challenges. This study evaluated the utility of dry plates (Dry Plate "Eiken"; DP1R) available in Japan, using the CLSI frozen plate method as a control.

Methods: We performed antimicrobial susceptibility testing on 197 clinical *Nocardia* isolates using both frozen and dry plates simultaneously. Minimum inhibitory concentrations (MICs) were measured, and categorical agreement was evaluated based on FDA performance metrics.

Results: For all 197 isolates, results for amikacin (AMK), tobramycin (TOB), imipenem (IPM), clarithromycin (CAM), sulfamethoxazole-trimethoprim (ST), and linezolid (LZD) met FDA criteria. However, species-specific analysis revealed discrepancies: CAM failed for the *N. abscessus* complex; IPM, CAM, and ST for the *N. transvalensis* complex; ST for *N. otitidiscaviarum*; and CAM and ST for other *Nocardia* spp. Notably, IPM and ST showed a 9.1% very major error (VME) rate in the *N. transvalensis* complex. While ceftriaxone, amoxicillin-clavulanate (AMPC/CVA), minocycline (MINO), and moxifloxacin did not meet overall criteria for all 197 strains, they showed acceptable performance in specific groups, such as AMPC/CVA in *N. farcinica*, *N. abscessus*, *N. transvalensis*, *N. otitidiscaviarum*, and *N. brasiliensis* complexes, and MINO in *N. farcinica* and *N. transvalensis* complexes.

Conclusions: The DP1R showed equivalent performance to the CLSI method for AMK, TOB, and LZD across all strains (species). For other antibiotics, however, since the accuracy of the test varies by bacterial species, it was determined that interpretations must take into account the test accuracy for each specific species. Further analysis using a larger number of strains for each bacterial species will be necessary.

P-1-21

一般演題 Microbiology

Comparison of the Current and the Old CLSI Method

M24-A3 vs M24-A2 for Antimicrobia Susceptibility Testing of Nocardia spp.

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Background: The Clinical and Laboratory Standards Institute (CLSI) has implemented a major revision of the antimicrobial susceptibility testing method for *Nocardia* species, transitioning from the previous standard method, M24-A2, to M24-A3. However, while changes in incubation time are likely to affect minimum inhibitory concentration (MIC) values, the CLSI has not published data regarding this impact. In this study, to clarify the effects of changes in incubation time, we performed susceptibility testing using both the new and old methods and examined the range of variation in MIC values as well as changes in susceptibility rates.

Materials/methods: A total of 195 clinical isolates of *Nocardia* species identified by 16S rRNA gene sequencing were used. The CLSI methods (M24-A3 and M24-A2) were performed simultaneously using a frozen panel (Eiken Chemical, Tokyo, Japan).

Results: Although a reduction in MIC values of up to fourfold was observed for amikacin (AMK), tobramycin (TOB), and linezolid (LZD) in M24-A3, the susceptibility rates were completely consistent; therefore, it was considered that the change in the standard method had no impact on the susceptibility results for these three agents. Regarding the concordance rate of MIC values between the new and old methods, high concordance rates (90-80%) were observed for moxifloxacin (MFLX), AMK, TOB, and sulfamethoxazole-trimethoprim, whereas the rate was 50% or less for minocycline (MINO) and LZD. The largest discrepancy in susceptibility rates between the new and old methods was observed for MINO; specifically, the susceptibility rate for *N. brasiliensis* increased from 16.7% under the old method to 77.8% under the new method. Although the extent of the impact on susceptibility rates varied by species, these results suggest that changes to standard testing methods could have a significant impact on the susceptibility results of many antibiotics used to treat *Nocardia* infections.

P-1-22

一般演題 Microbiology

Integrating FilmArray and Codehop RT-snPCR for Enterovirus Genotyping

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Introduction:
Rhinovirus (RV) and enterovirus (EV) are common respiratory pathogens with overlapping genetic characteristics, posing challenges for differentiation in routine diagnostics. Syndromic molecular platforms such as FilmArray RP2.1 enable rapid detection of RV/EV; however, they lack genotypic resolution, limiting their clinical and epidemiological utility. This study aimed to integrate multiplex PCR screening with Codehop RT-snPCR to enhance enterovirus detection and characterization.
Methods:
A retrospective study was conducted between 2024 and 2025 at a medical center in Northern Taiwan. A total of 105 respiratory specimens, initially positive for Rhinovirus/Enterovirus by FilmArray RP2.1, were included. Selected samples underwent Codehop RT-snPCR followed by sequencing for genotypic identification.
Results:
Among 105 FilmArray-positive specimens, 13 enterovirus-positive cases (12.4%) were confirmed by genotyping. CA6 was the predominant genotype, followed by EV-D68. Both are clinically significant and associated with outbreaks.
Discussion
This study demonstrates that a proportion of FilmArray RP2.1 RV/EV-positive results represent diverse enterovirus genotypes rather than rhinovirus alone. The integration of Codehop RT-snPCR enables accurate genotyping, detection of clinically relevant strains, and improved interpretation of syndromic testing results. This approach enhances outbreak surveillance and supports clinical decision-making.
Conclusion:
Combining FilmArray RP2.1 with Codehop RT-snPCR provides an effective strategy for improving enterovirus detection and genotyping. This integrated workflow enhances diagnostic accuracy, strengthens epidemiological surveillance, and supports precision infectious disease management.

P-1-23

一般演題 Microbiology

Evaluation of Accelerated Antimicrobial Susceptibility Testing Methods for Enterobacterales

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Early initiation of appropriate antimicrobial therapy is essential for managing infectious diseases effectively and improving patient outcomes. However, conventional culture-based antimicrobial susceptibility testing (AST) typically requires 16 to 20 hours to provide definitive results, creating a critical delay in clinical decision-making. Consequently, there is an urgent need for the development of innovative diagnostic devices that can significantly accelerate the susceptibility testing process.

RaST-TAS, developed by Fukoku, is a rapid testing system that utilizes advanced image analysis to monitor bacterial morphological changes induced by antimicrobial agents. This technology allows for the estimation of susceptibility profiles for Enterobacterales against eight distinct antimicrobials within a mere three hours. In this study, we conducted a performance evaluation of the RaST-TAS kit for Enterobacterales using 35 clinical strains of Enterobacterales isolated at our institution between December 2025 and March 2026. The susceptibility results obtained via RaST-TAS were compared with those from standard conventional methods to determine categorical agreement rates.

The overall agreement rate was 97.9%. Specifically, the agreement rates for individual agents were as follows: 100% for Ampicillin, 91.4% for Ampicillin/Sulbactam, 100% for Cefazolin, 100% for Cefmetazole, 97.1% for Cefotaxime, 100% for Cefepime, 100% for Meropenem, and 94.3% for Levofloxacin. The occurrence of very major errors (VMEs), where resistant strains are incorrectly classified as susceptible, is 0.3% (1/280).
In conclusion, RaST-TAS demonstrated high concordance with conventional AST and maintained a low incidence of critical errors. These results indicate that RaST-TAS is a highly useful tool for the rapid determination of antimicrobial susceptibility in clinical practice.

P-1-24

一般演題 Microbiology

Rapid Detection Epidemiological Shift of Carbapenemase-Producing Organisms

at a medical center in Northern Taiwan.

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Introduction

Carbapenemase-producing organisms (CPO) are a major global health threat due to rapid transmission and limited treatment options. However, conventional detection methods are time-consuming and may delay infection control and appropriate therapy. This study aimed to evaluate epidemiological trends and clinical impact using an integrated phenotypic detection system.

Methods

A retrospective study was conducted from Q4 2024 to Q3 2025 in a medical center. A total of 748 non-duplicate isolates were analyzed using the BD Phoenix CPO detect panel, enabling simultaneous antimicrobial susceptibility testing and carbapenemase classification (Class A, B, D).

Results

Class B carbapenemases were predominant (5.1%), exceeding Class D (2.0%) and Class A (0.8%). Quarterly analysis showed a dynamic shift: Class B increased from 24 (Q4 2024) to 54 (Q1 2025, +125%), decreased to 32 (Q2), and rebounded to 38 (Q3). In contrast, Class D declined markedly from 100 (Q1) to 15 (Q3, −85%). Trend analysis confirmed a significant increase in Class B ($p < 0.01$; OR = 2.87, 95% CI: 1.65–4.98).

Discussion

A significant shift toward Class B dominance was observed, suggesting evolving resistance dynamics. Rapid phenotypic classification supports earlier infection control and targeted therapy, highlighting the role of diagnostic stewardship.

Conclusion

A dynamic transition toward Class B carbapenemases was identified with strong statistical significance. Integrated phenotypic detection improves diagnostic speed and clinical decision-making, emphasizing the need for continuous surveillance in antimicrobial resistance management.

P-1-25

一般演題 Microbiology

Unmasking the Staphylococcus aureus Complex in Clinical Workflow

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Introduction

Accurate identification within the *Staphylococcus aureus* complex (SAC) remains challenging due to high phenotypic and genetic similarity. Misclassification may affect antimicrobial resistance interpretation and surveillance.

Methods

A total of 25 isolates initially identified as *Staphylococcus argenteus* by MALDI-TOF MS underwent 16S rRNA sequencing. Antimicrobial susceptibility testing (AST) was performed on 21 isolates and compared with hospital-wide S. aureus data (Year 114). Agreement was assessed using Cohen's kappa and McNemar's test.

Results

All isolates were reclassified as *Staphylococcus aureus* by 16S rRNA sequencing, showing complete discordance with MALDI-TOF MS ($p < 0.001$). Sequence similarity exceeded 99.5% with <0.5% variation and no discriminatory markers. AST demonstrated 100% susceptibility to vancomycin and linezolid, >95% to TMP-SMX, while penicillin resistance was 85–95% and erythromycin resistance 20–40%. These findings were consistent with hospital-wide Staphylococcus aureus data.

Discussion

The results confirm that 16S rRNA lacks resolution for SAC differentiation, while MALDI-TOF MS may introduce systematic misclassification. Concordant AST profiles support classification as Staphylococcus aureus and highlight the risk of misinterpreting resistance trends.

Conclusion

Complete diagnostic discordance ($p < 0.001$) underscores the need for integrated molecular and phenotypic approaches to ensure accurate SAC identification and reliable clinical interpretation.

P-1-26

一般演題 Microbiology

Rapid Molecular Testing and Traditional Culture: A Complementary Approach

Enhancing Clinical Microbiological Surveillance and Diagnostic Synergy

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[Background] Rapid molecular diagnostics offer high sensitivity and fast turnaround times, yet traditional culture remains the gold standard for live-bacteria confirmation and antimicrobial susceptibility testing (AST). This study evaluates the diagnostic performance and clinical complementarity of the Flimarry platform versus traditional culture methods. **[Methods]** This retrospective analysis of 103 clinical specimens (January–December 2025) compared Flimarry with conventional bacterial culture (positivity threshold: >10,000 CFU/mL), analyzing diagnostic concordance, pathogen diversity, overall detection rates, and antimicrobial resistance (AMR) profiles. **[Results]** Flimarry yielded a 35.9% (37/103) detection rate versus 34.7% (35/101) for culture, with 78.2% overall concordance (23.8% dual-positive; 54.5% dual-negative) and 21.8% specific discrepancy (6.8% Flimarry+/Culture-; 10.7% Flimarry-/Culture+). Culture dominance included *Corynebacterium striatum* (n=17) and *Stenotrophomonas maltophilia* (n=7), which were mostly off-panel. Conversely, Flimarry prominently excelled in detecting viral pathogens (e.g., Influenza A) and low-load or fastidious bacteria, identifying *P. aeruginosa* (n=10) and *Acinetobacter baumannii* complex (n=4) in completely culture-negative samples. Notably, Flimarry successfully detected one un-suspected *Legionella pneumophila* case without a requested targeted culture. Furthermore, AMR profiles showed that 7.9% of culture-positive cases were resistant, primarily driven by Carbapenem Resistance (CR). **[Conclusion]** Implementing a comprehensive dual-track strategy significantly enhances overall diagnostic sensitivity. Flimarry excels in rapid and fastidious pathogen detection, while traditional culture provides vital live-organism evidence and AST data. Future clinical efforts should optimize molecular panels for local pathogens (e.g., *C. striatum*, *S. maltophilia*) to improve patient outcomes, reduce unnecessary antibiotic exposure, and strongly support institutional antimicrobial stewardship (AMS) programs.

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P-1-27

一般演題 Microbiology

Conventional Candia Identification Matches MALDI-TOF MS

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Introduction *Candida* species are clinically significant opportunistic pathogens, and rapid, accurate species-level identification is essential for appropriate patient management. The introduction of matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) in our institution has improved the accuracy of yeast identification. This study aimed to retrospectively assess the concordance between MALDI-TOF MS and conventional identification methods, including the ID 32 C API system (bioMérieux Japan Ltd.; hereafter, ID 32 C) and CHROMagar™ Candida (Kanto Chemical Co., Inc.).

Materials and Methods A total of 30 yeast isolates recovered from clinical specimens between August 2025 and January 2026 were included. All isolates were identified using MALDI-TOF MS and re-evaluated using ID 32 C, and identification results obtained by two methods were compared. In addition, colony color on CHROMagar™ Candida was evaluated for its correlation with presumptive species identification.

Results The overall concordance rate between MALDI-TOF MS and ID 32 C was 86.7% (26/30 isolates).

All four discordant isolates were identified as *Candida parapsilosis* complex by MALDI-TOF MS, whereas they were identified as *C. parapsilosis* by ID 32 C. These isolates consistently produced white colonies on CHROMagar™ Candida, corresponding to the typical phenotype of *C. parapsilosis*.

Discussion A high level of concordance was observed between MALDI-TOF MS and ID 32 C. Since the *C. parapsilosis* complex is often treated as a single group in routine clinical practice, the observed discrepancies are unlikely to be clinically significant. Although this study has several limitations, the results obtained indicate that identification by conventional methods was generally consistent with those of MALDI-TOF MS, and also suggest that MALDI-TOF MS may provide higher taxonomic resolution.

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P-1-28

一般演題 Microbiology

Concordance Between Ampicillin/sulbactam and Amoxicillin/clavulanate in *Enterobacterales*

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Objective: Ampicillin/sulbactam (ABPC/SBT) and amoxicillin /clavulanate (AMPC/CVA) are potential treatment options for infections caused by ESBL-producing organisms. However, differences in inhibitory activity between SBT and CVA may result in discrepancies in antimicrobial susceptibility testing (AST) results. This study compared the susceptibility results of ABPC/SBT and AMPC/CVA and evaluated their categorical agreement (CA).

Materials and Methods: A total of 125 *Enterobacterales* isolates were included, comprising 100 ESBL-producing strains, 20 non-ESBL-producing strains, and 5 *E. coli* strains exhibiting chromosomal AmpC overexpression. AST was performed using dry plates by the broth microdilution method (BMD) in accordance with CLSI guidelines. Results were interpreted based on CLSI M100 (34th ed). The CA between ABPC/SBT and AMPC/CVA was calculated. In addition, disk diffusion (DD) testing was performed for selected isolates, and inter-method CA was also evaluated.

Results: The CA between ABPC/SBT and AMPC/CVA determined by BMD was 45.6%, indicating substantial discordance between the two agents. AMPC/CVA showed lower MIC values than ABPC/SBT. In contrast, the CA by DD was higher at 76.5%. Agreement between BMD and DD for each agent exceeded 75%. However, when limited to ESBL-producing isolates, while DD showed a relatively high CA (70.8%), it remained low by BMD (39.1%).

Conclusion: A considerable proportion of isolates showed discordant categorical interpretations between ABPC/SBT and AMPC/CVA, when limited to ESBL-producing isolates. Differences in β-lactamase inhibition likely contribute to these discrepancies, especially in isolates with MIC values close to clinical breakpoints, where a one-dilution difference in MIC may alter categorical interpretation. As such discrepancies may impact clinical treatment decisions, careful interpretation of susceptibility results is considered necessary.

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P-1-29

一般演題 Microbiology

Comparison of laboratory-developed Cytomegalovirus PCR against Cobas 5800 Cytomegalovirus assay

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Background
Our laboratory screens urine specimens from newborns for congenital cytomegalovirus (CMV) infection. Congenital CMV infection can lead to hearing loss, vision loss or developmental delay and occurs in about 1 in 200 births. We also screen blood (plasma) specimens collected from our haematology-oncology patients to monitor CMV levels. Both tests play an important role in managing paediatric patients.

Materials and Methods
Testing for CMV in our laboratory is currently performed by a lab-developed real-time PCR test (LDT) adapted from a publication by Leruez-Ville et al. (2003). We validated this assay on plasma and urine specimens. Our LDT was compared with the Cobas CMV assay run on the Roche Cobas 5800 instrument. We used 60 plasma samples and 68 urine samples collected from our inpatients for comparison of the two assays.

Results
For the plasma samples, 21/60 (35.0%) were positive and 31/60 (51.7%) were negative for both assays. Eight plasma samples (13.3%) contained low viral loads (Ct>35) according to Cobas 5800 but were negative by the LDT. For the urine samples, 5/68 (7.4%) were positive and 62/68 (91.2%) were negative for both assays. One urine sample (1.5%) contained low viral load (Ct=36.42) according to Cobas 5800 but was negative by the LDT.

Conclusions
The CMV assay performed by the Cobas 5800 is comparable to the LDT for viral loads within the sensitivity range of the LDT. There were a few samples where the Cobas 5800 assay was able to detect CMV at lower viral loads than our LDT. This observation requires further study with a larger number of samples and another assay to confirm discrepant results. The Cobas CMV assay has the potential to replace our current LDT for urine and blood specimens.

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P-1-30

一般演題 Microbiology

floR as a Marker of Meat-Derived Resistant *E. coli*

Whole-Genome Sequencing Analysis of Broad-Spectrum Cephalosporin-Resistant Isolates from Retail Chicken Meat

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Background: Antimicrobial-resistant bacteria from livestock are an increasing clinical concern. Broad-spectrum cephalosporin-resistant Gram-negative bacteria have been detected in retail chicken meat and frequently isolated from patients. Notably, bacteria carrying *floR* are occasionally identified among clinical isolates, although florfenicol is approved only for veterinary use in Japan. Previously, we investigated *floR*-positive strains from retail meat and compared them with clinical isolates, suggesting *floR* as a useful epidemiological marker of meat-to-human transmission. In this study, we further examined this relationship using whole-genome sequence data.

Methods: Eighteen *floR*-positive, broad-spectrum cephalosporin-resistant *Escherichia coli* isolates from retail chicken meat were analyzed. Antimicrobial susceptibility testing was performed. Draft genomes were obtained by short-read sequencing and annotated using PATRIC/RAST. Resistance genes, sequence types (STs), and plasmid incompatibility types were identified using the Center for Genomic Epidemiology tools. Conjugation experiments assessed plasmid transferability.

Results: All isolates were resistant to cefotaxime and florfenicol; more than 50% were also resistant to ciprofloxacin, levofloxacin, and fosfomycin. Broad-spectrum cephalosporin resistance genes included $bla_{\text{CTX-M-55}}$, $bla_{\text{CTX-M-65}}$, $bla_{\text{CTX-M-2}}$, and $bla_{\text{CMY-2}}$. Conjugative transfer was observed in 9 isolates, with *floR* carried on transferable plasmids in 2. ST162 was identified in 5 isolates; each showed core-genome similarity to the same clinical ST162 isolate, differing by 80–90 SNPs.

Discussion: These findings suggest that meat-associated *E. coli* ST162 may have entered the clinical setting, likely representing a fraction of the overall meat-to-human strain influx. *floR* may serve as a useful epidemiological marker for identifying broad-spectrum cephalosporin-resistant *E. coli* clinical isolates of potential meat origin.

P-1-31

一般演題 Microbiology

Comparing Immunochromatography and Nucleic Acid Amplification Tests for *Clostridioides difficile*

Immunochromatography and Nucleic Acid Amplification Tests Evaluated Against Toxigenic Culture

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Objective: The rapid and accurate diagnosis of *Clostridioides difficile* infection (CDI) is crucial for effective patient management. This study aimed to evaluate and compare the diagnostic performance of immunochromatographic assays (ICAs), nucleic acid amplification tests (NAATs), and toxigenic culture (TC) to establish an optimal diagnostic strategy for toxigenic *C. difficile* detection.

Methods: Stool specimens submitted for *C. difficile* testing between March 2024 and May 2025 were evaluated. Two ICAs (GE Test Immunochromato-CD GDH/TOX [Shimadzu Diagnostics] and Quick Chaser CD GDH/TOX [Mizuho Medy]) and two NAATs (Xpert C. difficile [Cepheid] and SmartGene CD Toxin B [Mizuho Medy]) were compared using TC as the reference.

Results: Of 498 specimens screened, 47 culture-positive samples were included in the analysis. The sensitivity of the ICAs for toxin detection was significantly low, with GE Test at 13.8% and Quick Chaser at 20.7%. In contrast, NAATs showed higher sensitivity, with Xpert at 86.2% and SmartGene at 62.1%. Notably, 13.8% of Xpert-negative and 37.9% of SmartGene-negative specimens were TC-positive, indicating that these cases could only be captured by culture methods. Specimens that were Xpert-positive but SmartGene-negative typically possessed low bacterial loads, just under the analytical detection limit. However, extending the vortexing time during the pre-processing stage significantly improved SmartGene's sensitivity to 89.7%, a level comparable to Xpert. All testing modalities demonstrated 100% specificity.

Conclusion: While NAATs outperformed ICAs, a substantial proportion of NAAT-negative specimens were TC-positive, suggesting that TC remains essential when CDI is clinically suspected despite negative NAAT results. Additionally, extending vortexing time during SmartGene pre-processing improved its sensitivity to a level comparable to Xpert.

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P-1-32

一般演題 Microbiology

Efficacy of a Resistant-Starch-Encapsulated Probiotics Supplement on Gastrointestinal Function

A 4-Week Longitudinal User Experience Study

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Background: Gastrointestinal (GI) disorders like constipation and bloating significantly diminish quality of life. While probiotics are common interventions, efficacy depends on strain specificity and delivery stability. This study evaluated the subjective physical sensations and safety of "Gene Young Plus," a probiotic supplement containing *Bifidobacterium longum, Bifidobacterium animalis,* and *Lactobacillus reuteri* encapsulated in resistant starch.
Methods: This 4-week descriptive observational study enrolled 30 participants (73% female; age range <18 to >60) via open online recruitment. At baseline, 56.7% and 50.0% of the cohort reported constipation and bloating, respectively. Following daily product consumption, participants completed Likert-scale questionnaires at weeks 2, 3, and 4. Primary endpoints included subjective improvements in bowel movement frequency, ease of defecation, bloating, and digestive discomfort (acid reflux/indigestion). Safety and tolerability were monitored via self-reported adverse events.
Results: High engagement was maintained with a 90% completion rate. Subjective scores for all indicators peaked at Week 3, suggesting a cumulative rather than immediate effect. "Bowel movement ease" consistently earned the highest ratings (3.9-4.0 points). By Week 4, 75% of participants reported improved regularity and a 75% reduction in bloating or gas. Qualitative feedback noted shorter toilet times and softer stools. Regarding safety, 82–90% of participants reported no GI discomfort, and 98.9% reported no systemic or neurological adverse reactions, indicating high tolerability.
Conclusion: Continuous use of resistant-starch-encapsulated probiotics for at least 2-3 weeks significantly improves subjective intestinal comfort and bowel regularity. These findings support its potential as a daily functional supplement for intestinal health with high compliance and minimal adverse effects.
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P-1-33

一般演題 Microbiology

ATR-FTIR for Rapid Microbial Identification

A Cost-Effective and Reagent-Free Alternative to MALDI-TOF MS

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Background
Rapid microbial identification is essential for timely antimicrobial therapy. Although MALDI-TOF MS is the current laboratory standard, its cost and maintenance limit widespread use. ATR-FTIR spectroscopy provides a reagent-free alternative with minimal sample preparation. This study evaluated the clinical feasibility of the I-dOne ATR-FTIR system using MALDI-TOF MS as the reference method.
Methods
A total of 158 clinical isolates, including Gram-positive (GP), Gram-negative (GN) bacteria, and yeasts, were tested. Identification performance was compared with MALDI-TOF MS results.
Results
At the genus level, 152 of 158 isolates were correctly identified, with an overall accuracy of 96.2%. At the species level, 142 isolates were correctly identified, yielding an accuracy of 89.0%, with 6 misidentifications.
Among GP organisms (n=27), genus-level accuracy was 100% and species-level accuracy was 92.6%, with no misidentifications. GN organisms (n=63) showed genus- and species-level accuracies of 92.1% and 90.5%, with 5 misidentifications, representing the highest error rate. For yeasts (n=68), genus-level accuracy was 98.5% and species-level accuracy was 92.6%, with 1 misidentification.
Discussion
ATR-FTIR spectroscopy demonstrated high diagnostic accuracy, particularly for Gram-positive bacteria and yeasts, whereas lower performance in Gram-negative bacteria may be associated with spectral similarity among closely related species and current database limitations. Compared with MALDI-TOF MS, ATR-FTIR is characterized by a reagent-free workflow, minimal sample preparation, and lower operational costs, although it requires a higher inoculum and does not support high-throughput batch processing. Our 2025 institutional data indicated that this approach covered 94% of routine clinical isolates in a tertiary medical center. Overall, the I-dOne ATR-FTIR system may serve as an alternative method for microbial identification, including clinically relevant Candida species, with potential application in small- to mid-sized laboratories or as a complementary system in high-volume settings. Nevertheless, further studies are warranted to comprehensively evaluate its overall performance.

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P-1-34

一般演題 Microbiology

Rapid Molecular Diagnosis of CMV-induced Frosted Branch Angiitis

Off-label Multiplex PCR Panel for Aqueous Humor in an Immunocompromised Patient

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Background
Intraocular and central nervous system (CNS) infections share a significant overlap in etiology, particularly regarding human herpesviruses. Frosted branch angiitis (FBA) is a severe, vision-threatening retinal vasculitis frequently driven by these neurotropic viruses in immunocompromised patients. Traditional aqueous humor PCR testing requires sample splitting, which risks false-negative results in low-volume specimens. Given the biological overlap between CNS and ocular pathogens, we evaluated an off-label use of a syndromic Meningitis/Encephalitis (ME) multiplex PCR panel for rapid detection of ocular pathogens to overcome current diagnostic limitations.
Methods
A 74-year-old highly immunocompromised female with a history of kidney transplantation and diffuse large B-cell lymphoma presented with severe visual impairment (left eye visual acuity: 20/1000) and diffuse FBA. Initial systemic blood tests revealed cytomegalovirus (CMV) viremia (854 IU/mL). To rapidly and comprehensively differentiate intraocular pathogens without sample dilution, an anterior chamber tap was performed. The collected aqueous humor was directly analyzed using the BioFire FilmArray ME Panel, which requires only 0.2 mL of specimen to simultaneously screen for 14 common CNS targets.
Results
The multiplex ME panel successfully identified CMV DNA in the aqueous humor within one hour, definitively confirming the diagnosis of CMV-induced FBA. This rapid, single-test molecular profiling effectively circumvented the delays of sequential PCRs. An intravitreal anti-viral injection was performed immediately, preventing disease progression. Subsequent systemic monitoring demonstrated a precipitous drop in the blood CMV viral load from 854 to <34.5 IU/mL. Monitoring systemic viremia offered a valuable additional biomarker for evaluating the patient's overall response to targeted antimicrobial therapy alongside ocular examinations.
Conclusion
Repurposing the ME panel for aqueous humor testing leverages the distinct biological overlap between CNS and ocular pathogens. This syndromic approach delivers a rapid, comprehensive diagnostic yield from minute sample volumes. Integrating rapid intraocular molecular diagnostics with longitudinal monitoring of blood viral load establishes a robust paradigm for managing sight-threatening infections.

P-1-35

一般演題 Microbiology

Analysis of Misidentification and Carbapenem Resistance in Clinical Serratia Isolates

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Background: The genus *Serratia* comprises clinically important Gram-negative bacilli, with *Serratia marcescens* being the major pathogen associated with nosocomial infections and antimicrobial resistance. Recent taxonomic updates have increased the complexity of species classification within the genus, posing challenges for accurate identification. Although matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) is widely used in clinical microbiology, inconsistent identification results are frequently observed among *Serratia* isolates.
Methods: We retrospectively collected all clinical isolates initially identified as *Serratia* spp. over a three-month period in a tertiary medical center. Identification consistency was evaluated based on concordance among the top five MALDI-TOF MS candidate species. Species distribution and carbapenem-resistance profiles were further analyzed.
Results: Among 428 *Serratia* isolates, 315 (73.6%) showed discordant MALDI-TOF MS identification, markedly exceeding the 113 (26.4%) with concordant results.(Fig.A) Overall, 84 isolates (19.6%) were carbapenem-resistant; the proportion was higher in the discordant group than in the concordant group (21.0%, 66/315 vs. 15.9%, 18/113). (Fig.B) Among the 66 carbapenem-resistant discordant isolates, the top-ranked candidate species was *S. marcescens* in 35 isolates (53.0%), followed by *S. nematodiphila* in 16 (24.2%) and *S. ureilytica* in 15 (22.7%).(Fig.C) When the representative result was assigned by majority vote across the top five candidates, 65 isolates (98.5%) were classified as *S. marcescens* and only 1 (1.5%) as *S. nematodiphila*. (Fig.D)
Conclusion: A remarkably high rate of inconsistent MALDI-TOF MS identification was observed among *Serratia* isolates in real-world clinical settings, supporting the use of the term *Serratia marcescens* complex in routine reporting. Integration of molecular methods and expansion of local spectral databases are essential to improve identification accuracy and optimize clinical decision-making.

P-1-36

一般演題 Microbiology

Performance Comparison of Panther Fusion and LabTurbo AIO

Evaluation of Diagnostic Accuracy and Efficiency in Respiratory Virus Testing

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Background: Upper respiratory viral infections cause seasonal epidemics and can lead to severe illness, particularly in pediatric and elderly populations, often requiring hospitalization. Because clinical symptoms are insufficient to differentiate causative pathogens, rapid and accurate diagnostic tools are critical for appropriate clinical management. This study compares the performance of the Panther Fusion Respiratory Panel and the LabTurbo AIO system.

Methods: A total of 1,018 throat swab specimens were collected from multiple clinics and hospitals. Samples were tested for SARS-CoV-2, influenza A and B, respiratory syncytial virus, adenovirus, human metapneumovirus, rhinovirus, and parainfluenza virus types 1–4 using both platforms. The LabTurbo AIO system uses 300 µL extraction and 60 µL elution volumes, while the Panther Fusion system uses 500 µL and 50 µL, respectively. PCR cycling conditions differ slightly, with 40 cycles for Panther Fusion and 43–45 cycles for LabTurbo, while reaction volumes are comparable (approximately 25–30 µL). Both systems employ three panels targeting similar pathogens, with turnaround times of approximately 2.4–2.5 hours.

Results: Median cycle threshold (Ct) values were consistently higher with the Panther Fusion platform, with statistically significant differences observed for SARS-CoV-2, influenza A, influenza B, adenovirus, and human metapneumovirus. Both systems demonstrated high negative percent agreement (NPA), exceeding 95% across all targets. The Panther Fusion panel achieved positive percent agreement (PPA) above 90% for most analytes, except parainfluenza virus types 1 and 2. In contrast, the LabTurbo AIO system showed a wider PPA range, from 66.2% to 100%. Overall, the Panther Fusion platform demonstrated greater sensitivity in detecting respiratory viruses.

Conclusion: The Panther Fusion Respiratory Panel demonstrated superior analytical sensitivity compared with the LabTurbo AIO system, as reflected by higher Ct values and stronger PPA across most targets. Both platforms showed excellent specificity, supporting their reliability in respiratory virus diagnostics.

P-1-37

一般演題 Microbiology

Five-Year Blood Culture Trends at Eiju General Hospital

Aiming to Improve the Specific Detection of Pathogenic Microorganisms

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Introduction
Blood culture testing is a critical diagnostic tool for the management of systemic infections. To ensure appropriate testing, objective and quantifiable indicators are required. This study evaluated the status of blood culture testing and the distribution of isolated microorganisms at our facility over the past five years.
Methods
A total of 26,020 blood culture sets were analyzed between January 2021 and December 2025. Based on the guidance of the Japanese Society of Clinical Microbiology, indicators included the number of sets per 1,000 patient-days, multiple-set collection rate, positivity rate, and contamination rate. Specimens with persistent positivity on confirmatory cultures were excluded from the calculation of the contamination rate. Bacterial distribution and trends were analyzed across all wards, with a focus on the hematology department.
Results
The mean number of blood culture sets per 1,000 patient-days was 16.2. The multiple-set collection rate was 91.7% in 2024 and 95.4% in other years. The positivity and contamination rates were 13.0% and 3.7%, respectively. In hematology patients, most common species was MRSE, accounted for 20.1%, followed by *E. coli* at 14.7%, and *E. faecium* at 10.8%. In other departments, *E. coli* at 24.0% and *K. pneumoniae* at 11.0% predominated, while MRSE accounted for only 7.6%. In the hematology department in 2025, *S. mitis* increased to 9.3%, and oral microbiota, including *S. mitis*, accounted for 11.8% of all isolates.
Discussion
Compared with data from the J-SIPHE, our facility showed a higher number of collection sets, with no major differences in other indicators. The decrease in 2024 was likely due to limited culture bottle supply. Skin commensals were frequently detected in hematology patients, requiring careful differentiation from contamination and consideration of catheter-related infection. Viridans group streptococci may also cause bacteremia in patients undergoing anticancer therapy. Continued monitoring using multiple indicators is essential to improve pathogen identification.
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P-1-38

一般演題 Microbiology

Galactomannan vs. PCR in Aspergillus Diagnosis

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Introduction
Invasive aspergillosis (IA) is a life-threatening infection in immunocompromised patients. Early diagnosis is challenging due to non-specific clinical manifestations and low sensitivity of conventional culture methods. The galactomannan (GM) assay is widely used but may be affected by false positives and limited species detection. PCR-based methods provide broader detection and improved specificity. This study aimed to evaluate the agreement between GM and Aspergillus PCR and their clinical diagnostic roles.

Methods
A retrospective study was conducted using 176 clinical specimens with paired GM and Aspergillus PCR results collected in 2025. GM was performed by ELISA, and PCR assays were conducted using commercial kits with real-time PCR.

Results
Concordant positive (n=21), concordant negative (n=125), GM-positive/PCR-negative (n=26), and GM-negative/PCR-positive (n=12). The overall agreement between GM and PCR was 83% (146/176). PCR detected fewer total positives than GM (30 vs 39) but identified 12 additional GM-negative cases, suggesting improved detection in early infection or low fungal burden. In contrast, 26 GM-positive/PCR-negative cases were observed, likely reflecting false-positive GM results.

Discussion
GM is suitable for screening but prone to false positives, while PCR offers higher specificity and broader detection, including cryptic species.

Conclusion
GM and PCR demonstrate moderate agreement but complementary roles. Combined use improves diagnostic accuracy and supports precision microbiology.

P-1-39

一般演題 Microbiology

Exploring serum IgG responses to oral commensal bacteria across individuals

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Background: The oral cavity contains over 700 bacterial species that may contribute not only to oral diseases but also to systemic conditions and chronic inflammation. However, antibody responses to individual oral bacteria remain poorly understood. This study examined serum IgG reactivity against oral bacteria isolated from each subject.
Materials and Methods: Nine healthy volunteers (22–64 years) provided dental plaque and blood samples. Bacteria were cultured under aerobic and anaerobic conditions, then isolated, and lysed for antigen preparation. Serum IgG reactivity was measured using an in-house ELISA. Highly reactive isolates (top 15%) were identified by 16S rRNA gene sequencing.
Results and Discussion: Each subject yielded 16–49 isolates, with variable IgG responses. IgG reactivity was selective, targeting a limited subset of bacteria. While individual profiles differed markedly, certain taxa were consistently recognized across subjects. At the genus level, *Staphylococcus*, *Prevotella*, *Cutibacterium* and *Haemophilus* were commonly identified. These findings suggest that IgG responses reflect cumulative immune exposure rather than acute infection. Some of the identified taxa included bacteria that may contribute to systemic inflammation and cardiovascular disease through platelet-mediated activation pathways. Limitations include the small sample size and reliance on culture-based methods.
Conclusion: Serum IgG responses to oral commensal bacteria show marked interindividual variability along with shared recognition patterns. This approach provides insight into host–microbe interactions and their potential systemic implications.
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P-1-40

一般演題 Microbiology

Rapid and Reliable

Emergency Implementation of Molecular Testing

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During peak seasons of respiratory viruses, healthcare facilities often face a massive influx of patients. While traditional **Rapid Antigen (Rapid Ag)** tests offer the advantage of speed, their sensitivity is limited—particularly during the early stages of infection when viral loads are low—leading to frequent false negatives. For high-risk groups such as children, the elderly, or those with chronic conditions, a false negative result can delay the administration of antiviral medication, thereby increasing the risk of respiratory failure or nosocomial outbreaks. This study aimed to evaluate whether rapid molecular testing could be integrated into emergency workflows while maintaining clinically acceptable turnaround time. Furthermore, it explores how rapid molecular diagnostics can bridge diagnostic gaps to optimize clinical decision-making and emergency department resource management.

This study retrospectively analyzed respiratory infection testing data (covering **Flu A/B, RSV, and GAS**) collected at our institution during 2025 to evaluate the **positive detection rates** and **turnaround times (TAT)** of **NAAT** compared to **Rapid Antigen tests**. The results indicate a significant increase in clinical positivity rates, with no substantial difference in TAT metrics. These findings suggest that rapid molecular diagnostics can enhance diagnostic breadth and early warning systems, facilitate precision medicine, and optimize overall system performance and resource allocation.

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一般演題 Microbiology

Bacterial Safety of Street-Vended Ready-to-Eat Fruits and KAP of Vendors

A Correlational Study on Ready-to-Eat Watermelons and Pineapples in Manila

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Background: Street-vended ready-to-eat (RTE) fruits are popular foods, posing public health risks with the lack of heat-killing step and exposure to environmental pollutants. A critical gap remains in understanding how vendor knowledge, attitude, and practices (KAP) translate to actual bacterial safety in high-traffic areas.

Objective: This study aimed to evaluate the bacterial contamination levels of RTE watermelons and pineapples in Quiapo and Divisoria and determine their relationship with vendor KAP.

Methods: Following descriptive cross-sectional design, 52 fruit samples were collected from 26 vendors. Socio-demographic, occupational, and fruit sourcing profiles were determined. Bacterial quality was assessed through total viable count (TVC), total coliform count (TCC), and identification via VITEK 2. A KAP survey was used, and data were analyzed using independent sample t-test and correlational analysis.

Results: Most vendors were male (80.8%), aged 30-44 (42.3%), and sourced fruits from Balintawak Public Market (80.8%). Nineteen bacterial species were highly presumptive, including *Enterobacter cloacae* (21.1%) and *Klebsiella pneumoniae* (11.6%). Mean TVC (4.85 $\log_{10}$ CFU/g) and TCC (4.19 $\log_{10}$ CFU/g) exceeded Philippine FDA safety threshold (10^4-10^5 CFU/g), despite good knowledge (96.2%) and safe practices (92.3%). Watermelons (M=5.29) showed higher contamination than pineapples (M=4.42). While positive attitudes (92.3%) correlated negatively with TVC, no significant correlation was found with TCC, highlighting environmental challenges.

Conclusion: The study reveals that street-vended RTE fruits in Manila pose a significant public health risk, with contamination levels frequently exceeding FDA safety thresholds. A distinct Knowledge-Practice Gap exists. Furthermore, while vendor attitude is a significant predictor of lower bacterial loads (TVC), it is insufficient to mitigate fecal indicator counts (TCC) driven by systemic environmental factors. Effective food safety strategies must transition from individual training to integrated interventions that address fruit-specific susceptibility (notably in watermelons), resilient opportunistic pathogens, and urban sanitation infrastructure.

P-1-42

一般演題 Microbiology

Evaluation of AI-Assisted IR Biotyper for Hypervirulent Klebsiella pneumoniae

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Background: Hypervirulent *Klebsiella pneumoniae* (hvKp) is a clinically relevant pathogen associated with severe community-acquired infections. The hypervirulent phenotype has been reported to correlate with the carriage of specific virulence genes (*pegA-344, rmpA, rmpA2, iroB,* and *iucA*). However, routine genetic testing remains limited in clinical practice due to time and cost constraints. Although the string test is commonly used as a simple screening method, its diagnostic performance is generally considered suboptimal. The IR Biotyper® (Bruker Japan), based on Fourier-transform infrared (FT-IR) spectroscopy, enables strain-level discrimination through analysis of molecular spectral patterns.

Objectives: This study evaluated the association between string test results and the presence of all five virulence genes, and explored the feasibility of an artificial intelligence (AI)–assisted approach using the IR Biotyper for identifying hvKp-related isolates.

Methods:A total of 40 non-duplicate *K. pneumoniae* isolates derived from bacteremia cases were analyzed. Virulence gene profiles were determined by multiplex PCR. IR measurements were performed in quadruplicate. Nine isolates were used for AI training, and evaluation was conducted on string test–positive isolates.

Results: Among 29 string test–positive isolates, 20 (69.0%) harbored all five virulence genes, whereas none of the string test–negative isolates did. No apparent correlation was observed between string test results and IR Biotyper clustering based on principal component analysis. AI-assisted analysis yielded a positive predictive value of 81.3% and a negative predictive value of 75.0% for identifying five-gene–positive isolates.

Conclusions: These findings may indicate that AI-assisted IR analysis has potential as a supplementary screening approach for hvKp.

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一般演題 Microbiology

Imported Brucellosis in a Regional Hospital:

Biosafety and Infection Control Considerations

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Background:
Brucellosis is a zoonotic infection that remains rare in Taiwan, with most cases being imported. According to Taiwan CDC surveillance data, no human infections caused by *Brucella* species have been reported in the past 15 years. Due to their low infectious dose and aerosol transmission potential, *Brucella* species are considered high-risk laboratory-acquired pathogens, requiring appropriate biosafety measures during diagnostic procedures.
Case Presentation:
A patient presented with persistent fever to a regional hospital. Blood cultures were positive, and routine laboratory testing initially identified the organism as *Brucella melitensis*. The isolate was subsequently referred to the Taiwan CDC, where confirmatory testing identified *Brucella abortus*. The patient had a travel history to an endemic region with animal exposure. The patient had a travel history to an endemic region with animal exposure. Appropriate antimicrobial therapy was initiated with a favorable clinical response.
Biosafety and Infection Control Considerations:
This case highlights three key considerations. First, confirmatory testing is essential due to the risk of misidentification among *Brucella* species with similar phenotypic characteristics. Second, all specimens should be treated as potentially infectious, requiring strict adherence to biosafety practices, including appropriate use of personal protective equipment and safe handling procedures. Third, timely communication between laboratory and infection control teams is critical for risk assessment and post-exposure management. No laboratory-acquired infection occurred.
Conclusion:
This case underscores the importance of confirmatory identification and integrated biosafety and infection control practices in managing rare imported pathogens.
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一般演題 Microbiology

ITS rDNA Polymorphisms in Trichophyton verrucosum Complex Strains

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Trichophyton verrucosum is the most frequent etiologic agent of cattle dermatophytosis. Throughout the world it was the second most common agent of zoophilic dermatophytes in human.

Objective: The aim of our study was to evaluate the efficacy of the PCR-RFLP and PCR-Sequencing methods for the identification and differentiation of *T. verrucosum* strains.

Material and methods: Thirty-six clinical strains identified by morphological characteristics as *T. verrucosum* were isolated from patients referred to Parasitology-Mycology laboratory of Sfax University Hospital.

Results: Identification of our strains by conventional methods was confirmed by molecular methods in 94.4 % of cases. Two strains were reclassified as *T. violaceum*. PCR products digested with *Hinf* I produced three profiles and two profiles with *MvaI*. ITS sequence analysis revealed a polymorphism in the ITS1and 5.8S regions. Analysis and alignment of consensus sequences has distinguished two types of genotypes among our *T. verrucosum* strains. The type I was the dominant genotype (93.7%). Phylogenetic study showed that the first clade contained *T.verrucosum* strains with ITS type I and species of *T.mentagrophytes* complex. The second cluster contained two *T.verrucosum* strains with ITS type II.

Conclusion: PCR-RFLP of ITS regions provided excellent tool for identifying *T. verrucosum* but also for detecting intra-species polymorphisms. PCR sequencing was useful for distinction of strains. In this study, most of *T.verrucosum* isolates were type I, dissimilar to others rare studies where type II has been the most common.

P-1-45

一般演題 Microbiology

Discrepancy between visual cleanliness and microbiological contamination of ultrasound probes

a cross-sectional point prevalence study across clinical departments

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Background: Ultrasound probes are widely used in clinical practice and may act as vectors of healthcare-associated infections. However, most previous studies have focused on single departments, and comprehensive cross-departmental data remain limited.

Objective: To evaluate bacterial contamination of ultrasound probes across multiple clinical departments and identify challenges in infection control practices.

Methods: A cross-sectional point prevalence study was conducted at a tertiary care hospital. A total of 264 probes from 18 outpatient departments and 8 central clinical units were sampled once at arbitrary time points. Visual contamination was assessed using a three-point scale (0–2). Microbiological evaluation included agar plate culture and enrichment broth culture, with positivity in either method defined as bacterial detection. Bacterial identification and antimicrobial resistance testing were performed for selected isolates.

Results: Bacteria were detected in 192 of 264 probes (72.7%). *Staphylococcus spp*. were identified in 29.0% and spore-forming bacteria in 60.7%. Potentially pathogenic bacteria were detected in 47.0%, and antimicrobial-resistant organisms in 6.1% (overlapping categories). Among probes judged visually clean (score 0), pathogenic bacteria and antimicrobial-resistant organisms were detected in 47.0% and 6.0%, respectively, indicating a discrepancy between visual cleanliness and microbiological contamination. Contamination rates varied across departments, ranging from 22.2% in the ICU to approximately 80% in several outpatient and central units.

Conclusions: Ultrasound probes were frequently contaminated with bacteria, including pathogenic and resistant organisms. Visual assessment alone was insufficient to ensure microbiological safety. Standardized cleaning and disinfection protocols and improved compliance across departments are needed to reduce the risk of healthcare-associated infections.

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一般演題 Microbiology

A Study on Workload Units in Clinical Virology Laboratories, Taiwan

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To quantify staffing requirements in clinical virology laboratories, a multicenter study was conducted to assess laboratory workload across seven clinical virology services in medical centers in Taiwan. The study evaluated workload requirements for virus isolation, identification, and rapid viral antigen detection assays. Time measurements included pre-analytical(e.g., preparation of cell culture), analytical(e.g., specimen inoculation, and viral identification), and post-analytical processes(e.g., result verification, and reporting etc.) for virus isolation and identification. For each test, manual processing time was measured and averaged over three independent runs in each laboratory. Mean workload units were 35.46 minutes (0.59 hours) for positive virus isolation, 22.87 minutes (0.38 hours) for negative isolation, and 6.2 minutes (0.10 hours) for virus antigen detection (IF). The measured workload units for virus isolation and identification were further validated against actual laboratory operations, based on specimen volume and the number of medical technologists. The results demonstrated strong concordance between calculated workload units and observed staffing levels across participating laboratories. These findings strong support the use of these standardized workload units for workforce planning and resource allocation in clinical virology laboratories.

P-1-47

一般演題 Microbiology

The 16S rRNA gene nanopore sequencing

Evaluation of background contamination and sequencing depth

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Background: Oxford Nanopore Technologies (ONT) sequencing has seen rapid improvements in read accuracy, making the platform suitable for use in clinical microbiology. ONT sequencing provides fast results, reduces hand-on time, and has sufficient quality for infectious diseases diagnostics. Broad-range amplification of the 16S rRNA gene followed by ONT sequencing is now being implemented in many routine diagnostic laboratories. The major challenge with 16S rRNA amplicon sequencing is background bacterial DNA contamination from extraction kits and other PCR reagents. Correctly distinguishing between relevant pathogens and contaminant species is crucial for patients' treatment decisions. Moreover, to ensure detection of all bacteria, sequencing requires a sufficient number of reads for each individual sample. In this study, we describe the most commonly identified contaminants from 16S amplicon ONT sequencing. In addition, we evaluate the sequencing depth necessary for accurate analysis of clinical samples.
Material and methods: 30 extraction negative controls were investigated with ONT sequencing of the 16S rRNA gene. In addition, to evaluate sequencing depth, 50 clinical samples from various infections in sterile body sites were examined using the same method.
Results: The most frequent contaminants across all negative samples were *Cutibacterium acnes*, *Hydrotalea flava* and *Staphylococcus epidermidis*. However, contaminants patterns were not stable. All contaminants appeared to be present at low amounts and therefore randomly amplified and sequenced. The number of reads required for accurate detection and identification of bacteria in the clinical samples is between 100 000 and 250 000 reads per sample.
Conclusion: Filtering of background bacterial contaminants is challenging and requires high expertise. Our findings demonstrated inconsistent bacterial contamination patterns, demanding continuous monitoring of contaminant species to enable effective managing of contaminants in ONT amplicon sequencing. In addition, adequate sequencing depth is essential for the detection of all pathogenic bacteria in clinical samples.

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一般演題 Microbiology

Reconsidering Cerebrospinal Fluid Specimen Storage Practices in Japan

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Background: Cerebrospinal fluid (CSF) specimens have been stored at room temperature to maintain the viability of fastidious bacteria such as *Neisseria meningitidis*. Meanwhile, with the multiplex PCR assays, such as the FilmArray meningitis/encephalitis (ME) panel, require storage practice at 4℃. Difference in specimen storage requirements among diagnostic tests may result in missed diagnostic opportunities.
Methods: To evaluate the need for reconsideration of CSF storage practices, we retrospectively analyzed the results of bacterial cultures and multiplex PCR using the ME panel for CSF specimens collected and tested between July 2023 and March 2026.
Result: During the study period, a total of 825 CSF specimens were submitted, of which 244 (29.6%) were tested using the ME panel. Bacterial culture yielded positive results in 34 specimens (4.1% 34/825). The identified organisms include *Pseudomonas aeruginosa* (n = 6), CNS (n = 4), *Corynebacterium* spp. (n = 4), *Staphylococcus aureus* (n =3), *Propionibacterium* spp. (n = 3), *Streptococcus pneumoniae* (n = 2), *Listeria monocytogenes* (n = 2), *Escherichia coli* (n = 2), *Enterococcus faecium* (n = 2), GPR (n = 2), *Enterococcus faecalis* (n = 1), *Bacillus* sp. (n = 1), *Nocardia* sp. (n = 1), and *Roseomonas* sp. (n = 1).
The ME panel yielded positive results in 37 specimens (15.2% 37/244), including varicella-zoster virus (n = 15), enterovirus (n = 7), herpes simplex virus type 2 (n = 6), human herpesvirus 6 (n = 3), human parechovirus (n = 1), cytomegalovirus (n = 1), *S. pneumoniae* (n = 3), *E. coli* (n = 1). *N. meningitidis* was not detected by either method.
Conclusion: Given the decreasing incidence of meningitis caused by fastidious bacteria and the increasing diagnostic opportunities for meningitis/encephalitis associated with the widespread use of the ME panel, conventional CSF specimen storage practice may need to be considered.

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一般演題 Microbiology

Genomic Analysis of Resistant K. pneumoniae in Taiwan Retail Food

Evaluating Prevalence, Antimicrobial Resistance, and Genomic Characteristics within a One Health Framework

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Background: Within the "One Health" framework, the transmission of antimicrobial-resistant (AMR) bacteria between the food chain and humans is a critical public health priority. *Klebsiella pneumoniae*, a significant opportunistic pathogen and "ESKAPE" group member, is recognized for its multidrug resistance (MDR) and its capacity to disseminate AMR genes via plasmids. This study aims to characterize *K. pneumoniae* isolates from retail meat and seafood in Taiwan to evaluate their role as reservoirs for AMR transmission.
Materials and Methods: Ninety-eight samples—comprising pork, chicken, fish, shrimp, oyster, and squid—were collected from 15 regions across supermarkets and traditional markets in Taiwan. Isolates were identified and subjected to antimicrobial susceptibility testing (AST), whole-genome sequencing (WGS), and phenotypic assays, including biofilm formation experiments and string tests for hypermucoviscosity (HMV).
Results: *K. pneumoniae* was widely distributed, with high prevalence in pork, chicken, and fish. Of 59 tested isolates, 22% (13/59) were MDR, showing significant resistance to sulfonamides and quinolones. WGS revealed most isolates belonged to the Kp1 phylogroup with diverse sequence types, including ST11, ST15, ST37, and ST107. Critical resistance genes such as blaCTX-M, blaDHA, qnrB4, and qnrS1 were identified, frequently linked with IncFII(K) plasmids. Phylogenetic analysis indicated that certain food-derived isolates clustered closely with clinical reference strains like NTUH-K2044 and CG43. Furthermore, 10% of isolates were high biofilm producers, and 5% exhibited the HMV phenotype.
Conclusion: Retail food in Taiwan serves as a significant vehicle for MDR and potentially hypervirulent *K. pneumoniae*. These results highlight the urgent need for continuous foodborne surveillance and integrated One Health strategies to control resistance transmission from the food chain to clinical environments.
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一般演題 Microbiology

Quantification strategy affects Fusobacterium abundance in colorectal cancer

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It is well established that *Fusobacterium* species are enriched in colorectal tumours. Nonetheless, reported prevalence and abundance vary across studies, raising questions about their diagnostic and biological significance in colorectal cancer (CRC). Methodological differences likely contribute to these discrepancies, particularly the choice of PCR assay and normalization approach. Common strategies include: (i) relative quantification using 16S rRNA gene targets, expressing *Fusobacterium* as a proportion of total bacterial load; (ii) normalization to a human reference gene, expressing *Fusobacterium* relative to total human DNA; and (iii) absolute quantification using standard curves. Consequently, interpretation and cross-study comparisons depend heavily on how *Fusobacterium* DNA is quantified.

To determine which normalization approach better discriminates cancers from controls, we compare the strategies using colonic biopsy samples from individuals with CRC (n=29), those with advanced adenoma (n=25), and lesion-free controls (n=25). DNA was analysed with TaqMan based real-time PCR assays targeting 1) *nusG* from *Fusobacterium nucleatum sensu lato*, 2) 16S rRNA and 3) human beta globin. Relative quantification of *Fusobacterium* spp. was calculated by 2^-dCt after normalization with 16S rRNA and beta globin. For each normalization strategy, patient groups were compared using two-sided Mann–Whitney U-test. The area under the receiver operating characteristic curve (ROC AUC) was established to evaluate how the different normalization strategies discriminated CRC from non-CRC participants. Significant differences were observed between CRC patients and controls regardless of normalization strategy. However, normalization with 16S rRNA better discriminated cancer patients from controls with a higher AUC. This may reflect that the relative abundance of *Fusobacterium* to the total number of bacteria in the tumour microenvironment is of importance in CRC development. Contact information:

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一般演題 Microbiology

Microbiological and Clinical Features of Propionimicrobium lymphophilum Infection: Literature Review

Microbiological Findings and Clinical Features of Propionimicrobium lymphophilum Infection: A Literature Review

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Introduction: *Propionimicrobium lymphophilum* is an obligately anaerobic, Gram-positive rod rarely reported as a human pathogen. Its clinical features and antimicrobial susceptibility profile remain poorly characterized. We therefore reviewed previously reported cases of *P. lymphophilum* infection together with a case of bacteremia from our hospital.

Case: An 80-year-old man with prostate cancer and urethral stricture was admitted with fever and hematuria. Acute pyelonephritis was suspected. Urine Gram staining showed Gram-negative and Gram-positive rods, whereas routine urine culture yielded only *Escherichia coli* and *Enterococcus faecalis*. Two anaerobic blood culture bottles grew Gram-positive rods on day 4. MALDI-TOF MS presumptively identified the isolate as *P. lymphophilum* with a low score of 1.72, and the identification was confirmed by 16S rRNA gene sequencing. Antimicrobial susceptibility testing was performed using broth microdilution. After sequential antimicrobial therapy, blood cultures became negative and the patient's condition improved.

Discussion: Including this case, only six cases of *P. lymphophilum* infection have been reported. A review of these cases suggests that the urinary tract may serve as a portal of entry, although urinary involvement could not be confirmed in the present case because anaerobic urine culture was not performed. Beta-lactams showed low minimum inhibitory concentration (MIC) values in all cases and may be useful therapeutic options, whereas metronidazole showed high MIC values. To our knowledge, this is the first reported case in which broth microdilution was used to evaluate the antimicrobial susceptibility of *P. lymphophilum*.

Conclusion: This review highlights the importance of careful interpretation when urine Gram staining and routine culture results are discordant. Furthermore, it underscores the need to accumulate further antimicrobial susceptibility data for *P. lymphophilum*.

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一般演題 Microbiology

Swab-Based Saliva Collection for Reliable EBV PCR Detection

Optimization of Swab-Based Saliva Sampling for Accurate EBV Molecular Diagnosis

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Saliva-based molecular diagnostics have gained importance following the COVID-19 pandemic, highlighting the need for safe and standardized specimen collection. Epstein–Barr virus (EBV), which establishes lifelong latency and is continuously shed in saliva, is suitable for non-invasive monitoring and epidemiological surveillance. In our previous work, we established a validated PCR method targeting the BALF5 gene, forming the basis of this study. However, conventional saliva collection methods remain limited by variability in sampling conditions and droplet exposure risk. This study optimized pre-analytical conditions and evaluated whether a swab-based method provides comparable detection performance to passive drooling.

Twenty healthy adults (≥18 years) were enrolled with informed consent and ethical approval. Conditions were assessed under fasting (30 minutes) and post-gargling states. Swab sampling used three swab sizes. After optimization, paired samples were collected using both methods. DNA was extracted using the QIAamp DNA Mini Kit, and concentration and purity were assessed. EBV detection was performed using the established BALF5 PCR method with beta-globin as an internal control. Semi-quantitative analysis used ImageJ.

Most samples showed DNA concentrations below 10 ng/μL and A260/A280 ratios above 1.8, with no significant differences between methods. Beta-globin and EBV DNA were detected in all samples. Although band intensity analysis showed variability, the swab method demonstrated comparable detection performance.

These findings indicate that combining the established PCR method with swab-based collection provides a safe, simple, and standardized approach for EBV detection suitable for clinical use and large-scale epidemiological surveillance.

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一般演題 Microbiology

Laboratory Morphological Identification of Ancylostoma ceylanicum from Colonoscopy Specimen

Buccal Capsule Microscopic Evaluation for Definitive Zoonotic Hookworm Identification: A Case Report

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Background: *Ancylostoma ceylanicum* is an emerging zoonotic hookworm in Asia that primarily infects dogs and cats but increasingly threatens human health. Because its clinical manifestations are nonspecific and its eggs are morphologically similar to those of other hookworms, human infection is frequently underdiagnosed.

Case Presentation: A 65-year-old woman with a history of colonic polyps presented to the gastroenterology clinic of National Taiwan University Hospital Yunlin Branch with intermittent nocturnal epigastric colicky pain radiating to the back. Routine blood tests showed no peripheral eosinophilia, and stool examination revealed no parasite eggs. However, follow-up colonoscopy identified a motile nematode approximately 1.0-cm long attached to the transverse colon mucosa. The worm was removed endoscopically and submitted for laboratory examination.

Laboratory Identification: The retrieved specimen was carefully processed and mounted on a glass slide. Microscopic examination of the prepared slide specimen demonstrated characteristic buccal capsule structures, including one pair of large ventral teeth and one pair of smaller outer teeth, confirming A. ceylanicum infection. These findings differentiated it from *Ancylostoma duodenale*, which has two pairs of ventral teeth, and *Necator americanus*, which possesses cutting plates.The patient was treated with oral mebendazole (100 mg twice daily for 3 days), with complete symptom resolution and parasite eradication.

Conclusion: This case underscores the clinical necessity of professional laboratory morphological analysis as the gold standard when conventional stool microscopy encounters bottlenecks. From a One Health perspective, mitigating this zoonosis requires integrated cross-disciplinary epidemiological surveillance, pet deworming, environmental sanitation, and community health education.

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一般演題 Microbiology

Evaluation of Workflow Efficiency in CMV

Evaluation of Workflow Efficiency in CMV Quantification Using the Fully Automated System

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Background: Cytomegalovirus (CMV) viral load monitoring is essential for immunocompromised patients. Conventional semi-automated workflows involve multiple manual steps, leading to increased hands-on time and workflow inefficiencies in high-volume laboratories. This study evaluated the operational impact of transitioning to a fully automated system.

Methods: We implemented the Alinity m platform (Abbott Diagnostics), which integrates nucleic acid extraction and real-time PCR. The automated workflow was compared with the previous semi-automated process at an average daily volume of 88 tests to evaluate hands-on time, turnaround time (TAT), and throughput.

Results: The fully automated system eliminated separate extraction and PCR setup, reducing daily hands-on time from 180 to 45 minutes. Processing TAT and sample-on-board TAT were shortened by approximately 4 hours and 2.5 hours, respectively. Urgent STAT specimens were consistently resolved within 4 hours. Increased throughput reduced monthly run frequency from 28 to 8 runs, lowering quality control reagent consumption and improving staffing efficiency.

Conclusion: The fully automated workflow remarkably enhances efficiency and minimizes operator variability. For high-volume centers, these improvements optimize laboratory operations and accelerate clinically actionable results.

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P-1-55

一般演題 Microbiology

Uncertainty in the Reproducibility of ESBL-producing *Escherichia albertii*

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Introduction: *Escherichia albertii* is a recently recognized foodborne pathogen that has also been isolated from urinary tract infection specimens. Because *E. albertii* lacks distinctive biochemical characteristics, it is often misidentified as *Escherichia coli*. Although antimicrobial-resistant strains have been reported, information regarding ESBL-producing *E. albertii* remains limited. We investigated the effects of preservation methods on antimicrobial susceptibility test results in ESBL-producing strains.
Materials and Methods: Three ESBL-producing *E. albertii* strains preserved at room temperature and at −80°C were examined. After enrichment in HI broth, strains were cultured on HI agar plates, and 10 colonies from each plate were analyzed. Antimicrobial susceptibility testing was performed according to CLSI guidelines using ceftazidime, cefotaxime, and cefpodoxime. Molecular epidemiological analysis was conducted for colonies showing discrepant susceptibility results.
Results: Among the three strains preserved at room temperature, 80%, 30%, and 80% of colonies were classified as susceptible by antimicrobial susceptibility testing, respectively. In contrast, among the three strains preserved at −80°C, 10%, 0%, and 0% of colonies were classified as susceptible, respectively. Molecular epidemiological analysis revealed that all susceptible colonies and one resistant colony lacked ESBL-related genes.
Conclusion: The results suggest that preservation methods may influence antimicrobial resistance phenotypes in ESBL-producing *E. albertii*. Although one colony was classified as resistant by antimicrobial susceptibility testing, no ESBL-related genes were detected. This colony showed a double-zone appearance, and only a few colonies were observed inside the inhibition zone, suggesting that ESBL gene-carrying bacteria may have been present at low proportions. These findings indicate that −80°C preservation may provide more stable antimicrobial susceptibility results in ESBL-producing *E. albertii*.

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P-1-57

一般演題 Microbiology

FTIR-Based Identification of High-Risk ST316-*bla*$_{NDM}$ Carbapenem-Resistant *Enterobacter hormaechei*

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Background: Carbapenem-resistant *Enterobacter cloacae* complex (CR-ECC) is an emerging healthcare-associated pathogen with limited treatment options and potential nosocomial transmission. In previous surveillance of 263 CR-ECC blood isolates collected at National Taiwan University Hospital during 2011–2020, 29 carbapenemase-producing ECC (CP-ECC) isolates (11.0%) were identified by mCIM, most of which carried metallo-β-lactamases. A major *bla*$_{NDM}$-carrying clone emerged after 2019, was identified as ST316 by MLST and PFGE, and was confirmed as *Enterobacter hormaechei* by hsp60 sequencing.
Methods: Fifty-one CR-ECC isolates with known sequence types and carbapenemase gene profiles were analyzed using Fourier-transform infrared spectroscopy (FTIR). Representative isolates covering different STs and resistance genotypes were used to establish an FTIR-based AI/machine-learning reference library, while the remaining isolates were used as a test set. FTIR spectra were assessed by PCA and classification models, and the results were compared with MLST, resistance gene data, and hsp60-based species identification.
Results: The collection included 13 sequence types. ST316 was predominant (21/51, 41.2%) and strongly associated with *bla*$_{NDM}$ carriage, whereas ST90 and ST204 were mainly associated with *bla*$_{IMP}$. PCA of FTIR spectra in the 1300–800 cm^{-1} region demonstrated clustering of major lineages, particularly the ST316-*bla*$_{NDM}$-associated cluster. In the test-set analysis, the FTIR-based ST prediction model achieved 94% isolate-based accuracy. Class recall and precision were 100% for ST316 and most other evaluable STs. For ST90, two isolates were conservatively classified as uncertain, resulting in 50% class recall. Species-level prediction was limited: all hsp60-confirmed *E. cloacae* and *E. hormaechei* spectra were classified as uncertain, resulting in 0% spectrum-based accuracy.
Conclusions: FTIR may serve as a rapid tool for CR-ECC ST-level typing and resistance prediction, particularly for identifying ST316-*bla*$_{NDM}$-associated *E. hormaechei*, while species-level identification requires molecular confirmation.

P-1-58

一般演題 Microbiology

Mucorales Isolation Enabled by Antibacterial Suppression in Rhino-Orbital Mucormycosis

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Introduction: Rhino-orbital mucormycosis is a rapidly progressive fungal infection requiring early diagnosis. Mucorales are characterized by fragile hyphae and low culture recovery rates, and isolation from nasal swab specimens may be hindered by bacterial overgrowth. **Cases:** A woman in her 40s was admitted to our hospital with diabetic ketoacidosis (DKA) after presenting with impaired mobility, nausea and diarrhea. Following admission, she developed rapidly progressive right visual loss and proptosis. Nasal endoscopy revealed black necrotic tissue, and the specimen was submitted for microbiological testing.
Investigations: Gram staining of a nasal swab specimen demonstrated broad ribbon-like pauci-septate hyphae with irregular 90-degree branching, suggestive of Mucorales. Serum β-D-glucan was negative. Routine culture yielded only mixed bacterial overgrowth, including Pseudomonas aeruginosa, Escherichia coli, methicillin-susceptible Staphylococcus aureus, and Streptococcus agalactiae. Since bacterial overgrowth was considered to interfere with fungal isolation, the swab suspension was incubated with meropenem and penicillin discs prior to subculture onto chloramphenicol-containing potato dextrose agar. Following antibacterial suppression, Mucorales was successfully isolated. Findings suggestive of mucormycosis were immediately communicated to clinicians. Lactophenol cotton blue staining demonstrated characteristic rhizoids and sporangia. The isolate was identified as Rhizopus arrhizus by ITS region sequencing.
Conclusion: Careful examination of Gram-stained specimens enabled recognition of mucormycosis, contributing to early therapeutic intervention. Furthermore, suppression of bacterial overgrowth using antimicrobial discs enabled successful isolation of Mucorales, leading to species identification and antifungal susceptibility testing. Even when microorganism cannot be recovered by routine methods, clinical laboratories should optimize testing conditions for accurate and timely microbiological diagnosis.
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P-1-59

一般演題 Microbiology

Multiplex PCR vs. Culture in Pneumonia Diagnosis

Performance and Clinical Impact on Lower Respiratory Pathogen Detection

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Objective
Rapid identification of pneumonia pathogens is crucial for timely therapeutic intervention. This study evaluated the diagnostic performance of the FilmArray Pneumonia Panel (FA PN) compared with the standard of care (SOC) culture, focusing on pathogen detection rates, co-infection patterns, antimicrobial resistance (AMR) gene identification, and turnaround time (TAT).
Materials and Methods
A retrospective analysis was conducted on 209 bronchoalveolar lavage (BAL) specimens at a medical center in 2025. The cohort primarily consisted of ICU patients (75%) and individuals aged 65 years or older (57%). FA PN results were compared with SOC for detection sensitivity, co-infection rates, and AMR gene detection (MRSA and carbapenemases).
Results
The overall positivity rate for FA PN was 50.7%. The infection patterns identified included pure bacterial infections (23.4%), pure viral infections (14.8%), and viral-bacterial co-infections (12.4%), demonstrating the system's ability to provide a comprehensive pathogen profile. On average, FA PN reduced the identification TAT by 20.5 hours. Notably, FA PN showed 100% concordance with SOC for MRSA detection and provided AMR results (including carbapenemase genes) 2.6 to 2.8 days earlier than final antimicrobial susceptibility testing (AST).
Conclusion
FA PN offers high sensitivity and rapid detection of co-infections while significantly shortening laboratory TAT. By providing critical AMR information 2.5 to 3 days earlier than conventional methods, FA PN facilitates early antimicrobial de-escalation and targeted therapy, demonstrating substantial clinical value for infection control and patient management.

Keywords
FilmArray Pneumonia Panel, Pathogen Detection

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P-1-60

一般演題 Microbiology

Automated Blood Culture Impact

Workflow Optimization and Processing TAT

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Objective
Blood culture is a critical tool for diagnosing bacteremia, and timely specimen processing is essential for accurate and rapid pathogen detection. Delays in loading specimens or retrieving positive bottles can directly impair time-to-result and, consequently, clinical decision-making. This study evaluated the effectiveness of implementing an automated blood culture system combined with workflow optimization in reducing two critical time metrics: "Collection-to-Load" and "Detection-to-Unload".
Materials and Methods
The bioMérieux BacT/ALERT VirtuO system, featuring continuous random-access loading capability, was introduced. The operational workflow was re-engineered from a "scheduled batch loading" model to an "immediate loading upon receipt" protocol.
Results
Implementing the immediate loading protocol significantly reduced the overall loading delay from a median of 84 minutes to 7 minutes, representing an approximately 92% reduction. With respect to positive bottle management, the integration of remote monitoring reduced the unloading delay for geographically dispersed instruments from 88 minutes to 59 minutes, ensuring more timely initiation of downstream microbiological workup.
Conclusion
The synergy of hardware automation, workflow re-engineering, and real-time information visualization represents an effective strategy for optimizing laboratory turnaround time (TAT) in blood culture processing. These improvements facilitate earlier clinical decision-making, support antimicrobial stewardship, and reduce the window of empirical therapy, providing substantial value for the targeted treatment of patients with bacteremia.

Keywords
Blood Culture Automation, Workflow Optimization

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P-1-61

一般演題 Microbiology

Establishment of a Murine Sepsis Model in Acute Radiation Syndrome

Analysis of Intestinal Barrier Dysfunction After High-Dose Irradiation

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Objective
Exposure to high-dose ionizing radiation during nuclear disasters or radiation accidents can induce Acute Radiation Syndrome (ARS). The gastrointestinal tract is highly susceptible to radiation-induced injury. Damage to the intestinal epithelium impairs intestinal barrier integrity, allowing bacterial translocation into the bloodstream and leading to bacteremia and sepsis. This study aimed to determine the timing of sepsis onset in the ARS mouse model and to investigate the relationship between intestinal barrier dysfunction and sepsis development.
Methods
Male C57BL/6N mice were divided into a non-irradiated control group and a 9.0 Gy total-body X-irradiation group. Survival was monitored for 30 days after irradiation. Blood cultures and fluorescein isothiocyanate-dextran (FITC-dextran) permeability assays were performed to evaluate bacterial translocation. Intestinal barrier function was assessed using hematoxylin and eosin staining, Alcian blue staining, and immunofluorescence staining for Zonula Occludens-1 (ZO-1) and proliferating cell nuclear antigen (PCNA).
Results
No bacterial growth was detected in blood cultures obtained on day 5 after irradiation, and no significant increase in intestinal permeability was observed in the FITC-dextran assay on day 8. In contrast, bacterial growth was detected in blood and organ cultures on day 12 after irradiation, and all irradiated mice died on the same day. Histopathological analyses demonstrated epithelial detachment, depletion of the mucus layer, reduced ZO-1 expression, and decreased PCNA expression.
Conclusion
These findings suggest that sepsis in the ARS mouse model develops rapidly around day 12 after irradiation and appears to precede death. Future studies will focus on intervention strategies aimed at suppressing sepsis and improving survival based on the identified onset timing and irradiation dose.

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一般演題 Microbiology

Ceftazidime-Avibactam Susceptibility and Synergy Testing for Carbapenem resistant isolates

Ceftazidime-Avibactam and Aztreonam synergy testing in Carbapenem resistant Enterobacterales and Pseudomonas aeruginosa

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Background:Carbapenem-resistant Gram-negative pathogens pose a challenge due to limited therapeutic options and evolving resistance mechanisms. Ceftazidime–avibactam (CZA) and CZA–aztreonam synergy testing are critical for characterizing resistance patterns. This study aimed to evaluate the burden of carbapenem-resistant Enterobacterales (CRE) and carbapenem-resistant Pseudomonas aeruginosa (CRPA), assessing their CZA susceptibility and synergy profiles.
Methods:A laboratory-based study analysed one-year data (June 2025 - May 2026). Carbapenem-resistant isolates of Escherichia coli, Klebsiella pneumoniae, and Pseudomonas aeruginosa were included. CZA susceptibility and CZA-aztreonam synergy testing results were analyzed.
Results:Among 2,980 carbapenem-resistant isolates, 2,285 isolates were CRE and 695 were CRPA. CRE predominantly comprised Klebsiella pneumoniae (1,766/2,285;77.3%) followed by Escherichia coli (519/2,285; 22.7%). CZA susceptibility was observed in 518/2,285 (22.7%) CRE isolates. Overall, 1,535/2,285 (67.2%) CRE isolates demonstrated synergy positivity, while 232/2,285(10.15%) were synergy negative. The predominance of synergy-positive isolates suggests a substantial burden of MBL mediated resistance, particularly NDM associated resistance.Among E. coli, 119/519 (22.9%) isolates were synergy negative, compared to only 113/1,766 (6.4%) K. pneumoniae isolates, potentially suggesting additional non-MBL pathways like PBP3 insertions in E coli. Among CRPA isolates, 351/695 (50.5%) were synergy negative, which is considerably higher than observed in CRE.
Conclusion:CRE represents a major burden, with K. pneumoniae being the predominant pathogen. High synergy positivity among CRE suggests a substantial prevalence of MBL-mediated resistance, whereas a higher proportion of synergy-negative CRPA indicates differing resistance mechanisms. Continuous surveillance is essential to optimize antimicrobial stewardship and therapeutic decision-making.
Keywords:CRE, CRPA,Ceftazidime–Avibactam, Synergy testing, NDM

P-1-63

一般演題 Microbiology

Potential Food-Poisoning Risk of Toxin-Producing *Bacillus cereus* in Common Foods

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Background: *Bacillus cereus* is found in the environment and in food products, and it causes food poisoning, which is classified into diarrheal and emetic types. Although both types are generally considered mild, severe cases have been reported. Common food sources include rice, noodles, and pasteurized milk. In this study, we focused on these foods to investigate the contamination status of *B. cereus* and the prevalence of toxin-related genes.
Method: A total of 200 food samples were collected from Japan. The samples were processed in accordance with the Food Microbiology Manual, and a 10-fold stock solution was prepared. The stock solution was cultured onto the agar plate and also added to the HIB enrichment culture, and then cultured onto the agar plate. The resulting *Bacillus cereus*-like colonies were isolated and examined biochemically. Strains identified as the *B. cereus* group by biochemical characteristics and mass spectrometry were subjected to PCR for toxin-related genes.
Result: *B. cereus* was isolated from 42/200 samples (21%), yielding 44 strains. The toxin gene prevalence was: *hblA* and C 37%, *hblD* 41%, *nheA*, B, and C 100%, *cytK* 48%, *entFM* 100%, and *ces* 2%. Total bacterial counts ranged from 0-10^4 CFU/mL, with most at 10^2-10^3 CFU/mL. Discussion: Both the food contamination rate and the prevalence of toxin genes were generally consistent with previous studies. Bacterial counts were low, ranging from approximately 10^2-10^3 CFU/mL. Since these counts represent the total bacterial population, including *B. cereus*, the number of *B. cereus* itself was presumed to be even lower. However, strains carrying the *hbl* associated with diarrhea-type and the *ces* associated with emesis-type food poisoning were identified. These findings suggest that the risk of food poisoning may represent a hidden hazard in everyday life. In addition, low-temperature-growing strains have recently been reported, emphasizing the importance of proper storage and adherence to expiration dates.

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一般演題 Microbiology

Genetic analysis of *Enterococcus faecalis* thymidine-dependent small-colony variants

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Introduction: Thymidine-dependent small-colony variants (TD-SCVs) are auxotrophic mutants that require exogenous thymidine for growth. These variants harbor mutations in *thyA*, which encodes thymidylate synthase, leading to deficiency of the thymidylate synthesis pathway. TD-SCVs have been reported in several bacterial species, including *Staphylococcus aureus*, coagulase-negative staphylococci, and *Escherichia coli*; however, reports on *Enterococcus faecalis* remain limited.
Methods: Eleven TD-SCV strains of *E. faecalis* isolated from clinical specimens were analyzed. Species identification was performed using 16S rRNA gene sequencing, and mutation analysis of *thyA* was conducted. In addition, multilocus sequence typing (MLST) was performed to determine sequence types (STs), and a minimum spanning tree was constructed using the goeBURST algorithm via PHYLOViZ Online to assess genetic relatedness.
Results: All 11 isolates were identified as *E. faecalis* and were found to harbor mutations in *thyA*. Three strains exhibited missense mutations, and 8 exhibited frameshift mutations (3 deletions, 4 insertions, and 1 combined deletion/insertion). Notably, 2 of the insertion mutations involved an 817-bp sequence presumed to be derived from a transposon. Three of the 11 strains reverted to the wild-type phenotype after several subcultures, whereas the remaining strains did not. Phenotypic reversion coincided with restoration of the wild-type *thyA* sequence. Furthermore, MLST analysis classified the 11 strains into 6 distinct STs (ST4, ST16, ST179, ST223, ST616, and ST719), which belonged to different clonal complexes.
Discussion: Our findings suggest that, consistent with other bacterial species, *thyA* mutations are the primary genetic basis of the TD-SCV phenotype in *E. faecalis*. The strains were not closely related in the minimum spanning tree, suggesting that SCVs did not arise within a single clonal complex.
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P-1-65

一般演題 Microbiology

Detection of Cefiderocol-Resistant *Escherichia coli* in Wastewater.

Genomic analysis reveals international relatedness of $bla_{\text{NDM-5}}$-producing isolates.

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Antimicrobial-resistant (AMR) bacteria readily spread across national borders through human mobility and food distribution systems, emphasizing the need for coordinated international action. Among them, carbapenemase-producing Enterobacterales (CPE) represents a major global public health threat. However, in Japan current surveillance data are based predominantly on clinical isolates, and the distribution of CPE in community-associated environments remains poorly understood. To address this gap, we investigated carbapenemase-producing *Escherichia coli* recovered from wastewater in Saitama Prefecture, Japan. During this investigation, we identified cefiderocol (CFDC)-resistant strains and characterized their genomic features.

Influent wastewater samples were collected on seven occasions between October 2020 and August 2023. Red colonies grown on CHROMagar mSuperCARBA were identified as *E. coli* by MALDI-TOF MS, and two CFDC-resistant isolates were detected by antimicrobial susceptibility testing. Whole-genome sequencing and core-genome single-nucleotide polymorphism (cgSNP) analyses were performed. In addition, mutations in PBP3 and truncation mutations in *cirA*, both associated with reduced CFDC susceptibility, were examined.

Both isolates belonged to O25:H34-ST2973 and carried $bla_{\text{NDM-5}}$, bla_{TEM}, and *mcr*. They also harbored a YRIN insertion after position 333 in PBP3, together with E349K and I532L substitutions, as well as a truncation mutation of *cirA*. These alterations associated with reduced CFDC susceptibility were also identified in other sequence types. Phylogenetic analysis demonstrated that the isolates were closely related to bla_{NDM}-harboring *E. coli* recovered from human rectal swabs in China, which also harbored CFDC resistance-associated mutations.

These findings indicate that wastewater-derived isolates in Japan, which are genetically linked to internationally circulating lineages, have acquired multiple determinants associated with CFDC resistance. Continuous wastewater surveillance is important for monitoring the emergence and dissemination of clinically relevant resistant strains. Corr : +81-48-973-4727

P-1-66

一般演題 Microbiology

Evaluating Diverse Specimens for Newborn Congenital Cytomegalovirus Screening

: Diagnostic Performance of Saliva, Urine, and Oral Mucosa by qPCR

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Abstract Content:

Background: Congenital cytomegalovirus (cCMV) infection is a primary cause of non-genetic hearing loss and neurodevelopmental delays in newborns, making early detection through universal screening critical for timely intervention. This study aimed to screen for newborn cCMV infection and evaluate the clinical performance of various specimens—including saliva, urine, and oral mucosa—to identify a convenient and reliable screening tool for clinical practice.

Method: Paired biological specimens—including saliva swabs, urine, and oral mucosa swabs, were collected from a cohort of 1,800 newborns within 21 days of birth. Viral DNA was extracted from all specimens and analyzed using real-time polymerase chain reaction (qPCR). Positive specimens were further evaluated by comparing viral loads among different specimen types based on cycle threshold (Ct) values.

Results: Among the enrolled neonates, four were confirmed positive for cCMV, indicating a prevalence rate of approximately 0.22% in this cohort in Taiwan. Screening results demonstrated that saliva and oral mucosa specimens showed superior screening performance, achieving a diagnostic sensitivity of 100%, whereas urine specimens showed a sensitivity of 75%. Furthermore, saliva and oral mucosa specimens exhibited significantly higher viral loads than urine specimens.

Conclusions: This study confirms that saliva and oral mucosa specimens are highly effective and reliable for newborn cCMV screening because of their high sensitivity and viral loads. Although urine specimens may be useful for monitoring the progression of neonatal infection, they demonstrate lower sensitivity for screening purposes and present greater challenges in specimen collection. Considering multiple specimen types may help optimize universal screening strategies and facilitate the early detection and clinical management of cCMV infection.

P-1-67

一般演題 Microbiology

Pulmonary *Mycobacteroides hainanense* infection: The First Case Report from Japan

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Introduction： Accurate species identification is of the utmost importance, as treatment for non-tuberculous mycobacterial (NTM) infections varies significantly depending on the causative species. Although the widespread adoption of mass spectrometry has made rapid identification possible, it remains difficult in many cases when dealing with new or rare species.

Case： A woman in her 60s. Since 2013, the patient has had pulmonary NTM disease, with the bacteria repeatedly clearing and then recurring. Treatment continued until 2021, but was discontinued due to liver dysfunction, and the patient has been under observation since then. In October 2025, her cough and sputum output increased; a chest CT scan revealed increased opacities, confirming findings consistent with NTM disease.

Laboratory Investigations： Sputum smear of Miller and Jones classification P1 was positive (±) on Ziehl-Neelsen stain. Culture results yielded yellow, smooth colonies. Identification testing using the MALDI Biotyper® sirius one (Bruker Daltonics, Bremen, Germany) was inconclusive, with low-confidence matches for *M. nebraskense* (Score Value: 1.64) and *M. parascrofulaceum* (Score Value: 1.62). Subsequently, genetic analysis targeting multiple regions (*hsp65*, *rpoB*, *ITS*) identified the organism as *M. hainanense*.

Discussion： *M. hainanense* is a slow-growing bacterium first reported in China in 2025. In this case, the bacterium could not be identified using mass spectrometry because it was not yet included in the manufacturer's reference library. The low-confidence matches for *M. nebraskense* and *M. parascrofulaceum* are likely attributable to their phylogenetic proximity to *M. hainanense*.

Conclusion： We encountered a case of long-term pulmonary NTM disease caused by *M. hainanense*. When mass spectrometry results are unreliable for NTM identification, the possibility of a new or rare species must be considered; therefore, genetic analysis targeting multiple regions is essential for a definitive diagnosis.

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P-1-68

一般演題 Microbiology

Diagnostic Value of Francisella tularensis in a Low-Incidence Setting

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Introduction: *Francisella tularensis* causes tularemia, a rare but potentially serious zoonotic bacterial disease. In Norway incidence is low, with cases typically occurring in localized clusters linked to environmental factors such as contaminated freshwater and fluctuations in rodent populations. This contributes to delayed diagnosis due to its rarity and unexpected presentation.Clinical manifestations are variable and often non-specific, commonly including influenza-like symptoms and regional lymphadenopathy. Consequently, patients may initially be evaluated for malignancy or other serious conditions. Diagnosis is further complicated by the difficulty of culturing the bacterium and associated biosafety risks.

Methods: Serological detection is performed using the automated VirClia® Lotus system. Serum samples are analysed for IgG and IgM antibodies using a chemiluminescence immunoassay (CLIA), based on antigen–antibody binding and emitted light measurement.Results are interpreted using manufacturer-defined cut-offs (negative, borderline, positive). The method is fully automated, enabling standardized processing with minimal hands-on time and safe integration into routine laboratory workflows.

Results: The VirClia® Lotus system enables reliable detection of *F. tularensis*-specific antibodies. Positive cases, though infrequent, are identified in patients with persistent lymphadenopathy and non-specific systemic symptoms.

In several cases, malignancy was initially suspected, highlighting diagnostic challenges. Serology supported confirmation of infection and clinical decision-making. The assay showed consistent, reproducible performance despite low testing volumes.

Conclusion: CLIA-based serology using the VirClia® Lotus system is suitable for routine detection of *F. tularensis*. Although rare in Norway, tularemia remains clinically significant due to variable presentation and its ability to mimic serious diseases.

Accurate diagnosis is essential, as untreated tularemia may cause prolonged illness and standard antibiotics are ineffective. Reliable serological testing enables timely diagnosis, reduces uncertainty, and supports appropriate treatment. Diagnostic readiness for low-incidence infections remains essential for patient care and laboratory preparedness.

P-1-69

一般演題 Microbiology

Fungal Skull Base Osteomyelitis

A Three-Case Series of Aspergillus and Candida Infections Highlighting Diagnostic Challenges

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Introduction: Skull base osteomyelitis (SBO) is rare and life-threatening, often linked to malignant otitis externa in elderly diabetics. While Pseudomonas is classical, fungal causes are increasingly recognized, causing delayed diagnosis, atypical features, and higher morbidity. We report three microbiologically confirmed fungal SBOs due to Aspergillus fumigatus, Aspergillus flavus, Candida parapsilosis, and Candida glabrata.

Material and Methods: Retrospective review of clinical records, imaging, operative notes, and microbiology of three patients with skull base infection. Data included presentation, radiology, microbiology, management, and outcomes.

Results:

Case I: A 65-year-old diabetic male with otalgia, otorrhea, and facial palsy; MRI showed mastoiditis, SBO, and temporal lobe abscess. Fungal Cultures grew A. fumigatus; improved with amphotericin B.

Case II: A 40-year-old female with prior ear trauma, chronic discharge and bleeding; imaging showed parietal–occipital–temporal bone erosion. Cultures grew A. flavus and C. parapsilosis; improved after surgical debridement.

Case III: A 60-year-old diabetic male with multiple cranial nerve palsies and right mastoiditis on CT; biopsy yielded C. glabrata; treated with amphotericin B then fluconazole, with full neurological recovery.

Diabetes, delayed presentation, and nonspecific symptoms hindered diagnosis. Imaging showed bone erosion; definitive diagnosis required fungal culture.

Conclusion: Fungal SBO should be considered in refractory or atypical skull base infections. Early imaging, comprehensive fungal microbiology, and prompt targeted antifungal therapy are essential to improve outcomes and prevent irreversible neurological sequelae.

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P-1-70

一般演題 Microbiology

HIV Notifiable Co-infections: Trends and Characteristics

A Laboratory-Based Retrospective Study

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Background

In Taiwan, acute hepatitis A virus (HAV) has shifted from foodborne routes toward sexual transmission, mirroring syphilis and gonorrhea patterns. Patients with HIV face elevated risks of notifiable co-infections. This study utilizes laboratory databases and statutory notification records to evaluate the prevalence and longitudinal trends of these infections from 2020 to 2026.

Materials and Methods

A retrospective cohort study was conducted by cross-matching an institutional HIV registry (n=163) with the statutory notifiable disease database (n=430) between 2020 and 2026. Medical record numbers were used for database linkage to identify overlapping cases and evaluate longitudinal infection patterns.

Results

Among 163 patients, 53 (32.5%) experienced at least one notifiable co-infection, totaling 88 records. Syphilis was the most prevalent co-infection (62.3%, 33/53), followed by gonorrhea (n=6) and acute hepatitis C (n=5). Notably, 19 patients (35.8%) presented with multi-pathogen infections during follow-up, including clusters of recurrent syphilis, gonorrhea, enteric pathogens, and Mpox. All secondary sexual and blood-borne infections occurred exclusively in male patients.

Conclusion

This study confirms a high burden of notifiable co-infections among patients with HIV, characterized by significant recurrence and multi-pathogen clustering. These findings support developing LIS-based Clinical Decision Support Systems (CDSS) to automatically identify high-risk cases and prompt clinicians for timely screening and proactive follow-up management.

Keywords

HIV, co-infections, Syphilis, Notifiable infectious diseases

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一般演題 Microbiology

The Association of Soil Factors on the Prevalence of Soil-Borne

Helminths in Organic and Conventional Farms in Selected Areas of Batangas, Philippines

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Soil-transmitted helminthiasis remains a significant health concern in the Philippines, particularly among agricultural workers who are in constant contact with soil. Previous research explored how certain physicochemical soil properties influence the presence and absence of soil-transmitted helminths (STHs), but further investigation is needed to determine how varying farming systems affect parasitic survival and contamination. This study aimed to determine how two different farming systems — organic and conventional — in selected farms in Batangas influence the presence and survival of STHs by examining five soil factors: depth, moisture, pH, temperature, and texture. Samples were collected from each site and analyzed at two depths. Using a modified flotation technique on the collected soil samples, the study identified a significant disparity in contamination rates between the farming systems. Specifically, the findings demonstrated a 40% contamination rate in the selected organic farm from the exclusively identified *Toxocara spp*. eggs, whereas the conventional farm exhibited 0% contamination rate. Additionally, results revealed warm soil temperatures as a common factor across both farm types although the farms differed entirely in soil chemistry. The selected conventional farm was found to be more acidic, whereas the selected organic farm featured a more stable, neutral environment. Statistical analysis showed that animal-based organic fertilizers and natural water sources were key predictors of STH presence ($p = 0.043$). Moreover, the equal prevalence across depths 1 and 2 suggests vertical movement of STH eggs, with the deeper layer providing protection from surface stressors.

Key Words: Soil-Transmitted, Conventional, Organic, Farming System, *Toxocara spp*.

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一般演題 Microbiology

Clinical Impact of Universal Sputum MTBC DNA Screening

Dual Benefits of Integrating Routine Molecular Diagnostics into Initial Sputum Workups

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Clinical Utility of Routine MTBC DNA Testing in Initial Sputum Specimens: A Retrospective Analysis from a TB Reference Laboratory in Taiwan

Background and Objectives: Following Taiwan CDC's March 2025 mandate for routine Mycobacterium tuberculosis complex (MTBC) DNA testing alongside acid-fast staining (AFS) for suspected TB patients, this study evaluated the clinical and workflow impacts using full-year data from a contracted reference laboratory.

Methods: We retrospectively analyzed 31,042 sputum sets from 2025. Patients submitting three or more specimens with at least one MTBC DNA result (n = 2,281) were stratified into Phase 1 (Jan–Feb; reflex testing for AFS-positive cases; n = 82) and Phase 2 (Mar–Dec; routine universal testing; n = 2,199).

Results: Phase 1 MTBC DNA positivity was 25.6% (21/82), restricted to AFS-positive cases. In Phase 2, universal screening yielded 4.0% (89/2,199) positivity; 7.9% (7/89) were AFS-negative, avoiding diagnostic delays. Among 323 Phase 2 AFS-positive patients, 74.0% (239/323) were DNA-negative, with 67.8% (162/239) confirmed as non-tuberculous mycobacteria (NTM). MTBC culture confirmation rates for DNA+/AFS+ patients remained consistent between phases (Phase 1: 81.0%; Phase 2: 78.6%).

Conclusions: Routine initial MTBC DNA testing provides significant dual benefits: reliable detection of smear-negative TB and rapid differentiation of TB from NTM (which accounted for nearly three-quarters of AFS-positive cases). These findings validate integrating molecular testing into standard initial TB screening to optimize workflow and patient care.

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一般演題 Microbiology

Isolation and Antibiotic Susceptibility of *Klebsiella oxytoca* and *Acinetobacter junii*

from Well Waters in Selected Barangays of Lubao, Pampanga

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Well water serves as an essential and accessible resource for rural areas across the Philippines. However, it often lacks adequate water treatment and regular monitoring systems to prevent the accumulation of microbiological contaminants, thereby increasing the risk of compromised public health. Several studies conducted across the country have reported well water contamination involving multidrug-resistant pathogens, yet studies remain limited in understanding contamination in other regions. This study aimed to quantify microbial counts in well waters, identify microbial species and antibiotic-resistance profiles, and evaluate the occurrence and distribution of antibiotic-resistant bacteria (ARB) across selected barangays in Lubao, Pampanga. The study analyzed the bacterial profile present in twenty-three well water samples from selected barangays (Santiago, San Isidro, Lourdes) of Lubao, Pampanga. The samples were quantified using the Heterotrophic Plate Count (HPC) method and further identified through isolation onto Sheep Blood Agar and MacConkey Agar. Two out of twenty-three samples were confirmed to have bacterial contamination and were subsequently subjected to VITEK®2's automated system for particular microbial identification and antimicrobial susceptibility testing. Results identified *Klebsiella oxytoc*a in one sample from Barangay Lourdes and *Acinetobacter junii* in another sample from Barangay San Isidro. *Klebsiella oxytoca* exhibited resistance to ampicillin but remained susceptible to other antibiotics, whereas *Acinetobacter junii* was susceptible to all antibiotics tested. Findings indicate low distribution patterns of antibiotic-resistant bacteria in Lubao, Pampanga, yet provide insight into the occurrence of potentially resistant microorganisms in community well waters. The findings highlight the potential health risks associated with contaminated water sources and emphasize the importance of routine monitoring and water safety management.

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一般演題 Microbiology

Evaluation of a Multi-step Diagnostic Algorithm for *Clostridioides difficile* Infection

Comparison of GDH and Toxin A/B Assays Using RT-PCR and Culture

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Background

Clostridioides difficile infection (CDI) is a major cause of healthcare-associated diarrhea. Because no single assay provides optimal diagnostic accuracy, multi-step testing algorithms are increasingly recommended.

Materials and Methods

This retrospective study evaluated a CDI diagnostic algorithm at a medical center in Northern Taiwan from May 2024 to April 2026. GDH antigen and toxin A/B assays were compared with real-time polymerase chain reaction (RT-PCR) in 2,522 specimens and anaerobic culture in 1,248 specimens. Diagnostic performance was assessed using sensitivity, specificity, predictive values, likelihood ratios, and Cohen's kappa coefficient.

Results

Among 12,762 stool specimens, positivity rates were 28.1% for GDH and 6.9% for toxin A/B. Using RT-PCR as reference, GDH showed higher sensitivity (76.1% vs. 9.3%) and negative predictive value (80.9% vs. 69.4%), whereas toxin A/B demonstrated higher specificity (93.0% vs. 45.9%). Similar results were observed using anaerobic culture, with GDH showing higher sensitivity (72.7% vs. 12.0%) and toxin A/B higher specificity (93.4% vs. 62.9%). Agreement was fair between GDH and culture (κ=0.344) but slight between toxin A/B and either RT-PCR (κ=0.028) or culture (κ=0.061). Overall, GDH provided superior screening performance, whereas toxin A/B offered greater specificity.

Conclusion

GDH demonstrated superior sensitivity and screening utility, while toxin A/B provided higher specificity. Their complementary strengths support a stepwise diagnostic algorithm that may improve CDI diagnosis and laboratory efficiency.

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一般演題 Microbiology

NGS-Based Gut Microbiota Modulation by Green Banana Oat Beverage

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Insufficient dietary fiber intake is closely associated with gut dysbiosis and metabolic disorders. Green banana provides resistant starch (RS2) and oats supply β-glucan, both acting as natural prebiotics. A plant-based green banana oat beverage (GBOB) was prepared via enzymatic hydrolysis using α-amylase, cellulase, and protease. To evaluate its effects on the gut microbiota, a 12-week animal trial was conducted with three groups: normal control (C), dysbiosis model (MG, 1% methylglyoxal), and treatment (GBOB, MG plus 600 mg/kg/day). Fecal bacterial DNA was extracted using the QIAamp kit and analyzed by Illumina next-generation sequencing, with assessment of diversity indices, principal coordinate analysis (PCoA), heatmap clustering, and PICRUSt2 functional prediction. GBOB significantly restored α-diversity and produced distinct community clustering ($p = 0.001$) relative to the MG group. Beneficial and short-chain fatty acid (SCFA)–producing taxa, including Blautia spp., Bifidobacterium pseudocatenulatum, Romboutsia spp., Phocaeicola vulgatus, and Allobaculum spp., were significantly enriched, while obesity-associated taxa were reduced. Functional prediction further indicated GBOB-specific regulations of starch and sucrose metabolism, galactose metabolism, and insulin signaling pathways.

These findings demonstrate that GBOB reverses MG-induced gut dysbiosis, increases microbial diversity, and modulates carbohydrate metabolism, supporting its potential as a plant-based functional beverage for gut health and metabolic management.

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一般演題 Microbiology

Investigation the Clinical Performance of PCR for Detecting Mycoplasma pneumoniae

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Introduction

Mycoplasma pneumoniae is a leading cause of community-acquired pneumonia (CAP), particularly in children, adolescents, and young adults. Among these diagnostic approaches, PCR has emerged as a rapid and highly sensitive method for the detection of *M. pneumoniae*, enabling early diagnosis and timely initiation of appropriate therapy.

Material and method

This study enrolled 140 patients with an initial diagnosis of community-acquired pneumonia (CAP). Information regarding prior antimicrobial exposure was obtained through a review of medical records and prescription histories available through Taiwan's National Health Insurance database.

Result

Using culture as the reference standard, the diagnostic performance of the rapid antigen test and PCR assay was assessed. The rapid antigen test yielded a sensitivity of 58.97%, specificity of 100%, positive predictive value (PPV) of 100%, and negative predictive value (NPV) of 65.96%.

The PCR assay demonstrated markedly improved sensitivity (93.59%) and NPV (92.54%), while maintaining a specificity and PPV of 100%. Compared with the rapid antigen test, PCR showed superior overall diagnostic accuracy for the detection of *Mycoplasma pneumoniae* in patients with community-acquired pneumonia.

Discussion

These results suggest that PCR is a more reliable diagnostic tool than rapid antigen testing, particularly for the diagnosis of *Mycoplasma pneumoniae* infection in clinically suspected cases. However, PCR still has several limitations. One important limitation is that PCR detects bacterial nucleic acids regardless of whether the organisms are viable or nonviable. Therefore, if a patient has received antimicrobial treatment before specimen collection, residual DNA from dead bacteria may still be detected, potentially leading to false-positive results regarding active infection.

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一般演題 Microbiology

Enhancing Blood Culture Specimen Quality

A Regional Hospital QI Project

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Background: Rapid identification through blood culture is essential for guiding appropriate antimicrobial therapy. However, diagnostic accuracy is highly dependent on specimen collection quality. Inappropriate practices, including inadequate adherence to aseptic technique, suboptimal skin disinfection, improper venipuncture handling, and non-compliance with two-set collection protocols, may introduce skin flora contamination, increase false-positive results, and compromise diagnostic reliability. We aimed to setup programs to improve the blood culture specimen quality.

Materials and Methods: A multidisciplinary quality improvement program was conducted from Jul. 2025 to Feb. 2026 in a regional hospital. Data from an automated blood culture system, the Laboratory Information System (LIS), and Power BI dashboards were continuously monitored. Root cause analysis was performed using fishbone analysis, workflow observation, staff surveys, and order pattern review. Key contributing factors included non-standardized procedures, low physician compliance with two-set collection, insufficient computerized physician order entry (CPOE) prompts, limited staff awareness, lack of routine monitoring, and inadequate feedback mechanisms. Interventions included CPOE redesign to promote two-set collection, revision of collection procedures, visual reminders, interdisciplinary education, monthly performance feedback, and incorporation of single-set rate into quality indicators.

Results: The single-set blood culture rate decreased from 64% to 19.5%, and contamination rate decreased from 1.9% to 1.45%. Blood culture positivity increased by 2.16 percentage points, corresponding to approximately 518 additional bloodstream infection diagnoses annually. Time to detection improved by 60 minutes, enabling earlier targeted antimicrobial therapy.

Conclusion: Continuous monitoring, standardized workflows, and structured feedback from a multidisciplinary system-based intervention were essential for sustaining improvement and enhancing diagnostic performance and patient safety.

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一般演題 Microbiology

The analyzation of Helicobacter pylori Stool Antigen Screening Outcome

Analyzing the Outcome of Helicobacter pylori Antigen Screening at a Medical Center in Taiwan

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Purpose: Up to 90% of gastric cancer cases are caused by Helicobacter pylori infection. The Taipei Global Consensus II (2025) provided recommendations on Helicobacter pylori screening for gastric cancer prevention. Therefore, beginning in 2026, Taiwan's Ministry of Health and Welfare has provided citizens aged 45 to 74 with a once-in-a-lifetime, government-funded Helicobacter pylori stool antigen screening. This study aims to analyze the outcomes of this expanded screening program.

Methodology: This medical center encouraged eligible outpatients to undergo screening and actively promoted cancer prevention screening in local communities. The results of the Helicobacter pylori stool antigen screenings were analyzed by gender and age group.

Results: From January to April of 2026, a total of 2,133 people were tested, including 562 males and 1,571 females. The age distribution was 726 people aged 45–54 years, 750 aged 55–64 years, and 657 aged 65–74 years. The overall positivity rate was 16.7%. The positivity rate was slightly higher among males than females, at 18.2% and 16.2%, respectively. Overall, the positivity rate increased with age in both genders. Although the male group showed lower screening participation, its overall positivity rate was as high as 18.2%, indicating a potentially higher infection risk.

Conclusion: Through screening, those with positive results can be assisted in returning for medical care, receiving further examinations, which can effectively reduce the prevalence of Helicobacter pylori. Early treatment can stop disease progression sooner and reduce the incidence of gastric cancer. For men, who have lower screening rates but higher positivity rates, targeted health education should be developed to increase screening rates and achieve early diagnosis and precise eradication for gastric cancer prevention.

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一般演題 Microbiology

Genomic Characterization of Carbapenemase-Producing Klebsiella pneumoniae ST218

Delineating Variants in Putative Phage Resistance-Associated Surface Receptor, Capsule, and CRISPR-Cas Loci

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Background: Carbapenemase-producing Klebsiella pneumoniae (CPKP) is a major multidrug-resistant nosocomial pathogen recently gaining focus in therapeutics. The resurgence of bacteriophage therapy offers another viable prospective; however, ongoing phage receptor bacterial mutations may intercept long-term phage susceptibility. This study aimed to investigate CPKP phage resistance and provide insights into the epigenetic determinants of antimicrobial discordance.

Design and Methods: Descriptive bioinformatic whole-genome analysis was performed on raw Illumina sequencing reads of a *CPKB* ST218 isolate retrieved from the NCBI Sequence Read Archive (SRR9635391; BioProject PRJNA552636) aligned to the complete ST218 reference genome with BWA-MEM after FastQC. Variants were called utilizing FreeBayes. Functional annotations were performed using SnpEff. Putative phage resistance-associated genes were analyzed via JBrowse.

Results: A total of 108 variants were identified across the five target loci, including 89 upstream/promoter, 17 missense, and 2 high-impact variants. Adenine insertion in *ompK36* was predicted to cause a frameshift mutation. High-impact insertion variants in *cas1* and *cas3* resulted in premature translational termination. Capsule-associated genes showed the highest regulatory variation. Read-alignment depicted localized sequence divergence and coverage decay relative to the reference genome.

Conclusion: Whole-genome variant analysis of CPKB ST218 revealed a diverse mutational landscape across putative phage resistance-associated receptor, capsule, and CRISPR-Cas loci. Recurrent variants in *ompK36*, capsule-associated genes, and CRISPR-Cas loci represent candidate mutational hotspots as targets for phage-based therapeutic design.

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一般演題 Microbiology

Does Cardiovascular Health Begin in the Gut?

The Impact of Dysbiosis and Intestinal Barrier Impairment on the Development of Cardiovascular Diseases

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Background: Cardiovascular diseases (CVD) are the leading global cause of mortality. As traditional risk factors do not fully explain atherosclerosis pathogenesis, research is shifting toward the gut-heart axis. Gut dysbiosis disrupts homeostasis and intestinal barrier integrity, promoting inflammation and the translocation of bacterial components and proatherogenic metabolites into circulation.

Objectives: To analyze the microbiota's role in cytoprotection and evaluate the impact of intestinal barrier impairment on CVD development.

Methods: A systematic PubMed search was conducted for English-language articles (2015–2025) using the keywords "gut microbiota," "dysbiosis," and "cardiovascular diseases."

Results: In eubiosis, short-chain fatty acids maintain tight junctions, exerting cytoprotective and cardioprotective effects. Dysbiosis and mucosal edema ("leaky gut") abrogate these mechanisms, permitting toxin translocation. Trimethylamine N-oxide (TMAO) induces endothelial dysfunction and inhibits reverse cholesterol transport via the NF-κB pathway. Elevated TMAO and phenylacetylglutamine (PAGln) levels correlate with myocardial infarction, stroke, and heart failure risk. Lipopolysaccharide (LPS) activates innate immunity via TLRs; blood endotoxin >50 pg/mL triples atherosclerosis risk. Bacterial DNA (e.g., from *Proteobacteria* and *Firmicutes*) is present within plaques, promoting growth via direct vascular wall infection. In coronary artery disease, significant alterations occur in *Lactobacillales*, *Collinsella*, *Enterobacteriaceae*, and *Streptococcus*. *Bacteroides*, *Lactobacillales*, and *Clostridium* are potential noninvasive diagnostic markers.

Conclusion: Preserving intestinal barrier cytoprotection is paramount to preventing systemic inflammation and vascular damage. The gut microbiota and its metabolites offer novel opportunities for CVD diagnosis and therapy.

Keywords: cardiovascular diseases, cytoprotection, dysbiosis, gut microbiota.

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一般演題 Immunology

Kappa Free Light-Chain Index Predicts Long-Term Outcomes in Multiple Sclerosis

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Background
κ-FLC index predicts short-term disease activity in early MS. The prognostic value of this biomarker over the long term is largely unknown.
Objective
To investigate whether κ-FLC index determined at disease onset predicts multiple sclerosis (MS) disease activity over a period of 10 years.
Methods
Patients presenting with a first demyelinating event of the central nervous system who underwent CSF and serum sampling at disease onset were followed for 10 (±5) years. Baseline parameters included age, sex, disease duration, number of T2 hyperintense lesions (T2L), and contrast-enhancing lesions (CEL) on MRI. During follow-up, relapse occurrence, Expanded Disability Status Scale (EDSS) scores, and initiation of disease-modifying treatment (DMT) were documented. κ-FLC concentrations were measured by nephelometry, and the κ-FLC index was calculated as (CSF κ-FLC / serum κ-FLC) divided by the albumin quotient. Multivariable Cox regression analysis was performed adjusting for demographic, MRI, and treatment-related variables.
Results
Sixty-four patients (75% female) with a median age of 32 years [27–39] were followed for a median of 113 months [90–129]. During follow-up, 72% experienced relapses and 47% showed disability worsening. Higher κ-FLC index values independently predicted shorter time to relapse (HR 1.45, 95% CI lower limit 1.002, p=0.049) and disability worsening (HR 1.86, lower CI 1.22, p=0.008). After 10 years, patients with high κ-FLC index values had a 40% lower probability of remaining relapse-free and a 27% lower probability of remaining free of disability worsening.
Conclusions
The κ-FLC index predicts long-term MS disease activity and disability worsening independent of established clinical and MRI risk factors.

P-2-2

一般演題 Immunology

MLS-ERAS Framework Detects Gastrointestinal-Onset SLE Microperforation

Novel Three-Stage Protocol Overcomes Normal-CRP Pitfalls in High-Risk Case

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Background: Gastrointestinal-onset (GI-onset) SLE (1–5%) often presents with misleadingly normal CRP, masking rare jejunal microperforation. In an immunocompromised Taiwanese patient after thyroidectomy, progressive weight loss concealed a perforation, prompting an urgent need for coordinated monitoring. Co-first MLS–physician authors developed a three-stage ERAS-inspired framework for imaging–biomarker detection in high-risk non-surgical GI-SLE contexts. **Methods:** A 65-year-old Taiwanese male with post-thyroidectomy hypothyroidism and SLE presented with progressive epigastric pain, acid regurgitation, abdominal fullness, constipation, 10-kg weight loss over 1 year, FOBT (+), and ascites on outpatient evaluation. Physician-identified abnormalities activated an MLS-supported ERAS protocol: Stage 1: symptom- and laboratory-data-triggered POCUS; Stage 2: CT for pneumatosis intestinalis and free air; Stage 3: EULAR-guided MLS-based SLEDAI-2K (>4-point rise triggers escalation), core WBC/CRP trends, and postoperative lactate for tissue perfusion/sepsis risk assessment. **Results:** Admission: normal coagulation (PT-INR 1.23), LDH 154 U/L. POD 2: lactate 1.1 mmol/L (preserved perfusion), WBC 12.9×10³/μL. POD 4: CRP peaked at 58.1 mg/L, Hb 10.6 g/dL. POD 5: transient bradycardia, troponin I 6.5 pg/mL, NT-proBNP 322 pg/mL. SLEDAI-2K increased from 10 to 18. Discharge Day 13 post-laparotomy: CRP improved to 14.5 mg/L, WBC normalized to 6.8×10³/μL, Hb recovered to 12.5 g/dL, wound dry/clean, soft diet, no sepsis. **Conclusion:** Pioneering MLS-physician pilot ERAS framework-adapted from surgical protocols-establishes imaging-–biomarker monitoring for rare non-surgical GI-onset SLE microperforation after thyroidectomy. Three-stage protocol overcame normal-CRP pitfalls via lactate/SLEDAI-2K, enabling timely urgent intervention with sepsis-free discharge by Day 13 in a high-risk comorbid patient. MLS roles for proactive ICU risk stratification; multicenter Asia-Pacific GI-SLE validation needed. * These authors contributed equally.
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P-2-3

一般演題 Immunology

Unravelling rAAV-Serotype-Specific Cytokine Profiles in HEK293 cells

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With several recombinant adeno-associated virus (rAAVs)-based therapies already approved for clinical use, rAAVs are among the most promising vectors for gene therapy applications, combining an outstanding safety profile, extensive tissue tropism and the ability to consistently transduce dividing and non-dividing cells. One of the biggest obstacles in manufacturing, however, is the achievement of high yields, which affects scalability as well as manufacturing costs which in turn often leads to companies' decision to stop gene therapy projects. Therefore, a deeper understanding of critical steps in the manufacturing process is of utmost importance.

One of the critical leverage points in rAAV manufacturing is the expression system used, most commonly HEK293 cells. In this study, we focus on the cytokine response in HEK293 producer cells to detect possible inhibitor targets to thereby increase rAAV titers. Given that some inhibitory targets have been described previously, we further aim to uncover whether different rAAV serotypes trigger distinct cytokine patterns, providing serotype-specific insights relevant for process optimization.

In our study we produced AAV2, AAV8 and AAV9 vectors in the same HEK293 cell line and collected samples after defined time points (0 h, 4 h, 24 h, 48 h and 72 h) post-transfection. Cytokine expression in the sample set was analyzed using a multiplexed immunoassay (Luminex). Thus, we generated comprehensive kinetic cytokine profiles for each AAV serotype. Preliminary analyses indicate distinct cytokine expression patterns, suggesting serotype-dependent modulation of host cell immune signaling. These findings may reveal novel cellular targets for process optimization and ultimately contribute to improving rAAV yields. By elucidating serotype-specific host responses, our study adds an important layer to understanding rAAV production biology and supports the rational design of more efficient manufacturing strategies.

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P-2-4

一般演題 Immunology

Resolving Immunoglobulin Interference Reveals HLA DQ6 Antibodies in Transplant Rejection

Unmasking Clinically Actionable Donor-Specific Antibodies in Late-Onset Liver Transplant Rejection

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Introduction: Detection of donor-specific anti-HLA antibodies (DSAs) is essential in transplant immunological monitoring. Emerging evidence suggests that class II DSAs, particularly anti-HLA-DQ antibodies, may contribute to liver graft dysfunction.

Methods: Immunological evaluation was performed in a male patient who underwent living donor liver transplantation in 2010 and developed late-onset graft dysfunction in 2025. Crossmatch testing and liver biopsy with C4d staining were performed.

Results: Initial single antigen bead (SAB) testing demonstrated high background reactivity and atypical patterns, complicating interpretation. Recent intravenous immunoglobulin (IVIG) administration was considered a source of assay interference. Following PreSorb™ pretreatment, nonspecific reactivity was markedly reduced, revealing a donor-specific anti-HLA-DQ6 antibody with increased signal intensity. The antibody corresponded to donor HLA typing, confirming its clinical relevance. Crossmatch testing showed positive B-cell and negative T-cell reactivity, consistent with class II DSA. Histopathology demonstrated severe acute cellular rejection (RAI score 8) with C4d deposition. Integration of laboratory and pathological findings supported the diagnosis of mixed rejection involving both T cell–mediated and antibody-mediated mechanisms.

Conclusion: Anti-HLA-DQ donor-specific antibodies may play an important role in late-onset liver transplant rejection. Immunoglobulin-associated assay interference can obscure clinically relevant antibodies in standard SAB testing, whereas PreSorb™ pretreatment effectively resolves high background reactivity and enables accurate detection. Identification of DQ6 DSA in this case highlights its value as a potential immunological marker. Accurate DSA detection is critical for diagnosis and may directly influence clinical management. Resolving assay interference is not merely a technical refinement, but a critical step in uncovering clinically actionable DSAs that directly impact transplant risk assessment.

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P-2-5

一般演題 Immunology

Distinct Senescence States Converge on Sustained PD-L1 in HCC

Temporal uncoupling of PD-L1 mRNA and protein during senescence

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Distinct Senescence States Converge on Sustained PD-L1 in HCC

Background: Therapy-induced senescence (TIS) is increasingly recognized as a contributor to tumor persistence and immune evasion. However, how PD-L1 expression is regulated during senescence in hepatocellular carcinoma (HCC) remains unclear, particularly at the protein level.

Methods: Senescence was induced in HCC cells using ionizing radiation, doxorubicin, and sorafenib. Senescence phenotypes were assessed by SA-β-galactosidase staining and p21 expression. PD-L1 expression was evaluated at both mRNA and protein levels to examine transcriptional and post-transcriptional regulation. Immunofluorescence analysis was performed to assess PD-L1 expression patterns in senescent cells.

Results: HepG2 cells exhibited robust and reproducible senescence across treatments. Distinct senescence phenotypes were observed depending on the inducing stimulus: ionizing radiation and doxorubicin strongly induced p21, whereas sorafenib produced a p21-low senescence phenotype.

Despite these differences, all conditions led to increased PD-L1 protein levels, with sustained accumulation observed at later time points. In contrast, PD-L1 mRNA levels were transiently elevated and declined over time, indicating a temporal dissociation between transcriptional and protein-level regulation. Immunofluorescence further supported increased PD-L1 signal following ionizing radiation.

Conclusion: Distinct senescence states in HCC converge on sustained PD-L1 protein accumulation. The observed temporal uncoupling between mRNA and protein levels suggests regulation beyond transcription. These findings provide insight into persistent immune checkpoint expression following cancer therapy.

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P-2-6

一般演題 Immunology

Immunogenic efficacy of mRNA-based influenza vaccines in older adults

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Older adults (≥65 years) are at high risk for influenza-related complications, yet traditional vaccines often elicit weak immune responses due to immunosenescence. mRNA-based influenza vaccines may enhance immunogenicity in this population. This systematic review and meta-analysis assessed the seroconversion rate (SCR) of mRNA influenza vaccines in older adults using data from randomized controlled trials (RCTs). Databases (PubMed, Scopus, Web of Science, Google Scholar) were searched to July 2025. Eligible RCTs reported SCR at 29 days post-vaccination in adults ≥65 years. Pooled risk ratios (RRs) were calculated using random-effects models. Heterogeneity, publication bias, sensitivity, and meta-regression analyses were conducted. Seven studies (n=7114) from four publications were included. Compared to licensed vaccines, mRNA vaccines showed significantly higher SCR across strains: A/H1N1 (RR=3.41), A/H3N2 (RR=3.54), B/Victoria (RR=2.83), B/Yamagata (RR=3.34). Heterogeneity was high (I^2>80%), but sensitivity analyses supported result stability. Funnel plots suggested possible publication bias, while meta-regression showed vaccine dose was not a major source of heterogeneity. This first meta-analysis on mRNA influenza vaccines in older adults shows they elicit significantly stronger immune responses than licensed inactivated vaccines. Findings highlight the potential of mRNA technology in improving influenza protection in the elderly and support further large-scale trials.

P-2-7

一般演題 Immunology

Citrullinated Fibrinogen Suppresses Neutrophil Proinflammatory Functions.

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[Background]
Citrullinated fibrinogen (C-Fbg) is a post-translational modification of fibrinogen (Fbg) catalyzed by peptidyl arginine deiminases (PADs). C-Fbg is clinically detected in inflammatory conditions such as infections or autoimmune diseases. While Fbg modulates immune responses through interactions with neutrophil integrins, the impact of C-Fbg on neutrophil function remains poorly understood. In this study, we investigated the effects of C-Fbg on neutrophil adhesion, interleukin (IL)-8 production, and CD66b expression as a degranulation marker.
[Methods]
C-Fbg was generated by incubating Fbg with recombinant human PAD2. Neutrophils isolated from healthy volunteers were stimulated with N-formyl-methionine-leucyl-phenylalanine. For adhesion assay, the neutrophils were seeded into 96-well plates coated with Fbg or C-Fbg (0, 2, 200, and 500 μg/mL). After incubation and washing, adherent cells were counted. For IL-8 production and CD66b expression assays, neutrophils were incubated in wells coated with Fbg or C-Fbg (500 μg/mL). IL-8 levels in the supernatants were measured by ELISA, and CD66b expression on the cell surface was analyzed by flow cytometry. Statistical analysis was performed using EZR software.
[Results]
Adhesion to C-Fbg (at 200 and 500 μg/mL) was significantly lower than that to Fbg ($p < 0.05$ and $p < 0.01$, respectively). IL-8 levels released from neutrophils incubated with C-Fbg were significantly lower than those from neutrophils incubated with Fbg ($p < 0.05$). Flow cytometric analysis revealed that the median fluorescence intensity of CD66b in neutrophils exposed to C-Fbg was significantly lower than in those exposed to Fbg ($p < 0.05$).
[Conclusion]
C-Fbg significantly suppresses neutrophil adhesion, IL-8 production, and degranulation. These findings suggest that C-Fbg acts as a negative regulator of neutrophil activity and may contribute to the pathophysiology of inflammatory conditions.
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P-2-9

一般演題 Immunology

Efforts and Challenges in HBV Reactivation Prevention

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Background: Hepatitis B virus (HBV) is known to persist in hepatocytes once infection occurs and can lead to liver fibrosis and HBV reactivation, particularly in the context of immunosuppression or chemotherapy. Preventing HBV reactivation is an important component of safety management in medical institutions. At our hospital, the Liver Disease Consultation Office, Safety Management Department, and Laboratory Department collaborate on various initiatives, including creating HBV reactivation test order sets and establishing a communication system for positive HBV-DNA results.
Objective: To assess the operational status of HBV reactivation prevention measures at our institution through case-based analysis, and to clarify their effectiveness and associated challenges, as well as to explore areas for future improvement.
Case: A teenage female diagnosed with systemic lupus erythematosus received intravenous immunoglobulin (IVIg) for thrombocytopenia, followed by prednisolone. Initial test showed HBsAg <0.005 IU/mL (−), HBsAb <1 mIU/L (−), and HBcAb 0.1 C.O.I. (−). After IVIg administration, HBsAb increased to 48 mIU/L (+) and HBcAb to 1.4 C.O.I. (+). Because the rapid rise suggested transient false positivity, the case was reported to the Liver Disease Consultation Office. Additional HBV-DNA testing was negative.
Results: Prompt recognition of possible false positivity by the clinical laboratory technologist and rapid communication within our institutional framework contributed to appropriate clinical decision-making. Although the patient was receiving immunosuppressive therapy and should have been tested using the HBV reactivation order set, the tests were submitted through the standard order set.
Discussion: To prevent missed identification of at-risk patients, further promotion of the specialized order set is necessary. Additionally, ensuring that hepatitis-related testing is performed prior to immunoglobulin administration remains an important area for improvement. (Contact: +81-88-633-9307)

P-2-10

一般演題 Immunology

Seroprevalence to Toxoplasma gondii Antibodies and Cat-Related Risk Factors

Among Women of Childbearing Age in Sampaloc, Manila

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Toxoplasma gondii is an intracellular protozoan parasite that causes toxoplasmosis, posing risks to women of childbearing age for congenital transmission with exposure to cats and related practices as major risk factors. Despite the potential health consequences, limited data exist on the seroprevalence of *T. gondii* infection among Filipino women. This study determined the seroprevalence of *T. gondii* antibodies and assessed cat-related risk factors among women of childbearing age in Sampaloc, Manila. A cross-sectional study was conducted among 157 women of childbearing age. Participants were screened for *T. gondii* IgG and IgM antibodies using a commercial lateral-flow immunochromatographic assay. Sociodemographic and cat exposure data were collected via structured questionnaires and analyzed using Pearson correlation, Chi-square, and Fisher's exact tests. The overall seroprevalence showed that IgG seropositivity was observed in 19.11% of participants (n=30), indicating established immunity from prior exposure. In contrast, IgM seropositivity was detected in only 1.27% (n=2), suggesting a low rate of recent or acute infection. Correlation analysis between IgM and IgG markers showed a weak, non-significant relationship ($r = 0.089$, $p = 0.266$), indicating the markers act independently. Statistical analysis revealed no significant associations ($p > 0.05$) between seropositivity and cat-related factors, such as pet ownership, frequency of contact, or volunteer activity. Similarly, demographic factors including age, pregnancy status, and miscarriage history did not demonstrate statistically significant relationships with *T. gondii* exposure. Nearly 20% of the surveyed women in Sampaloc, Manila, show evidence of past *T. gondii* infection. The lack of significant correlation with feline-related exposures suggests that other environmental or dietary factors may contribute to transmission in this urban population.

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P-2-11

一般演題 Immunology

Immune Cell Recruitment and Activation Factors as PRP Biomarkers

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Background: Platelet-rich plasma (PRP) is widely used in regenerative medicine, but its therapeutic efficacy varies among individuals despite standardized preparation. Conventional quality indicators, such as platelet counts and selected growth factor levels, do not fully explain this variability. This study explored immune cell-related plasma biomarkers associated with PRP functional quality and clinical response.

Methods: PRP samples from 23 subjects receiving pure PRP in a previous clinical trial were analyzed. In vitro bioactivity was evaluated using an RSC96 Schwann cell proliferation model, while clinical efficacy was assessed by changes in IIEF-5 scores. EGF, PDGF, VEGF, and BDNF levels were measured by ELISA, and a 440-cytokine profiling platform was used to compare good and poor responders.

Results: Although all subjects had baseline hematologic parameters within normal ranges, PRP from different individuals showed marked variability in promoting RSC96 cell proliferation, indicating functional heterogeneity despite standardized preparation. EGF, PDGF, and BDNF were significantly enriched in PRP compared with plasma and positively correlated with whole-blood platelet counts. However, these growth factors were not associated with RSC96 proliferative effects. Moreover, PDGF and BDNF were negatively correlated with IIEF-5 improvement. In contrast, cytokine profiling showed that PRP from good responders had higher expression of immune-related molecules involved in lymphocyte recruitment, dendritic cell chemotaxis, immune induction, and tissue-repair-associated cell activation.

Conclusion: PRP efficacy may depend more on immune-modulatory cytokine profiles than conventional growth factor content. Immune cell-related plasma biomarkers may support PRP quality stratification and therapeutic response prediction in precision regenerative medicine.

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P-2-12

一般演題 Immunology

ANA Immunofluorescence Patterns in Primary Biliary Cholangitis

Clinical Significance in AMA-Positive and AMA-Negative Cohorts

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Introduction: Although Anti-Mitochondrial Antibody (AMA) is the gold standard for diagnosing Primary Biliary Cholangitis (PBC), 5%–10% of patients remain AMA-negative. In such cases, diagnosis relies on clinical presentation, biochemical markers (GGT, ALP), and Antinuclear Antibody (ANA) patterns via Indirect Immunofluorescence (IIF). This study analyzed 215 subjects to compare liver function and ANA patterns (AC Codes) between AMA-positive and AMA-negative groups.Methods: ANA detection used HEp-2 cell-based IIF, with patterns classified according to the International Consensus on ANA Patterns (ICAP).Results: Analysis (n=229) highlighted the diagnostic importance of ANA patterns. AC-21 (Mitochondrial-like) was the primary pattern in AMA-positive cases. Notably, 45.5% (15/33) of the AMA-negative group with elevated liver enzymes (GGT+/ALP+) also exhibited AC-21, suggesting IIF may be more sensitive than AMA reagents in detecting latent autoimmunity.Furthermore, the AC-3(Centromere)pattern served as a crucial diagnostic supplement for AMA-negative patients; its prevalence was significantly higher in the AMA-negative group compared to the AMA-positive group(p<0.001), often correlating with Systemic Sclerosis (SSc).Conclusion: Our findings confirm that AC-21 is a strong indicator of AMA positivity. Interestingly, 35.19% of AMA-positive subjects with normal liver function exhibited AC-21, identifying them as high-risk individuals requiring long-term monitoring. Additionally, the AC-3 detection rate was 47.45% in the AMA-negative group versus 2.35% in the AMA-positive group. This supports the clinical correlation between anti-centromere antibodies and AMA-negative PBC, emphasizing the indispensable role of ANA IIF in comprehensive PBC screening.

P-2-13

一般演題 Immunology

Reverse Algorithm in Syphilis Testing

Evaluation in Routine Clinical Practice

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Syphilis, caused by Treponema pallidum (TP). Our hospital using the traditional algorithm for the diagnosis of syphilis, in which non-treponemal tests are used for initial screening, followed by treponemal-specific confirmation. The annual testing volume of non-treponemal assays in our institution exceeds 30,000 cases. Given this substantial workload, the manual, labor-intensive non-treponemal testing places a considerable burden and may increase the risk of human error. This study evaluated the performance and efficiency of the reverse syphilis algorithm.

A total of 521 residual serum samples were collected. Non-treponemal testing was performed using the Arlington Scientific, Inc. Rapid Plasma Reagin card test for syphilis (ASI). Treponemal-specific assays included the Abbott ARCHITECT Syphilis TP (Abbott) and the Roche cobas e601 Elecsys Syphilis assay (Roche). Agreement between methods was assessed with Cohen's kappa coefficient, and workflow efficiency was evaluated via time-cost simulation and paired sample t-tests.

The positive rates of ASI, Abbott, and Roche were 34.7%, 37.4%, and 38.2%, respectively. Agreement among the three methods was high, with Cohen's kappa values of 0.86, 0.85, and 0.98, respectively. Both algorithms identified the same number of dual-reactive cases (n = 172), indicating equivalent performance for active infection. However, the reverse algorithm yielded a higher number of discordant results, specifically treponemal-positive/non-treponemal-negative cases (n = 27), which may reflect past infection or post-treatment status. Time-cost analysis demonstrated that the reverse algorithm significantly reduced total turnaround time compared with the traditional algorithm (6.7 vs. 11.7 hours; 42.2% reduction, p < 0.0001).

The reverse algorithm improves automation and laboratory efficiency without compromising the detection of active infection; however, it increases the complexity of serological interpretation. Therefore, the selection of a testing algorithm should be guided by clinical risk stratification and overall resource allocation.

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P-2-14

一般演題 Immunology

DM

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Viral Hepatitis with Comorbid Diabetes Significantly Increases Risks of Vascular Stiffness and Hyperglycemia

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Purpose : To evaluate the independent and additive effects of viral hepatitis on vascular stiffness and hyperglycemia.

Methods : This cross-sectional study included 790 participants: healthy controls (n=123), hepatitis alone (n=48), diabetes alone (n=440), and hepatitis with diabetes (n=179). Vascular stiffness was measured by the vascular hardening index. Hyperglycemia was assessed by HbA1c. Insulin and HDL-C levels were also compared. Statistical analyses used ANOVA with post-hoc tests. Data are mean ± SD.

Results : The hepatitis-alone group showed no significant difference in vascular hardening index (p=0.139), but had significantly higher insulin (p=0.024) and lower HDL-C (p=0.003), indicating insulin resistance. The hepatitis-with-diabetes group exhibited a significantly elevated vascular hardening index (=0.012) and markedly higher HbA1c (p<0.001) compared to controls.

Conclusion :Viral hepatitis alone induces insulin resistance without overt vascular stiffening. However, when hepatitis coexists with diabetes, patients face significantly increased risks of both vascular stiffness and hyperglycemia. Screening for glucose metabolism and vascular function is essential in hepatitis patients.

Keywords: Viral hepatitis; vascular stiffness; hyperglycemia; insulin resistance; HbA1c

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P-2-15

一般演題 Immunology

Clarifying Causes of Optic Neuropathy via Laboratory Data

Case Reports

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Introduction:

Visual impairment and sudden vision loss are prevalent in autoimmune disorders. Neuromyelitis Optica Spectrum Disorder (NMOSD) is a rare central nervous system condition where the anti-aquaporin 4 (AQP4) antibody serves as a critical diagnostic marker. Similarly, Sjögren's syndrome, characterized by anti-SSA/SSB antibodies, often manifests as dry eyes. Furthermore, Anti-neutrophil cytoplasmic antibody (ANCA)-associated vasculitis and Behcet's disease can lead to severe optic nerve involvement. Serological testing is therefore essential for precise differential diagnosis and treatment.

Methods:

Indirect Immunofluorescence (IFA) detected anti-AQP4 (using transfected HEK293 cells) and ANCA (using neutrophils). Immunoblotting was employed for Anti-SSA and Anti-SSB detection.

Conclusion:

Clinical presentations of optic neuropathy often overlap across various autoimmune diseases. Beyond imaging, serological identification of autoantibodies provides indispensable evidence for clarifying etiology and guiding therapy. These cases highlight the high clinical value of laboratory science in preventing permanent blindness through accurate diagnosis. By integrating specific antibody profiles, clinicians can implement targeted treatments, significantly improving patient prognosis.

P-2-16

一般演題 Immunology

2025 Allergen Retrospective Analysis, Southern Taiwan Lab

Statistical analysis of allergen positivity rates and age distribution

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Allergic diseases are common and increasingly prevalent in Taiwan due to variations in climate, diet, housing, and environment. Clinically, total and specific IgE testing helps identify allergens and guide personalized treatment and prevention. This study analyzes specific IgE positivity rates and age-specific IgE distribution in the Kaohsiung area, aiming to support local clinical strategies. Total and specific IgE data were collected from January to December 2025 (age range: 0–99 years). Total IgE was measured by ECLIA, and specific IgE was detected using the BioIC Allergen Specific-IgE Detection Kit, an indirect enzyme-linked chemiluminescent immunoassay. Specific IgE grades: Class 0 (<1 AU) to Class 6 (≥32 AU); ≥1 AU = positive. Positivity rates by age group were analyzed for total IgE and 40 specific allergens. Among total IgE tests, 3,888 were positive and 4,037 negative. By gender, males had 1,890 positive and 1,576 negative; females had 1,998 positive and 2,461 negative; 88 positive and 95 negative had unrecorded gender. The highest positivity rate in both sexes was in the 0–10 age group (males: 74.0%; females: 67.4%). The highest negativity rate was in 51–60 for males (52.3%) and 61–70 for females (64.0%). Among 40 allergens, dust mites showed the highest positivity: house dust mite (56.77%), followed by *D. farinae* (55.84%) and *B. tropicalis* (21.72%). In food allergens, hen's egg white ranked highest (14.14%), followed by peanut (10.70%) and potato (10.64%). Latex showed 10.75%, and cat dander showed 11.46%. This study reveals that dust mite reactivity is common in southern Taiwan. About 10% of individuals are allergic to egg white, peanut, potato, latex, and cat dander. Males are more allergy-prone than females, with peak positivity at ages 0–10. Early prevention and allergen testing in children are strongly recommended to identify and avoid triggers effectively.
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P-2-17

一般演題 Immunology

Anti-rituximab assay formats and analytical interference

Comparison of three different in-house bridging immunoassays in rheumatological serum samples

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Background

Anti-drug antibodies (ADAb) against biologic therapies may reduce treatment efficacy, alter pharmacokinetics and contribute to adverse events. Reliable laboratory detection is therefore clinically important. Bridging immunoassays are widely used for ADAb testing, but may be vulnerable to analytical interference, particularly in patients with rheumatological disease, where rheumatoid factor and heterophilic antibodies may cause non-specific reactivity.

Materials and methods

This study compares three in-house immunoassay formats for detection of anti-rituximab antibodies in biobanked serum samples from patients with rheumatoid arthritis treated with rituximab. Samples originate from the ULRABIT and NOR-DMARD cohorts at Diakonhjemmet Hospital, Norway. In total, 328 serum samples from 95 patients are included, comprising longitudinal samples from six visits in ULRABIT and two visits in NOR-DMARD. The assay formats include IgG–IgG, $F(ab')_2$–IgG and $F(ab')_2$–$F(ab')_2$ bridging assays, performed on the automated AutoDELFIA platform (Revvity, Waltham, MA). Samples collected prior to treatment initiation are included to assess baseline reactivity as a marker of potential analytical interference. Positive rates and agreement between assay formats will be compared.

Expected results

We hypothesise that assay formats based on $F(ab')_2$-fragments will demonstrate lower baseline reactivity and fewer potentially false positive results compared with whole-IgG formats, indicating reduced susceptibility to interference. Data analysis is ongoing and final results will be presented at the congress.

Conclusion

Assay design may substantially influence ADAb results. Optimisation of analytical format is important for robust immunogenicity testing, and biomedical scientists play a key role in development, validation and quality assurance of such methods in clinical laboratories. (*Contact: aagwin@ous-hf.no*)

P-2-18

一般演題 Immunology

Diagnostic Utility of Pleural Fluid Mesothelin-Related Peptides in Asbestos-Related Diseases

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【Background and Aims】

Asbestos exposure is a well-established risk factor for lung cancer and other asbestos-related diseases. This study evaluated the diagnostic utility of pleural fluid soluble mesothelin-related peptides (P-SMRPs) in patients with asbestos-related diseases.

【Methods】

A total of 250 pleural effusion cases were classified into four groups for comparative analysis.

Group I : Benin asbestos-related diseases

Group II : Malignant asbestos-related diseases (mesothelioma)

Group III: Benign non-asbestos-related diseases

Group IV: Malignant non-asbestos-related diseases

【Results】

P-SMRP levels were significantly higher in the asbestos-related disease group (Groups I･II; n = 47, median 12.00 nmol/L, range 1.91 - 446.93 nmol/L) than in the non-asbestos-related disease group (Groups III･IV; n = 203, median 5.00 nmol/L, range 0.01-100.4 nmol/L) ($P < 0.05$).

P-SMRP levels did not differ significantly between the benign asbestos-related disease group (Group I; n = 15, median 7.79 nmol/L, range 2.08 - 33.37 nmol/L) and the malignant asbestos-related disease group (Group II; n = 32, median 14.05 nmol/L, range 1.91 - 446.93 nmol/L) ($P = 0.13$).

P-SMRP levels were significantly higher in the malignant asbestos-related disease group (Group II; n = 32, median 14.05 nmol/L, range 1.91 - 446.93 nmol/L) than in the malignant non-asbestos-related disease group (Group IV; n = 69, median 6.87 nmol/L, range 0.84 - 100.4 nmol/L) ($P < 0.05$).

【Conclusion】

P-SMRPs may serve as a useful biomarker for the diagnosis of asbestos-related diseases. Further investigation is needed to determine whether combining P-SMRPs with occupational history, smoking history, and imaging findings can improve diagnostic accuracy. We will report on the details on the day of the conference.

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P-2-19

一般演題 Immunology

Oral mucositis signals acute but not chronic immune complications

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Oral mucositis (OM) presents a common complication of conditioning-related mucosal barrier damage and may contribute to the activation of systemic immune responses in patients undergoing hematopoietic stem cell transplantation. This retrospective study aimed to investigate whether early mucosal toxicity is associated with the later development of graft-versus-host disease (GVHD). A cohort of 439 adult allogeneic stem cell transplant recipients at the Medical University of Vienna (2015–2022) was analyzed with up to seven years of follow-up.

Among transplant recipients, oral mucositis occurred in 70.6%, with severe manifestations (WHO grades III/IV) observed in 127 individuals. Moderate-to-severe OM (grades II-IV) was associated with a significantly higher incidence of acute GVHD ($p = 0.0056$), whereas no such correlation was observed in chronic cGVHD ($p = 0.0582$). Importantly, the severity of oral mucositis did not correlate with the severity of either acute ($p = 0.071$; $r = 0.087$) or chronic graft-versus-host disease ($p = 0.0649$; $r = 0.088$). Multivariate competing risks models further identified independent risk factors for GVHD development, including myeloablative conditioning regimens ($p = 0.014$), total body irradiation doses of 10 Gy or higher ($p = 0.026$), donor type ($p = 0.004$), and the degree of HLA-mismatch ($p = 0.049$). These findings suggest that while early mucosal barrier damage may indicate an increased risk for acute disease, the progression and severity of graft-versus-host disease are influenced by broader immunological and transplant-related factors.

In conclusion, oral mucositis appears to be a relevant marker for the occurrence of acute graft-versus-host disease, but its severity does not predict disease severity or the development of chronic graft-versus-host disease in this large, single center cohort.

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P-2-20

一般演題 Immunology

Keratinocyte Injury and Cell Death Pathways in Long COVID Alopecia

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Background
Alopecia is common in patients with Long COVID; however, its pathophysiological mechanisms remain insufficiently understood. This study aimed to investigate the effects of acute-phase serum from patients with Long COVID on keratinocytes and to clarify its association with cellular injury and cell death–related pathways.
Methods
Acute-phase serum samples collected from hospitalized patients with COVID-19 in a prospective study were used for serum stimulation experiments. Participants were classified into a Long COVID alopecia group (LC alopecia group, n=17), a Long COVID non-alopecia group (LC non-alopecia group, n=9), and a non-Long COVID group (non-LC group, n=9). HaCaT cells were treated with acute-phase patient serum and control serum samples (n=10). Cell viability was assessed using the CCK-8 assay. In addition, RT-qPCR was performed to evaluate the *BAX/BCL2* ratio as an apoptosis-related marker and *MLKL* expression as a marker of necroptosis execution.
Results
Acute-phase serum from all three groups significantly reduced HaCaT cell viability compared with control ($p<0.01$). The *BAX/BCL2* ratio was significantly increased only in the LC alopecia group ($p<0.001$), primarily due to decreased *BCL2* expression. Furthermore, *MLKL* expression was significantly upregulated in both the LC alopecia and LC non-alopecia groups ($p<0.01$).
Conclusion
Increased *MLKL* expression in both the LC alopecia and LC non-alopecia groups suggests the involvement of necroptosis-related pathways in Long COVID. In addition, the LC alopecia group showed an increased *BAX/BCL2* ratio, indicating dysregulation of apoptosis-related balance and involvement of more extensive cellular injury and complex cell death mechanisms in Long COVID–associated alopecia. In contrast, no increases in the *BAX/BCL2* ratio or *MLKL* expression were observed in the non-LC group, suggesting that abnormalities in cell death pathways may be associated with the persistence of Long COVID pathology.

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P-2-21

一般演題 Immunology

Reducing False-Positives in Fourth-Generation IGRA Screening

Balancing Laboratory Quality and Cost Through Retest Criteria Optimization

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Optimizing Retest Criteria to Reduce False-Positives in Fourth-Generation IGRA Screening: Balancing Quality and Cost
Background: The fourth-generation Interferon-Gamma Release Assay, QuantiFERON-TB Gold Plus (QFT-Plus), introduces a second antigen tube (TB2) to detect CD8+ T-cell responses alongside CD4+ responses (TB1). While enhancing sensitivity for latent tuberculosis infection, single-tube positivity (TB1-only or TB2-only) poses a risk of false positives. This study investigates potential automated ELISA pipetting splash contamination and evaluates optimized retest algorithms to mitigate these errors.
Methods: We retrospectively analyzed 16,959 QFT-Plus screening samples from tuberculosis contacts and high-risk populations, including long-term care facility and mountainous area residents, between 2024 and 2025. Tests were performed using a DYNEX DS2 automated ELISA system. The laboratory's initial protocol triggered a retest if a sample exhibited single-tube positivity with a response difference (|TB1 - TB2|) 0.4 IU/mL. An optimized model was further evaluated to balance quality control and reagent costs.
Results: Among 16,959 samples, 1,743 (10.2%) were positive, including 265 (15.2% of positives) single-tube positives (120 TB1-only, 145 TB2-only). Under the initial protocol, 65 samples (24.5% of single-tube positives) met the retest criteria, and 21 were ultimately confirmed as negative false positives. Adjusting the threshold to a positive tube value minus Nil ≥0.5 IU/mL and a |TB1 - TB2| difference ≥ 0.5 IU/mL reduces retests to 38 samples but misses 2 potential false positives caused by instrument splashing.
Conclusion: Establishing an optimized retest algorithm for single-tube positive results is critical for maintaining high-quality reporting while managing high reagent costs. Although more stringent criteria significantly reduce the laboratory retest workload, facilities must carefully weigh these cost savings against the potential risk of issuing false-positive reports.
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P-2-22

一般演題 Immunology

Evaluation of HLA antibodies against recombinant and native HLA

A HLA proficiency testing survey

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Background: Luminex single antigen bead assay (SABA) has become the “gold standard” for human leukocyte antigen (HLA) antibody detection and identification. However, some studies had reported an antibody against denatured HLA found in SABA could result in a false positive reaction. The aim of this study was to measure the concordance and discordance of the results among laboratories in testing anti-HLA antibodies with LABScreen™ Single Antigen (One Lambda, USA) and LIFECODES® Class I and Class II ID (Abbr. IDs) (Immucor, USA).

Materials and Methods: The sera were from Asia-Pacific Histocompatibility and Immunogenetics Association (APHIA) and distributed by the Proficiency Testing Program to 15 HLA laboratories. We analyzed 3 test results (XmAbSER22-01, XmAbSER-22-02, AbSER-22-03) for HLA class I and class II antibodies submitted by participating laboratories.

Results: The concordance rate for HLA class I antibodies between SABA and IDs for the 3 tests were 75.0%, 72.7% and 82.1% respectively. Additionally, the concordance rate for HLA class II antibodies for each test was 100%, given that the IDs was not assigned to the serological DQA1 and DP typing. Relatively the discordances found between SABA and IDs assay were that the IDs assay, which the beads are coated with purified human HLA, showed positive reactions against Cw7 and Cw10 with median fluorescent intensity in XmAbSER22-01, A29, A33, A34, and Cw10 with in XmAbSER-22-02, and A1, A2, A3, A30 and Cw6 in AbSER-22-03, respectively. While the SABA showed positive reaction against B27, B38, B39, B48, B54, B71, B76 and Cw2 in XmAbSER-22-01, A69, B27, B44, B51, B58, B76, B78, Cw6 and Cw15 in XmAbSER-22-02 and B38, B48, B58, B59 and B76 in AbSER-22-03, in which IDs assay showed negative reaction to these antigens.

Conclusions: The discordances found between SABA and IDs are worth further investigation by consolidating the results using different methods and assays.

P-2-23

一般演題 Immunology

Modulation of NLRP3 Inflammasome-related Cytokines by Fatty Acids

Differential Modulation of NLRP3 Inflammasome-related Cytokines by Palmitic Acid and Docosahexaenoic Acid

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Nucleotide-binding oligomerization domain (NOD)-like receptors (NLRs) are a newly identified class of pattern recognition receptors (PRRs). Alongside Toll-like receptors (TLRs), C-type lectins (CTLs), and galectins, NLRs mediate the innate immune response by detecting pathogenic microbes and other endogenous or exogenous pathogens. Inhibition of the NLRP3 inflammasome is a promising strategy for developing novel treatments for inflammatory diseases. For instance, MCC950 is a potent and specific small-molecule inhibitor of the NLRP3 pathway. Previous studies have shown that saturated fatty acids, such as palmitic acid (PA), induce chronic inflammation, while omega-3 polyunsaturated fatty acids like docosahexaenoic acid (DHA) possess potent anti-inflammatory and immunomodulatory properties. To clarify these pathways, this study investigated the regulatory mechanisms of PA and DHA on NLRP3 inflammasome-related cytokine expression in RAW 264.7 macrophages. Cells were treated with various concentrations (1, 10, and 50 μM) of DHA or PA, then mRNA expression levels of IL-1β, IL-18, NLRP3, Caspase-1, and TNF-α were measured using qPCR. The results indicated that DHA significantly decreased the expression of IL-1β, NLRP3, IL-18, Caspase-1, and TNF-α ($p < 0.05$). In contrast, PA significantly increased the expression of these cytokines ($p < 0.05$). In particular, mRNA expression comparisons between DHA and PA treatment highlighted their differential impact on NLRP3-related inflammatory cytokines. Therefore, these findings reveal that PA and DHA possess the potential to modulate the NLRP3 inflammasome.

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一般演題 Immunology

POLKESMAS COVID-19 ANTIGEN: Innovative Diagnostic Kit Based Local Indonesian Isolates

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INTRODUCTION: The development of rapid and accurate diagnostic tools remains essential for controlling Coronavirus Disease 2019 (COVID-19). This study aimed to develop POLKESMAS COVID-19 Antigen, an innovative immunochromatographic diagnostic kit designed to qualitatively detect the SARS-CoV-2 nucleocapsid antigen using recombinant protein derived from local Indonesian SARS-CoV-2 isolates.

METHODS: This laboratory experimental study was conducted from March 2021 to November 2024. The research included sample collection and confirmation using the real-time reverse transcription polymerase chain reaction (rRT-PCR) method, followed by whole genome sequencing and strain mapping through homology and phylogenetic analyses. The SARS-CoV-2 nucleocapsid gene was cloned and expressed as a recombinant protein in Escherichia coli BL-21. Monoclonal antibodies were subsequently produced and integrated into an immunochromatographic platform through conjugate coating optimization. The diagnostic kit was then manufactured and validated against the rRT-PCR gold standard.

RESULTS: Whole genome sequencing of 111 randomly selected Indonesian isolates identified Delta lineage variants consisting of AY.23 (85.6%; n=95), AY.24 (12.6%; n=14), and AY.127 (1.8%; n=2). Phylogenetic analysis revealed that the isolates formed distinct genetic clusters, suggesting predominantly local transmission. Recombinant nucleocapsid proteins derived from these isolates were successfully utilized in the development of the diagnostic kit. Validation testing demonstrated excellent diagnostic performance, with sensitivity of 100%, specificity of 96.9%, positive predictive value of 98.4%, negative predictive value of 100%, and overall accuracy of 98.9% compared with rRT-PCR.

CONCLUSION: POLKESMAS COVID-19 Antigen demonstrated high diagnostic performance and accuracy, indicating its potential as a reliable diagnostic tool for COVID-19 detection. The use of recombinant proteins derived from local Indonesian isolates provides a novel approach that may enhance diagnostic relevance and effectiveness in the Indonesian population.

KEYWORDS: COVID-19; SARS-CoV-2; Antigen Diagnostic Kit; POLKESMAS COVID-19 Antigen; Local Indonesian Isolates.

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P-2-25

一般演題 Immunology

Targeting the NLRP3 Inflammasome for Inflammation Control

Potassium Channels as Targets for Inhibiting NLRP3 Inflammasome Activation

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The NLRP3 inflammasome is a critical component of the innate immune system and plays an important role in the pathogenesis of various inflammatory diseases, including chronic kidney disease and nephritis. Upon activation, the NLRP3 inflammasome promotes the cleavage of pro-caspase-1 into active caspase-1, leading to the maturation and secretion of pro-inflammatory cytokines such as interleukin-1β (IL-1β) and interleukin-18 (IL-18), as well as the induction of pyroptotic cell death. Recent studies have identified potassium ion efflux as a common upstream signal required for NLRP3 inflammasome activation. This reduction in intracellular potassium serves as a key signal that promotes NLRP3 inflammasome assembly and activation. Consequently, this study targeted the inhibition of potassium channels as a potential strategy to suppress NLRP3 activation and regulate inflammatory responses. Inhibiting potassium efflux successfully reduced NLRP3 activation and decreased the production of IL-1β and IL-18. Furthermore, anti-inflammatory agents such as docosahexaenoic acid (DHA) and vitamin D were evaluated for their protective effects, specifically regarding how they modulate potassium channel activity and suppress the NLRP3 inflammasome. These results demonstrate that potassium channels are important molecular targets in the regulation of NLRP3 inflammasome activity. Further investigation of potassium channel-mediated signaling pathways may provide novel therapeutic approaches for treating chronic inflammatory disorders.

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P-2-26

一般演題 Immunology

Laboratory Method Verification of Urit IA-200 Chemiluminescence Immunoassay Anayser

Laboratory Method Verification of Urit IA-200 Analyser at Regional Hospital Bamenda, Cameroon

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Background: The URIT IA-200 is a fully automated chemiluminescence immunoassay analyser used for quantitative testing in clinical laboratories. Before use, the instrument must be verified to ensure that its performance under local laboratory conditions meets the manufacturer-specified specifications in accordance with ISO 15189 Standards. As this instrument is the first of its kind in our setting and in Sub-Saharan Africa, formal verification is needed to improve patient care.

Objective: To verify the performance characteristics of the Urit IA 200, including precision, linearity, and carryover, using the Total Prostate-Specific Antigen

Methods: This was a cross-sectional, prospective study conducted between February 2026 and May 2026 at the Bamenda Regional Hospital Laboratory, Cameroon. Precision was assessed using normal and pathological controls, and the percentage coefficient of variation (%CV) was expected to be within the manufacturer's specifications. Very high and very low specimens were analysed, and the expected carryover should be within the manufacturer-provided specification. Several dilutions of the standard specimen were analysed, and the linearity correlation coefficient was expected to be greater than 0.975, with the slope closer to one and the y-intercept closer to zero.

Results: The %CV precision experiments were less than 2.58 for both controls. The carryover was −0.035%, the correlation coefficient r = 0.995, the slope was 0.944, and the y-intercept was -0.536, all within manufacturer- provided specifications.

Conclusion: The URIT IA-200 demonstrated acceptable precision, carryover, and linearity under local conditions, confirming its suitability for routine use and for improving workflow, patient management and research.

Keywords: Performance evaluation; Precision; Carryover; Linearity; Total Prostate Specific Antigen.

P-3-1

一般演題 Hematology

Vit B12 deficiency among AML patients in Riyadh, retrospective study

Vit B12 deficiency among AML patients in Riyadh, Saudi Arabia; a retrospective study

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Acute myeloid leukaemia (AML) is one of the most prevalent types among patients in many regions and countries. Some laboratory diagnostic and biomarkers can be used to diagnose and follow up on AML cases and their exacerbation. In some cases, AML may be linked with a decrease in vitamin B12 levels (pg/mL). This study investigates the correlation between vitamin B12 deficiency and the exacerbation of diagnostic markers in AML patients. A retrospective study was conducted to collect demographic and clinical outcomes data for patients who have histologically confirmed diagnoses with AML and met specific inclusion criteria, which included assessing their vitamin B12 levels and eligibility for vitamin B12 deficiency evaluation. The data was retrieved from King Fahad Medical City (KFMC, Riyadh, Saudi Arabia) covering the period from 2015 to 2023, and then data was statistically analysed using the SPSS program. From 242 reported cases diagnosed with malignant AML, the mean age is 37 ± 22.9 years, and the mean B12 level is 96.6 ± 42.7. More than half of the AML cases are females (n=128), most of them are adults (n=194), and most of them are from Saudi Arabian nationality (n=197). Regarding the type of AML reported in this study, most of the cases (n=180) were acute myeloid leukaemia, NOS, and most cases were tested against different laboratory markers for diagnosing AML, such as Jak2, CD44, CD45RA, and CD123, most of the cases were tested against Jak2 (n=135). It has been reported that CD44 is significantly correlated with iron levels (p=0.029). AML could be diagnosed and followed up using different biomarkers rather than vitamin B12, and it has been suggested that vitamin B12 levels may decrease among cases with and without AML.

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P-3-2

一般演題 Hematology

Assessing the association between neutrophil-to-lymphocyte ratio and bacteremia

A Case Study of a Teaching Hospital in Hsinchu, Taiwan

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This study explores the relationship between the neutrophil-to-lymphocyte ratio (NLR) and bacteremia, a severe bloodstream infection often linked to immune dysfunction. NLR, representing the balance between neutrophils (acute inflammation) and lymphocytes (specific immunity), can serve as a predictive biomarker for infection. Neutrophils are key in acute responses, while lymphocytes contribute to specific immune defenses, making NLR a potential marker for predicting bacteremia onset and progression.

A retrospective analysis of blood data from 9,633 hospitalized patients at a teaching hospital in Taiwan was conducted. Blood cultures were processed with the Vitek 2 Compact system, and hematologic data were obtained using the Sysmex XN-2000 analyzer. The dataset included white blood cell count (WBC), neutrophil percentage (NEU%), and NLR, with 7,633 valid data points 6,993 in the blood culture-negative (BCN) group and 640 in the blood culture-positive (BCP) group.

The results showed significantly higher WBC, NEU%, and NLR values in the BCP group compared to the BCN group (all $P < 0.001$). Specifically, WBC was 11.3 vs. 9.67 $\times 10^9$/L, NEU% was 90.5% vs. 80.8%, and NLR was 19.65 vs. 7.48. Receiver operating characteristic analysis revealed that NLR effectively discriminated between BCP and BCN groups, with an area under the curve (AUC) of 0.879, sensitivity of 98.9%, and specificity of 69.4%.

Elevated NLR was associated with prolonged bacteremia and increased mortality. As a simple, cost-effective biomarker, NLR can aid early bacteremia detection, especially when infection sources are unclear, helping guide timely diagnosis and treatment.

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P-3-3

一般演題 Hematology

Epigenetic and MYC Signaling Modulation by Vault RNA1-1 in AML

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Introduction: Vault RNA1-1 (vtRNA1-1) is a non-coding RNA associated with multidrug resistance. We previously correlated serum vtRNA1-1 levels with bone marrow cellularity in Acute Myeloid Leukemia (AML) patients, implying its role in leukemic expansion. This study elucidates the underlying regulatory networks of vtRNA1-1 in AML via comprehensive bioinformatic profiling.
Methods: We established stable vtRNA1-1 knockdowns (KD) and controls in the THP-1 AML cell line using shRNA. Proliferation was assessed via flow cytometry. To uncover downstream mechanisms, RNA sequencing (48h post-transduction) and Biojupies analyses (KEGG/Reactome, motif discovery, L1000 Connectivity Map) were performed.
Results: vtRNA1-1 KD significantly suppressed THP-1 proliferation. Transcriptomic profiling revealed profound reprogramming: down-regulated genes were enriched for cell cycle and ribosome biogenesis pathways, prominently featuring MYC/MAX binding motifs. Conversely, apoptosis, p53, TNF signaling, and metabolic pathways (e.g., glycolysis) were markedly upregulated. Crucially, Connectivity Map analysis revealed that the KD signature mimics the effects of the HDAC inhibitor Vorinostat. Supported by ENCODE H3K27ac data, this suggests vtRNA1-1 maintains an epigenetic state favoring proliferation.
Conclusions: vtRNA1-1 is critical for maintaining AML cell growth by sustaining MYC-driven progression and repressing apoptotic/inflammatory stress responses. Its connections to HDAC activity and metabolism highlight vtRNA1-1 as a multifaceted therapeutic target in AML.

P-3-4

一般演題 Hematology

Smart System Reduces Peak-Hour Blood Draw Waiting Time

©CHING CHAO LIANG[1)]、Chin Chao Liang[1)]、Yi Pen Chin[1)]、Mu Ching Hsueh[1)]、Hsu Han Chien[1)]、Chin Yi Chien[1)]
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Smart System Reduces Peak-Hour Blood Draw Waiting Time
To reduce peak-hour (9–11 AM) blood draw wait times and improve urgent report turnaround through a smart monitoring and backup system. Baseline (Jan–Jun 2024) showed an average wait of 12.2 min. Fishbone analysis revealed three gaps: no peak-volume data, no surge backup, and unmeasured phlebotomist performance. Three countermeasures were implemented: (1) real-time monitoring dashboard; (2) music alert when queue exceeded 20 patients; (3) staff performance ranking with monthly review. Target: 50% wait-time reduction. Post-implementation (Jan–Dec 2025): peak-hour wait fell to 4.8 min (−60.7%; 121.3% of target). Urgent report turnaround improved from 37.7 to 26.2 min; support response time from 8 to 1 min. Performance transparency also boosted phlebotomist morale. The integrated smart system benefited patients, phlebotomists, and physicians by optimizing staffing and enabling timely clinical decisions, with strong potential for broader hospital adoption.

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P-3-5

一般演題 Hematology

Comparison of Two Cases of T-PLL with Contrasting Clinical Courses

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[Introduction]T-cell prolymphocytic leukemia (T-PLL) is an aggressive and rare. We encountered one case with a clinical course typical of aggressive T-PLL and another with a relatively indolent course. Here, we report a comparative analysis of these two cases.

[Clinical course] (Case1) A man in his 70s. Twelve years after treatment for diffuse large B-cell lymphoma (DLBCL), thrombocytopenia was detected during follow-up, and diagnosed with T-PLL. Four months later, the disease transformed into T-cell acute lymphoblastic leukemia (T-ALL). The patient died approximately seven months after the diagnosis of T-PLL. (Case2) A man in his 50s. Leukocytosis was identified during a routine medical checkup three years ago. He was referred to our hospital and was suspected of having small cell variant of T-PLL. During the evaluation, lung cancer was diagnosed, and he is currently under observation without progression of T-PLL.

[Test results]< blood test> (Case1) WBC 6.1×10^3/μL, RBC 4.48×10^6/μL, Hgb 13.1g/dL, PLT 62.0×10^3/μL, Ly 67.0% (Small to large lymphocytes with basophilic cytoplasm, high N/C ratio, condensed nuclear chromatin, and prominent nucleoli), LD 301U/L (Case2)WBC 17.9×10^3/μL, RBC 5.10×10^6/μL, Hgb 15.0g/dL, PLT 315×10^3/μL, Ly 68.0%(small and prominent nucleoli), LD 166U/L <FCM> (Case1) positive cyCD3, CD2dim, CD5dim, CD7, CD4dim, CD52, CD13, CD34, CD117 negative sCD3, cyMPO, TdT(After transformation, get TdT positive) (Case2) positive cyCD3, sCD3, CD4, CD5, TCRab, CD43 negative CD8, CD7, TCRgd, CD30, CD38, CD16, CD56, TdT <Chromosome, Gene> (Case1) normal karyotype, TCRγ rearrangement (Case2) normal karyotype, TCRβ rearrangement

[Conclusion] Case 1 exhibited typical aggressive features whereas Case 2 demonstrated a more indolent course. Compared with Case 1, Case 2 had lower LD levels, lymphocyte morphology closer to normal lymphocytes, and fewer abberant marker in FCM. The small cell variant of T-PLL might be associated with a relatively indolent course in some cases.

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P-3-6

一般演題 Hematology

Andrographolide Induces Ferroptosis and Enhances Bortezomib in Plasma Cell Neoplasms

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Background: Ferroptosis is an iron-dependent, lipid peroxidation–driven form of regulated cell death and a potential therapeutic target in hematological malignancies. Andrographolide (Andro) induces oxidative stress–related cell death, but its involvement in ferroptosis and its combinatorial effects with bortezomib (Btz) remain unclear.

Methods: Human plasma cell neoplasm cell lines H929 and ARH77 were treated with Andro alone or in combination with Btz. Cell viability was measured by MTT assays. Ferroptosis was assessed by ROS production, lipid peroxidation (Liperfluo), and FACL4/GPX4 modulation, with Ferrostatin-1 (Fer-1) used for validation. Apoptosis and drug interactions were analyzed by Annexin V/7-AAD flow cytometry and combination index (CI) analysis, respectively.

Results: Andro reduced cell viability in both H929 and ARH77 cells in a dose-dependent manner (H929 IC_{50}: 7.0 μM, ARH77 IC_{50}: 10.1 μM), accompanied by significant ROS accumulation and lipid peroxidation. These effects were partially reversed by Fer-1, supporting involvement of ferroptosis-associated lipid peroxidation. Mechanistically, Andro upregulated FACL4 expression (control: 15.7 vs Andro: 44.3; 2.8-fold) while downregulating GPX4 (control: 52.9 vs Andro: 24.1 0.45-fold) in H929 cells. Although Andro also induced apoptosis, ferroptosis-associated markers were preserved independently of apoptotic features. Notably, co-treatment with Andro enhanced Btz-induced cytotoxicity, yielding synergistic or additive interactions depending on dose and cell line; synergism was observed with Andro 7.0 μM plus Btz 2 nM (CI = 0.68) in H929 cells. This enhanced efficacy was associated with augmented oxidative stress and cell death, which was partially Fer-1–sensitive.

Conclusion: Andrographolide induces ferroptosis in plasma cell neoplasm cells and potentiates the antitumor activity of bortezomib through oxidative stress–dependent mechanisms. Andro-based ferroptosis targeting may enhance proteasome inhibitor therapy in plasma cell neoplasms.

P-3-7

一般演題 Hematology

AI-Driven Morphological Recognition of Myeloma Cells

Enhancing Efficiency and Accuracy in Bone Marrow Smear Morphological Screening

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Introduction: In multiple myeloma (MM), neoplastic plasma cells proliferate uncontrollably, disrupting normal hematopoiesis and leading to severe systemic complications. Myeloma cells exhibit significant hematopathological heterogeneity; specifically, the presence of plasmablasts indicates high-grade malignancy and poor prognosis. While early detection is clinically vital, differentiating these cells morphologically remains challenging even for experienced hematologists. Deep learning, particularly Convolutional Neural Networks (CNNs), provides advanced image recognition capabilities. This study aims to develop a high-precision AI-driven system for the automated identification and hematopathological differentiation of myeloma cells.

Methods: We utilized ResNet-18, 34, 50, and 101 architectures. The training dataset consisted of 895 microscopic bone marrow smear images, categorized into three classes (lymphocytes, normal plasma cells, and myeloma cells) by expert consensus. The data augmentation was applied to the original images, and transfer learning or fine-tuning was performed on the AI models. For clinical validation, we analyzed 11,180 images from 31 healthy and 15 MM cases, evaluating the agreement between manual expert classification and AI-based recognition.

Results: The best-performing model achieved a holdout validation accuracy of 0.994, with an average recall of 0.994 and an F-measure of 0.994. In clinical assessment, the model demonstrated robust performance across all datasets. For healthy subjects, the median accuracy (MID) was 0.987 (range: 0.620–1.000). In MM cases, the MID was 0.976 (range: 0.690–1.000). The overall system maintained a median accuracy of 0.985, showing high consistency with expert findings.

Conclusion: Our CNN-based models accurately differentiated normal plasma cells from malignant myeloma cells. By minimizing the risk of overlooking hematopathological cells, this AI-driven approach enhances both the efficiency and accuracy of bone marrow smear screening, offering a superior alternative to conventional manual microscopy.

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P-3-8

一般演題 Hematology

Preventing Oversight of Non-Specific Reactions in FDP and D-dimer

Utility of Alert Settings for Detecting and Establishing Practical Identification Procedures

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Immunochemical assays based on antigen-antibody reactions are sometimes problematic due to non-specific reactions that can compromise diagnostic accuracy. This study aimed to evaluate an alert system and establish a clinically applicable identification protocol for non-specific reactions in fibrin/fibrinogen degradation products (FDP) and D-dimer assays using latex agglutination turbidimetric immunoassays. We analyzed a total of 10,915 samples with simultaneous FDP and D-dimer orders to define the alert thresholds. The alert thresholds were defined as a D-dimer/FDP ratio of > 60% and <20% when FDP was < 10 μg/mL, and of > 60% and < 25% when FDP was > 10 μg/mL, respectively. Nanopia P-FDP and Nanopia D-dimer reagents (SEKISUI MEDICAL) were employed for measuring FDP and D-dimer, and the assays were performed on the Coapresta 2000 analyzer (SEKISUI MEDICAL). Over a five-year period, 53 cases were detected by the alert criteria, of which 16 cases demonstrated non-specific reactivity, indicating the clinical utility of the alert system. Although dilution testing revealed no consistent trends relative to undiluted values, absolute variation analysis identified a 3-fold dilution as optimal, yielding the highest sensitivity and specificity. Consequently, we propose a diagnostic algorithm: perform a 3-fold dilution test upon alert activation. If the change variation is greater than ±9.1% for FDP or ±20.0% for D-dimer, a non-specific reaction should be suspected. Upon suspicion of a non-specific reaction, confirmation via dithiothreitol (DTT) treatment or immunoglobulin absorption testing is recommended to identify the cause of non-specific reaction. This protocol enhances the detection and characterization of non-specific reactions in routine immunoassay.

P-3-9

一般演題 Hematology

Evaluation of Internal Quality Control Strategy in Peripheral Blood Morphology

Establishing Objective Criteria for leukocyte differentials

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Background: Our laboratory performs monthly internal quality control (IQC) of peripheral blood smear leukocyte differentials for technologists using both normal and abnormal specimens. The conventional acceptance criterion has been defined as the mean value of four expert morphologists ± 5% for each cell category. However, this uniform criterion does not account for differences in cell frequency or clinical relevance. In addition, differences in the starting position for cell counting may result in variability in the proportions of detected cell types among technologists. To establish a more appropriate QC strategy, we evaluated alternative acceptance criteria.
Methods: Peripheral blood smears have been assessed since October 2025 using differential counts of 200 cells under five criteria: (1) the conventional method (mean ± 5%); (2) a non-specified starting position with an SD-based criterion (mean ± 3 SD of four experts); (3) a specified starting position with an SD-based criterion (mean ± 3 SD); (4) a non-specified starting position with a fixed-percentage criterion (mean ± 3%); and (5) a specified starting position with a fixed-percentage criterion (mean ± 3%). For each method, deviations were analyzed by cell type, and detection performance was evaluated.
Results: Compared with the conventional method, the SD-based criteria and the specified-position ± 3% criterion identified a greater number of technologists exceeding the acceptance limits. Deviations were particularly evident in low-frequency cell populations under the SD-based criteria.
Discussion: The conventional ± 5% acceptance criterion appears overly permissive for rare cell types and may overlook inadequate performance. In contrast, the SD-based and specified-position ± 3% criteria more effectively identify variability in cell classification and clarify misclassified cell types, suggesting improved educational value. Further refinement of the criteria and structured feedback may enhance reproducibility and overall IQC effectiveness in peripheral blood smear morphology assessment.

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一般演題 Hematology

Rapid Histiocytic Sarcoma with Hemophagocytosis and Hematoidin Crystals Case

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Histiocytic sarcoma (HS) is an extremely rare and highly aggressive hematopoietic malignancy arising from mature histiocytes, characterized by rapid progression and poor prognosis. We report a 51-year-old man presenting with fever, significant weight loss, night sweats, progressive weakness, and cytopenia. Initial imaging revealed a large retroperitoneal mass with widespread metastases involving the lungs, liver, adrenal glands, pre-sacral region, and soft tissues, suggesting systemic and highly proliferative disease. Laboratory findings included anemia, thrombocytopenia, elevated lactate dehydrogenase, and inflammatory markers, while tumor markers were normal. Bone marrow aspiration and biopsy revealed hypocellularity with diffuse infiltration of pleomorphic histiocytic tumor cells containing vacuolated cytoplasm and hemosiderin. Prominent hemophagocytosis and bright-orange hematoidin crystals were observed within tumor cells, indicating tissue necrosis and chronic hemorrhage. Immunohistochemical analysis demonstrated positivity for CD163, CD68, CD4, and CD45, and negativity for lymphoid, epithelial, myeloid, dendritic cell, and BRAF V600E markers, confirming HS with bone marrow involvement. The clinical course was fulminant; despite supportive care, the patient rapidly progressed to multiple organ failure and died 11 days after admission. HS is diagnostically challenging due to its rarity, heterogeneous morphology, and overlap with other hematologic and solid malignancies, making histiocytic markers such as CD163 critical for accurate diagnosis. Notably, hematoidin crystals in bone marrow are rarely reported and may represent an important histopathological clue of ongoing necrosis and chronic bleeding. This case highlights the aggressive nature of primary HS, underscores the significance of hemophagocytosis and hematoidin crystal deposition for diagnosis, and emphasizes the importance of early recognition, prompt diagnosis, and timely intervention to guide clinical management in this rare and often fatal malignancy.

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一般演題 Hematology

Alternative Erythrocyte Sedimentation Rate Systems After Tube Discontinuation

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Erythrocyte sedimentation rate is a widely used, nonspecific marker of inflammation. Following the discontinuation of the reference collection tube for the VACUETTE SRS20/II reference method, laboratories need practical alternatives for routine testing. This study evaluated three K_2EDTA-compatible systems— CUBE 30 Touch, ALIFAX Roller 20PN, and iSED ELITE—for analytical performance, reference interval verification, and suitability for routine laboratory workflow. This evaluation was conducted from November 1 to November 20, 2025. Within-run precision, between-day precision, accuracy, reference interval verification, method correlation, and carryover were assessed. Reference interval verification was performed using 20 healthy individuals. Method comparison included 60 clinical specimens across low, medium, and high erythrocyte sedimentation rate ranges. Hematocrit values were recorded for all specimens, and samples with a hematocrit below 35% were corrected using Fabry's formula. Carryover testing was performed for ALIFAX Roller 20PN and iSED ELITE. All three systems met predefined validation criteria and were considered acceptable alternatives. After Fabry's formula correction, the correlation between each method and the VACUETTE SRS20/II method showed Pearson's *r* values of 0.883 for CUBE 30 Touch, 0.858 for iSED ELITE, and 0.835 for ALIFAX Roller 20PN. Importantly, all three systems also passed reference interval verification, while iSED ELITE showed the closest alignment with the current reference interval framework. Carryover results were acceptable for both ALIFAX Roller 20PN and iSED ELITE. Furthermore, iSED ELITE demonstrated favorable workflow characteristics and the broadest CAP participation among the evaluated platforms. In summary, all three K_2EDTA-compatible systems are suitable alternatives for routine laboratory practice after discontinuation of the reference collection tube. Among them, iSED ELITE showed the best alignment with the current reference interval framework and overall workflow suitability.
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一般演題 Hematology

Lymphoma involving cerebrospinal fluid confirmed by flow cytometry

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Background: Flow cytometry is powerful in determing the cellular lineage of hematological malignancies, particularly for lymphoid vs. myeloid neoplasms. It is routinley employed using bone marrow and/or peripheral blood samples, bu less frequently used in evaluating cerebrospinal fluid specimens. Here we present a case of lymphoma with cerebrospinal fluid involvement confirmed by flow cytometry.

Materials and Methods:

We reviewed a patient wtih diffusel large B cell lymphoma who had neurological symptoms. We perfomred flow cytometric stuty using cerebrospinal fluid specimen and reported the phenotypic findings.

Results: A 26 years old female presened with left side numbness and weakness for about ten days to the Emergency Deparment on March 18, 2026. Physical examination showed weakness of bilateral lower legs, slurred speech and neck tenderness. Laboratory data showed acute kidney injury, hypercalcemia. Brain CT showed diffuse bilateral brain swelling. Abdominal CT showed large infiltrative retroperitoneal tumors. Under the impression of malignant lymphoma, needle biopsy of the retroperitoneal mass and cerebrospinal fluid tapping were performed. Histological examination revealed diffuse large B-cell lymphoma. The cerebrospinal fluid was highly cellular compring large cells with pleomrophic nuclei. The population of CD45 bright cells with intermediate to high farward scatter signals was gated for flow cytometric immunophenotyping. These cells expressed CD10 (partial), CD19, CD20, but not CD3, CD5, CD23, CD79b, CD81, or ROR1. They were monotypic for cytoplasmic kappa light chain expression. These findings confirmed large B-cell lymphoma invovling the cerebrospinal fluid.

Conclusion: Our case showed that flow cytometric immunophenotyping is a powerful tool for confirming large cell lymphoma with secondary involvement of cerebrospinal fluid.
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一般演題 Hematology

Dependent Platelet Clumping

A Reversible Pseudothrombocytopenia Case

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Temperature-Dependent Platelet Aggregation Leading to Reversible Pseudothrombocytopenia: A Case Report

Objective：

Pseudothrombocytopenia is a common laboratory artifact, most often associated with platelet aggregation induced by EDTA anticoagulant, which may lead to an underestimation of platelet counts by automated hematology analyzers. In clinical practice, most cases can be confirmed by changing the anticoagulant or by reviewing a peripheral blood smear. However, non–EDTA-dependent or temperature-related cases are relatively uncommon and may lead to misinterpretation.

Methods:

Blood samples were collected in EDTA and sodium citrate tubes. Platelet counts and peripheral smears were evaluated at room temperature, followed by reanalysis after incubation at 37°C for 20 minutes. Morphological assessment focused on platelet aggregation and red blood cell (RBC) agglutination.

Results:

Platelet clumping was observed in both EDTA and citrate samples, resulting in falsely low platelet counts. Peripheral smear confirmed marked platelet aggregation without RBC agglutination. After warming at 37°C, platelet aggregates resolved completely, and counts returned to normal ranges. These findings indicate a temperature-dependent, platelet-specific agglutination rather than EDTA-induced pseudothrombocytopenia.

Conclusion:

This case highlights a rare, reversible form of platelet aggregation likely mediated by cold-reactive antibodies. Recognition of this phenomenon is essential to avoid misdiagnosis. Appropriate pre-analytical handling, including temperature control and smear review, is crucial for accurate platelet evaluation.

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一般演題 Hematology

Using erythrocyte sedimentation rate as a novel application of biomarker

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Background：Erythrocyte sedimentation rate (ESR) is a widely used non-specific inflammatory marker; however, it is influenced by hematological factors such as hematocrit and red blood cell morphology. With the introduction of high-precision photometric rheology (ALCOR iSED), ESR measurement has become more rapid and less susceptible to interference. This study aimed to evaluate the association between ESR and tumor markers (CEA, CA125, and CA19-9), and to assess its potential as a clinically useful biomarker. **Methods**：A retrospective study was conducted using patient data from 2020 to 2025 at Taichung Veterans General Hospital. ESR values obtained by the conventional Westergren method and the ALCOR iSED system were analyzed in conjunction with tumor marker levels. Patients with hematological abnormalities (Hct <30%, MCV >100 fL) or chronic inflammatory diseases were excluded. Data were stratified by sex and categorized according to established reference ranges. Statistical comparisons were performed to evaluate differences between groups. **Results**：In male patients, no significant association was observed between ESR and tumor markers. In female patients, although CEA and CA19-9 showed increasing trends with elevated ESR, these did not reach statistical significance. In contrast, CA125 levels were significantly higher in patients with elevated ESR using both methods (Westergren: p=0.0297; iSED: p=0.0020). Furthermore, the iSED method significantly reduced turnaround time from 69 minutes to 39 minutes (p<0.001), improving laboratory efficiency. **Conclusion**：A significant association between ESR and CA125 was observed in female patients, suggesting that ESR may serve as a supportive biomarker in cancer-related conditions, particularly in gynecological diseases. The iSED method demonstrated superior efficiency, reduced interference, and improved analytical performance, supporting its potential application in clinical practice for cancer risk assessment and monitoring.

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一般演題 Hematology

Development and evaluation of an automated CLEIA measurement for sCLEC-2

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Introduction

Soluble C-type lectin-like receptor 2 (sCLEC-2) has attracted attention as a novel biomarker for in vivo platelet activation. Conventionally, its measurement has been performed using the ELISA method, which requires complicated procedures and considerable time to obtain results. In this study, we developed a new automated measurement reagent based on the chemiluminescent enzyme immunoassay (CLEIA) principle, evaluated its analytical performance, and investigated several pre-analytical factors affecting its measurement.

Methods

Human citrated plasma samples were used. We examined the sensitivity, precision, linearity, influence of endogenous substances, the effect of residual platelets, and the correlation with ELISA for the sCLEC-2 CLEIA reagent. Furthermore, the reference range, molecular forms of sCLEC-2 detected by this assay, and the effects of centrifugation conditions and plasma sampling position were evaluated. The CLEIA was performed on the STACIA analyzer (PHC Corporation, Tokyo, Japan).

Results

The parametric LoD was 3.8 pg/mL and the LoQ was 14.1 pg/mL (10% CV). Using three samples, repeatability CVs ranged from 5.1 to 6.2% and intermediate precision CVs ranged from 6.2 to 6.6%. Linearity was confirmed up to 881.7 pg/mL. Most endogenous substances showed no interference except conjugated bilirubin. Platelets in plasma increased the measured sCLEC-2 values. The correlation equation with ELISA was $y = 24.21 + 1.155x$ ($r = 0.908$, $n = 59$). The reference range for males was significantly higher than that for females. The CLEIA assay showed stronger reactivity with the shed form than with the microparticle form. No problems were observed with sCLEC-2 measurements using normal centrifugation or plasma sampling.

Conclusions

The newly developed sCLEC-2 CLEIA reagent exhibits robust performance and is promising for clinical applications.

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一般演題 Hematology

Impact of permeabilization reagents on CKAP4 detection in myeloma cells

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Introduction CD38 is both a hallmark marker and a therapeutic target in multiple myeloma (MM) cells, which originate from plasma cells. However, treatment with the anti-CD38 therapeutic monoclonal antibodies (mAb), daratumumab (DARA) and isatuximab (ISA), is known to interfere with CD38 detection by flow cytometry (FCM).To overcome the limitations of CD38-based evaluation, the endoplasmic reticulum-associated protein CKAP4 has been proposed as an alternative marker for MM cell detection using intracellular FCM.In this study, we aimed to establish optimal methods for detecting CKAP4 in MM cells by FCM.

Methods MM cell lines (MM.1S and RPMI 8226) and primary CD138+ cells isolated from patients with MM (n = 5) were analyzed by FCM and quantitative PCR. Cell permeabilization was performed using IntraPrep, PerFix-nc, or IntraStain reagents. CD38 and CKAP4 expression were assessed using an anti-CD38 multiepitope Ab and an anti-CKAP4 mAb (VS38c clone), respectively.

Results CD38 and CKAP4 mRNA levels in MM cells were not significantly altered by DARA or ISA treatment compared with untreated controls. In contrast, surface CD38 detection by FCM was significantly reduced following DARA or ISA treatment (MFI on MM.1S cells: untreated 12.76, DARA 7.18, ISA 6.89; $P < 0.05$). CKAP4 expression by FCM was minimally affected by DARA or ISA treatment (MFI in MM.1S cells: untreated 46.5, DARA 46.2, ISA 46.9; not significant). Notably, CKAP4 expressions were significantly lower when using IntraPrep and IntraStain compared with PerFix-nc in MM cells. Furthermore, the proportion of CKAP4- cells was increased when using IntraPrep or IntraStain compared with PerFix-nc in primary CD138+ cells (22.6% vs 10.1% vs. 0.6%; $P < 0.05$).

Discussion and Conclusion CKAP4 is a promising marker for the detection of MM cells, even in patients treated with DARA or ISA. Further studies are warranted to optimize intracellular staining protocols for CKAP4-based detection in clinical settings.

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一般演題 Hematology

Evaluation of a Lupus Anticoagulant Sensitive Activated Partial Thromboplastin Reagent

Reduced Lot to Lot Variation Using Controlled Synthetic Phospholipid Composition

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[Purpose] Activated partial thromboplastin time (APTT) is reported as an uncalibrated clotting time, and lot-to-lot variation in reagent phospholipid composition may compromise comparability within and between laboratories. This study evaluated a new lupus anticoagulant (LA) sensitive APTT reagent using ellagic acid as the activator, developed with controlled synthetic phospholipids and a liposome-homogenization process to minimize lot-dependent variability.
[Methods] Lot-to-lot variability was compared using 10 reagent lots with normal, abnormal, and heparin control plasmas. Factor sensitivity to factors VIII, IX, XI, and XII was assessed using diluted factor-deficient plasmas. Method comparison was performed with 89 plasma specimens. LA sensitivity was evaluated using weak LA–positive control plasmas and LA–positive control plasmas. Unfractionated heparin sensitivity was evaluated using plasma spiked to 0.2–0.8 IU/mL.
[Results] Lot-to-lot coefficients of variation for the evaluated reagent were 0.8% (normal), 2.1% (abnormal), and 2.8% (heparin), compared with 2.3%, 1.7%, and 3.5% for a comparator reagent. The evaluated reagent showed strong LA responsiveness (APTT ratios 1.88–3.30), and LA controls in the comparison set were prolonged by 37.1–67.5 s relative to the comparator. Unfractionated heparin produced concentration-dependent increases (APTT ratios approximately 1.4–6.1 at 0.2–0.8 IU/mL). Factor activities at the upper reference limit were 46% (factor VIII), 33% (factor IX), 44% (factor XI), and 24% (factor XII). Passing–Bablok regression demonstrated good correlation between reagents after exclusion of lupus anticoagulant samples ($r = 0.968$).
[Conclusion] The evaluated ellagic acid–based APTT reagent demonstrated high LA sensitivity, consistent unfractionated heparin responsiveness, and reduced lot-related variability, which may contribute to improved reproducibility of APTT testing during reagent lot changes.

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一般演題 Hematology

p53 Expression by IHC and Cytogenetic-Morphological Findings in MDS

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Background: Myelodysplastic syndromes (MDS) are clonal hematopoietic stem cell disorders characterized by morphological dysplasia in the bone marrow. Morphological evaluation plays a central role in diagnosis and classification. TP53 (tumor protein p53) is a representative tumor suppressor gene, and its genetic alterations have been reported to be associated with poor prognostic subgroups in MDS. Although detection of TP53 mutations requires molecular genetic analysis, immunohistochemical (IHC) assessment of p53 protein expression is widely used as a surrogate marker. However, the relationship between p53 expression assessed by IHC, cytogenetic abnormalities, and lineage-specific morphological dysplasia remains unclear. **Objectives**: This study aimed to evaluate the association between p53 expression patterns assessed by IHC and cytogenetic abnormalities and morphological dysplasia in patients with MDS. **Methods**: We retrospectively analyzed 90 patients diagnosed with MDS at our institution between January 2020 and December 2025. Dysplastic features in erythroid, granulocytic, and megakaryocytic lineages were classified based on their specificity for MDS. p53 expression was categorized as strong, moderate, or negative/weak based on the distribution pattern and proportion of p53-positive cells. Associations between p53 expression, cytogenetic findings, and morphological dysplasia were analyzed using Fisher's exact test and the Mann–Whitney U test. **Results**: p53 overexpression was significantly associated with a complex karyotype (>3 abnormalities) ($p < 0.01$). It was more frequent in the poor prognostic group and less frequent in the favorable group ($p < 0.05$). No significant association was observed between p53 overexpression and dysplasia in granulocytic or megakaryocytic lineages. In contrast, p53 overexpression was significantly associated with erythroid dysplasia ($p < 0.05$). **Conclusions**: p53 overexpression assessed by IHC is associated with advanced cytogenetic abnormalities and poor prognosis in MDS and suggests a selective association with erythroid dysplasia.

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一般演題 Hematology

Iron Intake and Iron Status in Women of Manila, Philippines

Heme and Non-Heme Contributions and Determinants

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Iron deficiency remains a public health concern among women of reproductive age in the Philippines. Dietary iron occurs as heme and non-heme iron forms, but their contribution to iron status in this population is not well understood. This study aimed to assess iron intake, identify its determinants and major food sources, and examine the relationship between heme and non-heme iron intake and iron status. A cross-sectional study was conducted among 169 women residing in the City of Manila. Dietary intake was estimated using a semi-quantitative food frequency questionnaire. Hemoglobin and ferritin were measured from blood samples. Determinants of iron intake were analyzed using Spearman correlation, ANOVA, and multiple linear regression. Associations between iron intake and iron status were assessed using correlation and regression analyses adjusted for age, parity, and education. Ferritin was log-transformed prior to regression. Mean iron intake was 20.0 ± 10.2 mg/day, coming largely from non-heme iron with 17.5 mg/day as compared to 2.5 mg/day from heme iron. White rice alone contributed 21.0% of total iron intake, while cereals and bakery products accounted for 64.0%. No demographic or socioeconomic factors were associated with iron intake (R^2=0.14, p=0.45). Neither heme nor non-heme iron intake was correlated with hemoglobin (rho=0.11, p=0.16 and rho=0.10, p=0.21, respectively) or ferritin (rho=0.07, p=0.36 and rho=-0.05, p=0.53). These associations remained non-significant after adjustment for covariates. Iron intake in this population was primarily derived from non-heme sources, with cereals and bakery products as the main contributors. Despite seemingly adequate intake, dietary iron was not associated with iron status, suggesting that bioavailability, dietary inhibitors, and physiological regulation may play a greater role than total iron intake. These findings highlight the need to integrate bioavailability-focused dietary strategies into nutrition programs and use appropriate biochemical markers to better assess iron status.

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一般演題 Hematology

PFCT Reference Interval Establishment and Hemostatic Risks in Trauma Patients

A Retrospective Study of Interval Validation, Medication Effects, and Injury Severity

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Objective: This study aims to establish a new biological reference interval (RI) for Platelet Function Closure Time (PFCT) using the PFA-100 system. It further analyzes the impact of medications and underlying diseases on PFCT and explores its relationship with the Injury Severity Score (ISS) in trauma patients to fill the diagnostic gap in comprehensive preoperative assessment.

Methods: A retrospective cohort study analyzed 12,522 PFCT data points from December 2023 to September 2025. Strict pre-analytical controls were enforced, including the prohibition of pneumatic delivery and rejection of hemolyzed samples. To establish the RI, a near-healthy baseline (n=5,308) was selected by sequentially excluding individuals with abnormal platelet counts, abnormal hematocrit (<20%), specific medications, and underlying diseases. RIs were defined using the 2.5th–97.5th percentiles.

Results: The new RIs were established as 61–144 seconds for Col/ADP and 73–175 seconds for Col/EPI. Implementation of these intervals significantly reduced abnormal reporting rates (Col/ADP: 24.9% to 3.4%; Col/EPI: 22.8% to 16.8%). Data indicated that Col/ADP is highly sensitive to embolism (p=0.001), while Col/EPI is more sensitive to stroke (p<0.001). In severe trauma (ISS >= 16), while mean closure times showed no linear trend, platelet function heterogeneity (CV%) increased significantly up to 60%.

Conclusion: The updated PFCT reference intervals improve clinical credibility by reducing unnecessary follow-ups for false positives. Shortened closure times serve as a vital, often overlooked indicator of hypercoagulability and VTE risk. Integrating PFCT with ISS provides a promising framework for developing VTE risk prediction models in trauma care.

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一般演題 Hematology

Alternative D-dimer Cut-offs Corresponding to FDP Thresholds in DIC

A Nationwide Real-World Analysis of Acute-Care Inpatients

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【Background】In Japan, the JAAM criteria are widely used for the diagnosis of acute DIC, and either FDP or D-dimer (DD) is used as a fibrin-related marker. However, in clinical practice, due to insurance restrictions and facility conditions, only DD is often measured at the initial visit. Therefore, a conversion table has been created for the JAAM criteria, assuming that DD values are converted to FDP values for application. However, this conversion table does not reflect the characteristics of the latest reagents, posing challenges from the perspective of standardization; thus, it is desirable to establish cutoff values using unified numerical values, similar to those for FDP.

【Objective】 In this study, we used the DPC database to establish DD cutoff values corresponding to the FDP categories in the JAAM criteria and evaluated their utility.【Methods】 We used case data provided by JMDC for patients admitted to acute-care hospitals from 2014 to 2023. A retrospective observational study was conducted on patients aged 18 years or older (n = 35,370) who were hospitalized for acute conditions and had both DD and FDP measured simultaneously during the early phase of hospitalization. Based on the JAAM criteria, control categories were defined as FDP < 10, 10–< 25, and ≥ 25 μg/mL, and the DD values that best corresponded to these categories were examined.

【Results】 DD values of 4.5 μg/mL (AUC: 0.975) and 9.7 μg/mL (AUC: 0.985) were identified as corresponding to FDP cutoff values of 10 μg/mL and 25 μg/mL, respectively. These cutoff values showed higher consistency with the FDP categories compared to the 3 μg/mL and 7 μg/mL values reported as ISTH-high DD.

【Conclusion】 It was confirmed that the cutoff values of 4.5 μg/mL and 9.7 μg/mL show high consistency with the FDP categories in the JAAM criteria. Applying DD using standardized cutoff values rather than a conversion table may contribute to increased sensitivity in the diagnosis of acute DIC in JAAM-2. We plan to conduct detailed analyses of the association between these cutoff values and 28-day mortality and severity, as well as disease-specific cutoff values. TEL+81-72-683-1221 (Ext: 3305)

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一般演題 Hematology

Soluble C-Type Lectin-Like Receptor 2 After Transcatheter Aortic Valve Implantation

Association with Post-Procedural Clinical Status in Cardiovascular Practice

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Background: Patients after transcatheter aortic valve implantation (TAVI) remain at risk of thrombotic and heart failure-related complications and require ongoing follow-up. Soluble C-type lectin-like receptor 2 (sCLEC-2) is a biomarker associated with platelet activation and thrombo-inflammatory states. We investigated whether plasma sCLEC-2 is elevated in patients with prior TAVI and associated with post-procedural clinical status.**Methods:** This cross-sectional study included 119 cardiovascular patients with available plasma sCLEC-2 measurements, including 28 with prior TAVI and 91 without prior TAVI. Plasma sCLEC-2 levels and the sCLEC-2-to-platelet count ratio were compared between groups. Multivariable linear regression analysis was performed in the overall cohort. In the TAVI subgroup, correlation, tertile, and multivariable analyses were conducted to examine associations with clinical variables.
Results: Patients with prior TAVI were older and had lower platelet counts, higher creatinine levels, and lower estimated glomerular filtration rate (eGFR) than those without prior TAVI. Plasma sCLEC-2 levels and the sCLEC-2-to-platelet count ratio were significantly higher in the TAVI group than in the non-TAVI group (203.1 vs. 153.2 pg/mL, p=0.045; 1.043 vs. 0.835, p=0.002, respectively). In the overall cohort, prior TAVI remained independently associated with a higher sCLEC-2-to-platelet count ratio after adjustment for age, sex, eGFR, and B-type natriuretic peptide (BNP) (p=0.008). In the prior TAVI group, the sCLEC-2-to-platelet count ratio correlated positively with BNP and creatinine and negatively with eGFR. Across tertiles of the sCLEC-2-to-platelet count ratio, higher values were associated with higher BNP and creatinine levels and lower eGFR (p for trend = 0.007, 0.017, and 0.004, respectively). In multivariable analysis within the TAVI subgroup, eGFR remained independently associated with the sCLEC-2-to-platelet count ratio (p=0.013).**Conclusions:** Plasma sCLEC-2 is elevated in patients with prior TAVI and is associated with clinical status after TAVI. These findings suggest that sCLEC-2 may reflect post-procedural clinical status in this population.

P-3-23

一般演題 Hematology

Deep Learning for Morphological Erythroblast Analysis in MDS

Automated Detection of Erythroid Morphological Changes to Support Clinical Diagnostic Accuracy

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Introduction: Myelodysplastic Syndromes (MDS) require early differential diagnosis, yet distinguishing MDS from other hematological disorders is challenging even for experts. A key diagnostic hallmark is the presence of dysplastic erythroblasts (EB); however, their high morphological diversity makes manual identification and precise counting subjective and technically difficult. To overcome these limitations and ensure diagnostic objectivity, we employed Convolutional Neural Networks (CNNs) for automated image analysis of bone marrow smears. This study aims to establish a deep learning-based approach to accurately identify dysplastic features, supporting experts in achieving more reliable and standardized MDS diagnoses.
Methods: ResNet architectures single or ensemble models were applied to deep learning. The original dataset for AI training included 2229 microscopic images of EBs from MGG-stained bone marrow smears. Three experts classified these images into 5 categories (Pro/Baso/Poly/Ortho/MDS EB) and assigned the correct labels. The data augmentation was applied to the original images, and transfer learning or fine-tuning was performed on the AI models. The subjects for clinical assessment were 15 healthy and 15 MDS cases. We evaluated the agreement between microscopic classification by experts and AI classification.
Results: In holdout validation, our AI model demonstrated high total accuracy, ranging from 0.926 to 0.944 with single models, and ranging from 0.928 to 0.937 with ensemble models. In clinical assessments, the best single AI model showed 0.673 for healthy cases, 0.181 for MDS cases in total accuracy. The best ensemble AI model showed 0.626 for healthy cases and 0.163 for MDS cases in total accuracy. The low agreement in MDS cases was due to the AI classifying cells that experts had identified as normal EBs as MDS EBs.
Conclusion: The low agreement in MDS cases suggests that AI may be detecting subtle morphological changes in EBs that experts are unable to recognize. We need to re-examine the possibility that MDS EBs may show monomorphic changes.
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一般演題 Hematology

Verification of Immature Granulocyte and Myeloblast Detection Performance

Examination of Operational Workflows Using an Automated Digital Cell Imaging Analyzer(DI-60)

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Background: Automated hematology analyzers accurately perform five-part white blood cell (WBC) differentials, but classifying immature granulocytes requires manual review. The DI-60 streamlines this process, but accuracy reports are limited. We evaluated its classification performance against manual review. To prevent missing critical myeloblasts, we developed a hybrid workflow combining an ROC-derived absolute count cutoff with automated flags. **Methods:** We analyzed 223 peripheral blood smear samples (117 positive for immature cells, 106 negative) using the DI-60, and compared the results to manual reviews performed at our hospital (Feb-Oct 2025). We compared percentages and absolute counts for myeloblasts, promyelocytes, myelocytes, metamyelocytes, and band neutrophils. We evaluated correlation and Bland-Altman agreement for each cell type. For myeloblasts, ROC analysis was performed using manual peripheral blood smear review (≥0.5%) as the reference standard to determine the optimal absolute count cutoff. We further verified a hybrid method combining this cutoff with automated analyzer flags. **Results:** Myeloblasts and myelocytes showed strong correlation. While some parameters for promyelocytes, metamyelocytes, and band neutrophils showed good correlation, the overall correlation remained low. Bland-Altman analysis demonstrated proportional bias across cell types, with increasing differences at higher counts. ROC analysis demonstrated high accuracy with an area under the curve (AUC) of 0.902. The derived myeloblast cutoff (0.0065 × 10^9/L) achieved 80.3% sensitivity and 100% specificity. Combining this with the automated blast flag (OR condition) improved sensitivity to 88.9% with 96.2% specificity. **Conclusion:** Although the DI-60 cannot fully replace manual classification, it effectively tracks cell trends. The hybrid approach utilizing the specific cutoff and automated flags enables high-accuracy myeloblast detection. This workflow may minimize missed cases and contribute to standardization, suggesting its potential as a screening tool for determining manual review necessity.

P-3-25

一般演題 Hematology

Flow Cytometry for Erythrodermic Cutaneous T-Cell Lymphoma Diagnosis

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Sézary Syndrome (SS) is a rare, aggressive erythrodermic Cutaneous T-Cell Lymphoma (CTCL) characterized by the triad of erythroderma, lymphadenopathy, and circulating malignant Sézary cells. Early diagnosis is often challenging due to symptomatic overlap with chronic dermatitis.

A 70-year-old female presented with progressive palmoplantar keratoderma, pruritus, and pain since 2022. Physical examination revealed marked hyperkeratosis over bilateral palms and soles. Laboratory evaluation showed marked leukocytosis (WBC: 25,600/μL). Peripheral blood morphology identified atypical lymphocytes (25μm in diameter) with characteristic cerebriform nuclei with deep indentations. The absolute Sézary cell count was 8,960/μL (35% of differential), significantly exceeding the ISCL/EORTC threshold of >1,000/μL.

Flow cytometry demonstrated a predominant T-cell population (CD2+, CD3+, CD4+, CD5+) with profound loss of CD7 (8.3%) and CD8 (1.1%). CD4+ reached 97.9%, yielding a CD4/CD8 ratio that fully satisfies ISCL/EORTC diagnostic criteria (CD4/CD8 >10 or CD4+/CD7- >30%). CD30 negativity excluded Anaplastic Large Cell Lymphoma. Although skin biopsy was not performed due to patient defaulting on follow-up, the absolute Sézary cell count, immunophenotype, and loss of T-cell antigens collectively met diagnostic criteria without TCR gene rearrangement data from skin tissue.

The patient's findings highly align with Sézary Syndrome criteria. Despite the absence of skin biopsy data, a diagnosis of Erythodermic Cutaneous T-cell Lymphoma was established on the 2023 Taiwan Expert Consensus, which emphasizes the integration of clinical presentation, hematomorphology, and flow cytometric immune-phenotype as the core diagnostic strategy.

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一般演題 Hematology

Diagnostic Value of HYPO-He% and MicroR% in Microcytic Anemia Differentiation

Utilizing Parameter Ratios to Distinguish Iron Deficiency from Thalassemia and Chronic Disease Anemia

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Objective and methods: Microcytic hypochromic anemia, characterized by MCV < 80 fl and MCH < 25 pg, primarily encompasses iron deficiency anemia (IDA), thalassemia (THAL), and anemia of chronic disease (CDA). Accurate differential diagnosis is essential for determining appropriate clinical management. This study aimed to evaluate the diagnostic performance of advanced parameters, HYPO-He% and MicroR%, and the MicroR%/HYPO-He% ratio (M/H ratio) in discriminating these conditions. A retrospective analysis was conducted on clinical hematological data from January 2022 to January 2025. The study cohorts included healthy controls (n=74), IDA (n=155), CDA (n=71), and THAL (n=44) patients. All samples were analyzed using the Sysmex XN-9000 automated hematology analyzer. Statistical analysis involved Kruskal-Wallis and Mann-Whitney U tests. Diagnostic accuracy was evaluated via Receiver Operating Characteristic (ROC) curves to determine the Area Under the Curve (AUC), optimal cut-off values (Youden Index), sensitivity (SN), and specificity (SP).

Results and conclusion: HYPO-He% and MicroR% levels were significantly higher in the IDA group compared to both control and CDA groups ($P < 0.001$). For differentiating IDA from CDA, HYPO-He% (cut-off ≥ 10.0, SN: 96.4%, SP: 90.1%) and MicroR% (cut-off ≥ 25.15, SN: 96.4%, SP: 94.4%) demonstrated high accuracy with AUCs of 0.983 and 0.994, respectively. Regarding IDA and THAL discrimination, the M/H ratio was significantly lower in IDA (median: 0.857) than in THAL (median: 2.047). The M/H ratio achieved an outstanding AUC of 0.955 (cut-off 1.310, SN: 0.944, SP: 0.864), significantly outperforming the traditional Mentzer Index (AUC: 0.700). HYPO-He% and MicroR% are highly effective screening parameters for identifying IDA. Furthermore, the M/H ratio serves as a superior, automated diagnostic tool for discriminating between THAL and IDA compared to traditional RBC indices. These parameters provide rapid, reliable, and high-precision clinical evidence, facilitating the early diagnosis and management of microcytic anemias in laboratory medicine.

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一般演題 Hematology

Extracellular HSP70 Drives Platelet Hyperactivation Under Stress-Associated Thrombotic Disease Conditions

Circulating extracellular HSP70 may provide clinically valuable laboratory information for thrombosis evaluation

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Background: Thrombotic disorders, such as myocardial infarction, stroke, and disseminated intravascular coagulation (DIC), involve platelet activation. Heat shock protein 70 (HSP70) is an extracellular protein released under stress and may serve as a biomarker for cardiovascular disease. The clinical relevance of extracellular HSP70 in thrombotic disorders is unclear. This study examined HSP70's relationship between platelet activation and thrombosis.

Methods: Platelet aggregation was assessed using platelet-rich plasma from healthy volunteers stimulated with adenosine diphosphate (ADP), with or without recombinant HSP70. Plasma HSP70, anti-HSP70 antibodies, and the platelet activation marker APP770 were measured using ELISA in DIC patients and non-DIC controls. To understand the mechanisms of platelet activation, the toll-like receptor 4 (TLR4) inhibitor, TAK-242, was used. In addition, HSP70 expression in human umbilical vein endothelial cells stimulated with oxidized LDL was evaluated.

Results: HSP70 significantly increased platelet aggregation under low-dose ADP stimulation. This effect was reduced by TAK-242, indicating the involvement of TLR4 signaling. Plasma HSP70 concentrations were significantly higher in patients with DIC than in non-DIC patients. HSP70 levels were negatively correlated with platelet counts and positively correlated with plasma APP770 concentrations, suggesting an association with platelet activation and thrombosis. Oxidized LDL stimulation induces both intracellular expression and extracellular secretion of HSP70 from vascular endothelial cells.

Conclusion: Extracellular HSP70 may enhance platelet activation via the TLR4-mediated pathway, contributing to thrombosis. The elevation of plasma HSP70 concentrations and their correlation with platelet activation markers in DIC patients suggest HSP70's utility as a biomarker for reflecting thrombotic activity and vascular stress. Measuring circulating HSP70 levels may provide additional diagnostic information for assessing thrombotic disorders and platelet activation.

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一般演題 Hematology

Leukapheresis Variables in CAR-T Cell Therapy

Effects on Cell Yield, Collection Time, and Monocyte Purity

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Background and Objective: Chimeric Antigen Receptor T-cell (CAR-T) therapy is a crucial treatment for relapsed/refractory hematological malignancies. Its manufacturing requires collecting sufficient high-quality autologous T cells via leukapheresis. However, patients heavily pretreated with chemotherapy often present with severe lymphopenia and anemia, causing poor collection efficiency and prolonged times. This study investigates how pre-apheresis hematological parameters (absolute lymphocyte count [ALC] and hematocrit [Hct]) interact with apheresis variables (processed blood volume and cycle multiplier) to impact T cell and total nucleated cell (TNC) yields, collection duration, monocyte purity, and manufacturing outcomes.
Materials and Methods: We retrospectively analyzed 42 patients undergoing leukapheresis before CAR-T therapy. Stratifying patients by ALC, Hct, and cycle multipliers, we evaluated the effects of these variables on cell yield, apheresis time, leukopak monocyte percentage, and final manufacturing yield using descriptive and correlation analyses.
Results: Pre-apheresis ALC is the primary determinant of final T cell count. In patients with low ALC (< 500 cells/μL), significantly increasing the cycle multiplier (≥ 3.0) yielded diminishing marginal returns. A low Hct (< 30%) interfered with centrifugation interface stability, substantially prolonging operation time. A consecutive-day collection case confirmed that large-volume filtration led to further ALC depletion and abnormal monocyte surges. Furthermore, despite meeting quantity and purity targets, manufacturing could still fail due to factors unrelated to starting material quality.
Conclusions: Blindly employing large-volume leukapheresis (LVL) or consecutive-day collections to compensate for low ALC is inefficient and compromises cell quality through prolonged mechanical shear stress, anticoagulant exposure, and severe monocyte contamination. Future practices should incorporate algorithm-based predictive models to optimize processing volumes, balancing yield, purity, and clinical safety while preserving patient condition for potential secondary collections.

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一般演題 Hematology

Automated LTA for Antiplatelet Monitoring: Comparison and Throughput

Versus Conventional Semi-Automated Aggregometer in Method Performance and Workflow Efficiency

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[Purpose] Light transmission aggregometry (LTA) is a reference method for platelet function testing, but conventional manual LTA is labor-intensive and operator-dependent. To evaluate analytical performance and clinical utility of an automated LTA system (LTAauto) for monitoring antiplatelet therapy compared with conventional manual LTA (LTAman), with emphasis on throughput.

[Methods] We evaluated repeatability and processing time using samples from healthy volunteers. We also tested 94 patients on antiplatelet therapy (aspirin, clopidogrel, or dual therapy). The same platelet rich plasma was measured on both analyzers. Five agonists were used: ADP, collagen, ristocetin, epinephrine, and arachidonic acid. We evaluated maximum aggregation (MA) and compared results between methods using method comparison analysis.

[Results] LTAauto showed good repeatability for MA (CV 2.7–5.7%). The mean processing time per agonist was 6 min 51 s with LTAauto and 12 min 20 s with LTAman, which is about a 44% shorter time (about 1.8× higher throughput). In patients on antiplatelet therapy, MA was significantly lower than in healthy controls for all agonists except ristocetin. MA results were correlated between methods (r = 0.519–0.819).

[Conclusion] Automated LTA gives reliable MA results and shows antiplatelet effects similar to the conventional method, while clearly improving throughput. This supports its use in routine laboratory workflows.

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一般演題 Hematology

A Case Report of Disseminated Carcinomatosis of Bone Marrow

DCBM due to carcinoma of unknown primary diagnosed by bone marrow aspiration

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Case Presentation: A woman in her 50s was referred to our hospital for further evaluation due to severe anemia. The patient had a past medical history of lumbar disc herniation. Blood test revealed hemolytic anemia and disseminated intravascular coagulation (DIC) with schistocytes.

Course: The patient had severe lower back pain, making bone marrow aspiration highly difficult. Cells with indistinct borders were observed in the bone marrow, which were diagnosed as poorly differentiated adenocarcinoma by pathological examination. And Computed tomography (CT) showed multiple signs of osteosclerosis. Therefore, a diagnosis of disseminated carcinomatosis of born marrow (DCBM) due to Carcinoma of unknown origin was made.

Discussion: DCBM is characterized by anemia, lower back pain, and bleeding tendency, and is reportedly associated with a high incidence of DIC and microangiopathic hemolytic anemia, findings that were consistent with the laboratory results. Initially, the lower back pain was suspected to be due to the patient's pre-existing lumbar disc herniation. In addition, CT revealed no mass lesion in any organs except for splenomegaly, and malignancy was not initially suspected. The primary site of the cancer remained unknown despite antemortem investigations. Even at autopsy, no definite primary lesion could be identified in any organ. Although the primary site of the carcinoma was unknown, immunohistochemical staining of the tumor cells suggested gastric cancer.

Conclusion: This case underscored the importance of considering DCBM, in addition to hematological disorders, in patients presenting with severe anemia and lower back pain.

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一般演題 Hematology

Comparison of Clauss and PT-derived for measuring fibrinogen in hyperbilirubinemia

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[Background] In living donor liver transplant patients, markedly elevated bilirubin levels may interfere with fibrinogen measurements using the Clauss method. This study evaluated the performance of the Clauss method with two detection wavelengths and a PT-derived method in samples with high bilirubin concentrations. [Methods] Two Clauss-based measurement systems using COAG-GENESIS Fbg were established with detection wavelengths of 405 nm and 660 nm (Clauss-405 and Clauss-660, respectively). The PT-derived method used COAG-GENESIS PT (PT-Fbg). All measurements were performed on the fully automated clinical laboratory system STACIA (PHC Corporation). The evaluation included within-run precision, dilution linearity, and the effects of interfering substances. Correlation analyses were conducted using residual plasma samples with elevated bilirubin levels obtained from patients who underwent coagulation testing at our hospital. [Results and Discussion] All methods demonstrated good within-run precision and acceptable dilution linearity. For interference testing, changes in measured fibrinogen values remained within ±10% up to a bilirubin concentration of 30 mg/dL for all methods. However, Clauss-660 failed to produce results in the presence of severe lipemia (3,000 FTU) or hemolysis with hemoglobin concentrations ≥500 mg/dL. For high-bilirubin samples, reference values were obtained by mixing patient plasma with normal plasma of known fibrinogen concentration. When the results were compared with a control group, Clauss-405 showed that multiple samples exhibited significant discrepancies in bilirubin values. In contrast, PT-Fbg showed discrepancies mainly in samples with bilirubin ≥20 mg/dL and fibrinogen ≤200 mg/dL. Overall, PT-Fbg and Clauss-660 showed good agreement with reference values, with minimal discrepancies. [Conclusion] PT-Fbg and Clauss-660 may serve as useful reference methods for fibrinogen measurements in samples with elevated bilirubin levels.
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一般演題 Hematology

CBC-Derived Inflammatory Biomarkers in Diabetic Kidney Disease

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Background: Diabetic kidney disease (DKD) is a major microvascular complication of type 2 diabetes mellitus (T2DM) and a leading cause of chronic kidney disease worldwide. This study aimed to evaluate the clinical significance and diagnostic performance of complete blood count (CBC)-derived inflammatory biomarkers in DKD.

Methods: This retrospective observational study enrolled 678 participants, including healthy controls (n = 125), T2DM patients without complications (ICD-10 code E11.9) (n = 50), and T2DM patients with kidney complications (ICD-10 code E11.2) (n = 503). CBC-derived inflammatory biomarkers, including neutrophil-to-lymphocyte ratio (NLR), platelet-to-lymphocyte ratio (PLR), systemic immune-inflammation index (SII), and pan-immune-inflammation value (PIV), were calculated. Group comparisons were performed using Kruskal–Wallis and chi-square tests. Receiver operating characteristic (ROC) curve analysis was used to evaluate diagnostic performance.

Results: Patients with diabetic kidney complications demonstrated significantly elevated inflammatory biomarkers compared with controls. Lymphocyte counts were significantly decreased, whereas neutrophil and monocyte counts were significantly increased ($p < 0.001$). NLR, PIV, and SII levels were significantly higher in the kidney complication group than in controls (2.615 vs. 1.920, $p < 0.001$; 248.7 vs. 190.4, $p < 0.001$; 601.3 vs. 519.0, $p < 0.05$, respectively). ROC curve analysis demonstrated that NLR exhibited the best diagnostic performance with an area under the curve (AUC) of 0.716, while PIV demonstrated moderate predictive ability with an AUC of 0.621. PLR showed limited discriminatory performance.

Conclusion: CBC-derived inflammatory biomarkers are significantly associated with DKD in patients with T2DM. Among these biomarkers, NLR demonstrated the best diagnostic performance and may serve as a simple, low-cost, clinically useful marker for early identification of DKD. These findings support the clinical utility of CBC-derived inflammatory indices in early detection and disease monitoring of DKD.

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一般演題 Hematology

Rotational Thromboelastometry in the Perioperative Management of Cardiac Surgery

Hemostatic Assessment in Cardiac Surgery

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Background: Viscoelastic tests (rotational thromboelastometry), together with the implementation of a specific algorithm for coagulation management in cardiac surgery, enable perioperative coagulopathy to be better controlled.
Methods: Retrospective cohort study including 675 patients who underwent cardiac surgery with cardiopulmonary bypass. The incidence of allogeneic blood transfusions and clinical postoperative complications were analyzed before and after rotational thromboelastometry implementation.
Results: Following viscoelastic testing and the implementation of a specific algorithm for coagulation management, the incidence of any allogeneic blood transfusion decreased (41.4% vs 31.9%, p=0.026)during the perioperative period. In the group monitored with rotational thromboelastometry, decreased incidence of transfusion was observed for packed red blood cells (31.3% vs 19.8%, p =0.002), fresh frozen plasma (9.8% vs 3.8%, p =0.008), prothrombin complex concentrate administration (0.9% vs 0.3%, p =0.599) and activated recombinant factor VII (0.3% vs 0.0%, p=0.603). Increased incidence was observed for platelet transfusion (4.8% vs 6.8%, p =0.530) and fibrinogen concentrate (0.9% vs 3.5%, p=0.066), tranexamic acid (0.0% vs 0.6%, p=0.370) and protamine administration (0.6% vs 0.9%, p =0.908). Similar results were observed in the postoperative period, but with a decreased incidence of platelet transfusion(4.8% vs 3.8%, p =0.813). In addition, statistically significant reductions were detected in the incidence of postoperative bleeding (9.5% vs 5.3%, p=0..037), surgical reexploration (6.0% vs 2.9%, p=0.035), and length of Intensive Care Unit (ICU) stay (6.0 days vs 5.3 days, p =0.026).
Conclusions: The monitoring of hemostasis by rotational thromboelastometry in cardiac surgery, was associated with decreased incidence of allogeneic blood transfusion, clinical hematologic postoperative complications and lengths of ICU stay.

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一般演題 Hematology

Cold Agglutinin Syndrome as a Paraneoplastic Manifestation of Malignancy

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Background
Cold Agglutinin Syndrome (CAS) is a rare autoimmune hemolytic anemia that may occur as a paraneoplastic manifestation of renal cell carcinoma (RCC). Cold agglutinin interference can cause misleading hematology results and diagnostic challenges.
Methods
A 60-year-old woman with metastatic clear cell RCC presented with severe anemia. Laboratory investigations included CBC, hemolysis markers, DAT, immunoglobulin studies, cold agglutinin titration, and bone marrow analysis. Pre-warming at 37°C and a stepwise laboratory workflow were used to evaluate analytical interference.
Results
Initial findings showed severe anemia (Hb 6.9 g/dL), elevated LDH (481 U/L), and reticulocytosis (9.0%), indicating hemolysis. CBC revealed spuriously low RBC counts with elevated MCV and MCHC, suggestive of cold agglutinin interference. DAT was positive for C3d, with markedly elevated IgM (1347.0 mg/dL). High-titer anti-I cold agglutinins (1:2048) confirmed CAS. Hematological parameters normalized after pre-warming, confirming analytical interference. Bone marrow findings supported a paraneoplastic process. Early recognition prevented misinterpretation of macrocytic anemia and preventing unnecessary transfusion and potential overtreatment.
Conclusion
This case highlights a critical laboratory pitfall where analytical interference mimics hematologic abnormalities. A structured diagnostic workflow enables accurate identification of cold agglutinin interference and facilitates timely recognition of underlying malignancy. This approach is readily applicable in routine laboratory practice and provides important educational value for laboratory professionals to enhance diagnostic accuracy and patient safety. Although rare, such interference has significant implications in routine hematology practice.
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一般演題 Hematology

Cold Agglutinin Effects

Interference in CBC and Rh Typing in an Elderly Patient

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Purpose: Cold agglutinins, typically immunoglobulin M (IgM), can induce red blood cell (RBC) aggregation at low temperatures, leading to spurious results in laboratory tests. This case highlights their effects on complete blood count (CBC), antibody screening, and blood typing in an elderly patient.

Methods: A 97-year-old woman presented to the emergency department and underwent CBC analysis, antibody screening, and blood typing. Because the abnormal results suggested cold agglutinin interference, the specimen was prewarmed at 37°C, and RBCs were washed with warm saline before repeat testing.

Results: Initial CBC revealed a decreased RBC count (1.08 × 10^6/μL), hemoglobin of 7.2 g/dL, and hematocrit of 11.4%, alongside an elevated MCV (105.6 fL) and a markedly high MCHC (63.2 g/dL). MP antibody screening was weakly positive (1+), while gel card testing was negative. Blood typing yielded B (4+) and a false Rh-positive (1+) result by the tube method. After prewarming, hematocrit rose to 20.3%, MCV normalized to 91.7 fL, and MCHC corrected to 34.7 g/dL. MP antibody screening became negative, and the Rh(D) status was confirmed as negative.

Conclusion: Cold agglutinins can cause spurious CBC alterations, including falsely elevated MCHC and decreased hematocrit, as well as false-positive MP antibody screening and Rh typing results. Prewarming at 37 °C effectively resolves these interferences and ensures accurate laboratory interpretation. Washing red blood cells with warm saline can help remove cold-reactive autoantibodies, further reducing analytical errors. Awareness of cold agglutinin effects and appropriate corrective techniques, along with recognition of associated imaging findings, is essential to prevent inappropriate blood selection and minimize transfusion-related risks, especially in elderly patients.

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一般演題 Hematology

Seeing Before Sequencing: Early AML Treatment

Morphology and flow cytometry as rapid surrogates for AML decision-making

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Background:
Rapid risk stratification in acute myeloid leukemia (AML) is critical for timely therapeutic decisions, yet next-generation sequencing (NGS) often requires several days. Cup-like blast nuclei (CLB) morphology and its associated immunophenotype have been linked to NPM1-mutated AML, but their role in guiding immediate treatment remains underexplored.

Methods:
We describe a 61-year-old female presenting with AML (WBC 29,300/μL; blasts 81.5%). Peripheral blood smear morphology and flow cytometric immunophenotyping were evaluated prior to NGS analysis.

Results:
Morphological examination revealed prominent CLBs with nuclear invaginations. Flow cytometry demonstrated an MPO+/CD33+/CD34−/HLA-DR− immunophenotype, strongly suggestive of NPM1-mutated AML. Based on these early findings, targeted therapy with venetoclax and azacitidine was initiated prior to molecular confirmation. Subsequent NGS identified mutations in NPM1 (VAF 48.78%), FLT3-ITD (VAF 88%), IDH1, and DNMT3A. The patient achieved complete remission within one month, supporting the clinical validity of early morphology-immunophenotype correlation for therapeutic decision-making.

Conclusion:
This case highlights the diagnostic and clinical value of integrating CLB morphology with immunophenotypic findings as a rapid surrogate marker for NPM1-mutated AML. Early recognition enabled prompt treatment initiation several days before NGS confirmation, potentially improving patient outcomes. This approach may help bridge diagnostic delays in settings where immediate molecular testing is unavailable and provides important educational value for laboratory professionals in recognizing morphology–immunophenotype correlations in AML.

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一般演題 Hematology

Evaluating the Platelet Reactivity of Coronary Artery Disease Filipino Patients

Undergoing Aspirin Therapy Using VerifyNow: A Novel One-Shot Case Study

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Introduction: Coronary Artery Disease (CAD) is the leading cause of death in the Philippines. Aspirin Antiplatelet therapy is the standard of care for secondary cardiovascular prevention. However, variability in patient response to this therapy remains a clinical challenge, often going unnoticed due to the lack of routine platelet function testing in local hospitals. The VerifyNow test is a novel point-of-care tool that is still innovative and rare in the Philippine healthcare system. Prior to hospital discharge, this assay can measure the antiplatelet impact, verify a sufficient medication response, identify non-adherence to treatment, and stratify the risk of bleeding, thrombotic, or significant adverse cardiac events.

Methods: This study employed a one-shot case study design with eight (8) patients diagnosed with CAD and on chronic aspirin therapy, selected purposively. The platelet function was quantitatively measured using Aspirin Reaction Units (ARU).

Results: Descriptive statistics was used to evaluate anthropometric and treatment factors. Chronic aspirin therapy remains highly effective among Filipinos with CAD. A significant inverse relationship between age and ARU was observed (r -0.78, p <0.01), meaning that as patient ages increase, ARU values decrease. Multiple linear regression analysis determined that the greatest contributors to ARU are age (t 26.02, p <0.01), sex (t -11.79, p <0.01), BMI (t 23.32, p <0.01), and total duration of medication (t -3.23, p 0.02).

Conclusions: The findings of this study contribute to the limited data on platelet reactivity among Filipino patients; further studies should be performed to investigate its adaptability to the Philippine healthcare setting.

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一般演題 Hematology

Reclassification of Gamma W208L and S313I as Hypodysfibrinogenemia

NaCl-dependent Enhancement of Fibrin Polymerization Abnormalities

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Introduction: Congenital fibrinogen disorders are caused by mutations in fibrinogen genes and result in quantitative and/or qualitative abnormalities. We identified two patients carrying *FGG* variants, W208L and S313I, respectively, who were suspected of having hypodysfibrinogenemia, whereas previously reported families with the same variants had been classified as hypofibrinogenemia. To investigate this discrepant phenotypic classification, expression and functional analyses were performed.

Materials and Methods: Target mutations were introduced into a fibrinogen γ-chain expression vector by site-directed mutagenesis, and the constructs were transfected into Chinese hamster ovary (CHO) cells to produce recombinant fibrinogen. The assembly and secretion of recombinant fibrinogen were analyzed by immunoblotting and an enzyme-linked immunosorbent assay (ELISA). Patients' plasma fibrinogen was purified, and thrombin-catalyzed fibrin polymerization assays were conducted under different NaCl concentrations.

Results: Both variant γ-chains were synthesized in CHO cells and assembled into fibrinogen. ELISA showed that the amounts of recombinant γW208L and γS313I fibrinogen secreted were lower than that of wild-type fibrinogen. No significant differences were observed in intracellular localization. In comparisons with fibrin polymerization from normal plasma fibrinogen at 0.12 M NaCl, that from γW208L and γS313I plasma fibrinogen was impaired. Notably, this impairment became more pronounced as NaCl concentrations increased from 0.15 to 0.21.

Conclusion: Both variants were associated with hypodysfibrinogenemia because they showed impaired fibrinogen secretion and functional abnormalities. Differences in the NaCl concentrations used for a fibrinogen functional analysis may contribute to a discrepant phenotypic classification in congenital fibrinogen disorders.

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一般演題 Hematology

Nonspecific APTT Prolongation in Cross-Mixing Tests

Effects of Container Air Volume on pH and Coagulation Activity

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[Background]
APTT prolongation is attributed to either a deficiency in coagulation factors or the presence of inhibitors against coagulation factors. The Cross-Mixing Test is a procedure used to differentiate the causes of APTT prolongation. This test involves mixing both plasma from patient and healthy donor in a specific ratio, and then measuring the APTT before and after incubation at 37℃ for 2 hours. Generally, coagulation factors are unstable and their activity decreases at elevated pH values. When nonspecific APTT prolongation caused by high pH is observed, these tests cannot be performed accurately. Although this pH change is thought to result from the volume of air remaining in the container , a detailed investigation has not yet been conducted. We investigated how variations in the air volume affect nonspecific APTT prolongation in this test.
[Method]
The mixed plasma (0.15mL) was dispensed into containers of different volumes (A:0.2mL, B:0.5mL, C:1.5mL). After incubation at 37℃ for 2 hours, the APTT, pH and coagulation factor activities were measured. Percentage changes were calculated from measurements taken before and after incubation.
[Result]
The percentage changes in pH were 108% for A,111% for B, and 116% for C. In relation to the increase in air volume, the percentage changes in APTT were 110% for A, 112% for B, and 117% for C. Particularly, C showed an APPT extension of approximately 10% compared with A.The percentage changes in factorⅤ were 73% for A, 60% for B, and 55% for C, while those in factorⅧ were 79% for A, 70% for B, and 67% for C. C showed a decrease in activity of more than 10% compared with A.
[Conclusion]
An increase in the air volume inside the container may lead to a rise in pH resulting in decreased coagulation factor activity.

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P-3-40

一般演題 Hematology

CWA parameters as surrogate markers for hypercoagulability in warfarin-treated patients

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Background: Warfarin therapy is used to prevent and treat venous thrombosis. Optimal management would require assessing both anticoagulant and procoagulant activities, but only the former is routinely evaluated. Anticoagulation status can be monitored by prothrombin time (PT) assay, the most common and guideline-recommended coagulation test for the therapy. Procoagulant status can only be assessed by molecular markers, such as D-dimer (DD), thrombin-antithrombin complex (TAT), and soluble fibrin (SF), which are specialized tests and are often outsourced with turnaround time of several days. Readily available surrogate markers would therefore be useful in clinical settings.
Objectives: To evaluate whether clot waveform analysis (CWA) parameters obtained from routine PT and activated partial thromboplastin time (APTT) tests can serve as surrogate markers.
Methods: We analyzed 282 samples (41 warfarin-treated patients) and 22 normal samples, which were categorized into four groups: normal, all-marker negative, TAT or SF positive with DD negative, and TAT or SF positive with DD positive. Nine conventional CWA parameters were automatically obtained for each of PT and APTT in all samples. Two statistical analyses were performed. First, the four groups were compared using mixed-effects models. Second, CWA parameter-molecular marker associations were decomposed into within- and between-subject effects via mixed-effects models.
Results: The first analysis showed that PT-min1, APTT-min1, and APTT-min2 were significantly increased in TAT/SF-positive groups compared to all-negative and normal groups. The second analysis identified 10 of 54 parameter-marker pairs (6 for DD and 4 for SF) with both significant within- and between-subject associations; four parameters (PT-min1, PT-min2, APTT-min1, and APTT-min2) showed significance for both DD and SF.
Conclusion: CWA parameters, particularly PT-based parameters (e.g., PT-min1), may serve as readily available surrogate markers for procoagulant activity without additional cost and time, enabling earlier detection of hypercoagulability in patients on warfarin therapy. Contact Information: +81-24-581-5503

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一般演題 Hematology

Early T-Cell Precursor Acute Lymphoblastic Leukemia with DNMT3A Mutation

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Background:Early T-cell precursor acute lymphoblastic Leukemia/lymphoblastic lymphoma (ETP-ALL/LBL) is a hematological malignancy derived from progenitor cells shared by T lymphoid and myeloid lineages. It was newly established as a distinct diagnostic entity in the 5th edition of the WHO Classification. Here, we report a rare case of ETP-ALL occurring in an elderly patient.Case Presentation: The patient presented to a hospital for evaluation of persistent fever continuing since late January 20XX. Computed tomography revealed multiple enlarged lymph nodes, including cervical, submandibular, and paratracheal lymph nodes. Abnormal cells were detected in the peripheral blood, raising suspicion of hematological malignancy.Results:Laboratory findings showed a white blood cell count of 3.5×10⁹/L with 9.5% abnormal cells, hemoglobin 11.5 g/dL, and platelets 201×10⁹/L. Bone marrow examination revealed a hypercellular marrow with 72.2% blastoid cells. Flow cytometry of bone marrow demonstrated: CD2−, CD3−, CD4−, CD5+, CD7+, CD8−, CD13+, CD33^dim, cytoplasmic CD3+, MPO−, CD38+, CD117−, and TdT−. Lymph node specimens showed positivity for cytoplasmic CD3, CD5^dim, CD7, CD13, and CD38. HemeSight® gene panel testing identified mutations in DNMT3A, NOTCH1, and NRAS. Chromosome analysis revealed a normal karyotype.Discussions: While ETP-ALL predominantly occurs in the AYA population, its onset in an older adult suggests an underlying age-related clonal hematopoiesis, supported by the DNMT3A mutation. At presentation, the absence of TdT expression and presence of myeloid markers complicated cell lineage determination. Differential diagnoses included FAB M0 AML, ALL, and mixed phenotype acute leukemia (T/myeloid). Definitive diagnosis was established by immunohistochemistry and the gene panel identifying a DNMT3A mutation, reported in 16% of ETP-ALL cases.

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一般演題 Hematology

Can normalization save Automated Thrombin Generation

Quest for the best normalizator to allow clinical use of Automated Thrombin Generation

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Background: Automated thrombin generation (ATG) assessment has significant potential for evaluating anticoagulation, as well as hypercoagulable and bleeding phenotypes. However, its broader clinical application has been limited by considerable intra- and inter-assay variability, particularly due to reagent-dependent differences. These inconsistencies hinder comparability between centers and studies, reducing the assay's clinical utility. Aim: We hypothesized that within-run normalization of thrombin generation (TG) results using pooled normal plasma (PNP), combined with standardized reagents and calibrators, would reduce variability. Successful normalization could improve assay reliability and support the development of clinically meaningful ATG metrics. Methods: ATG and standard coagulation tests were measured by a single operator using a Calibrated Automated Thrombography (CAT), multiple reagent lots and a StarMax3 instrument. Various PNPs were evaluated, including an in-house double-centrifuged frozen plasma, multiple lots of commercial frozen PNPs, and a lyophilized PNP. Additionally, ATG was assessed in plasma samples from 30 healthy individuals. Particle debris in plasma samples was analyzed using flow cytometry. Results: Raw calibrated ATG showed low intra-assay variability (CV <6% for Peak TG, <3.7% for Endogenous Thrombin Potential (ETP)) and inter-assay variability (≤10.7% for Peak TG, ≤3.1% for ETP). Among tested PNPs, the commercial frozen plasma GK7370 matched the median ATG values of the healthy cohort best and was therefore selected for normalization. In-house and lyophilized PNPs were less suitable. With normalization, inter-assay variability was similar to the raw data (≤12% for Peak TG and ≤4.1% for ETP). However, reagent lot-to-lot variability was markedly reduced (by 74% for ETP, 78% for Peak TG, and 92% for time to peak). Flow cytometry detected no tissue factor in particle debris. Conclusion: Normalization of ATG using a well-characterized frozen PNP reduces reagent-dependent variability and may facilitate broader clinical application of ATG.

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一般演題 Hematology

Complete Blood Count Assessment with Health-Related Factors in Navotas City

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Background: Different studies have documented how reference values for Complete Blood Count (CBC) vary among different populations based on influences, including sex, age, race, and environment. A gap exists in previous studies, focusing on clinical populations and isolated determinants.

Objective: The study aims to assess CBC and its relationship with demographics, socioeconomic status, lifestyle, and health-related factors among community members in North Bay Boulevard South (NBBS) Dagat-Dagatan, Navotas City.

Methods: A cross-sectional quantitative approach was employed to examine the relationship between CBC and Social Determinants of Health (SDH). Sixty-five (65) subjects aged 20 to 59 were tested for CBC. Data regarding the SDOH was collected through structured questionnaires. Statistical analyses assess the relationship of CBC parameters with SDOH responses.

Results: Both male and female hematocrit and hemoglobin levels lower than the physiologically healthy Filipino. Conversely, platelet counts of males (<0.01) were found to be higher than those of females. Additionally, smokers had lower neutrophil percentages (0.03) than non-smokers and former smokers. An inverse relationship exists between perceived social conditions and platelet levels. Education Access and Quality showed a significant negative relationship with hematocrit levels (r=-0.25, p=0.05).

Conclusion: Unexpected findings suggest that although the study provides useful preliminary data and baseline hematologic profiles in NBBS Dagat-Dagatan, some significant results may be affected by sample distribution, limited subgroup representation, and possible confounding factors. Future studies may address these limitations with a larger sample size, stratified sampling, and a more detailed assessment of lifestyle and health-related exposures.

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一般演題 Hematology

Association Between sCLEC-2 and Renal Function in Plasma Samples

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Background: Renal dysfunction has been associated with enhanced platelet activation, potentially mediated by endothelial dysfunction and inflammation. Soluble C-type lectin-like receptor 2 (sCLEC-2) is a novel biomarker reflecting platelet activation; however, its relationship with renal function remains unclear. We investigated the association between sCLEC-2, the sCLEC-2/platelet ratio, and renal function.

Methods: A total of 124 plasma samples from patients with cardiovascular diseases were analyzed. Clinical variables including age, sex, platelet count, BNP, and eGFR were collected. Associations between sCLEC-2 and eGFR were evaluated using Spearman's correlation and group comparisons across eGFR categories (<30, 30–59, ≥60 mL/min/1.73 m²). Multivariable linear regression analysis was performed using log-transformed sCLEC-2/platelet ratio.

Results: Both sCLEC-2 and the sCLEC-2/platelet ratio were inversely correlated with eGFR; however, the association was stronger for the sCLEC-2/platelet ratio ($\rho = -0.584$, $P < 0.001$) than for sCLEC-2 alone ($\rho = -0.393$, $P < 0.001$). In group comparisons, the sCLEC-2/platelet ratio showed a significant stepwise increase with worsening renal function, with the highest levels observed in patients with eGFR <30 mL/min/1.73 m² ($P < 0.001$). In multivariable linear regression analysis, decreased eGFR was independently associated with higher log-transformed sCLEC-2/platelet ratio after adjustment for age, sex, and BNP ($\beta = -0.0151$, $P < 0.001$). Stratified analysis by BNP demonstrated that the inverse association between eGFR and the sCLEC-2/platelet ratio was observed in both groups and appeared stronger in patients with higher BNP levels.

Conclusion: The sCLEC-2/platelet ratio is more strongly associated with renal dysfunction than sCLEC-2 alone and may serve as a useful marker of platelet activation in patients with impaired renal function.

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一般演題 Hematology

Analysis of FXI Dimerization and Secretion Defects in *F11* Variants

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Background
Hereditary factor XI (FXI) deficiency is a rare bleeding disorder with poor correlation between FXI activity levels and bleeding symptoms. FXI is secreted as a homodimer, and impaired dimer formation reduces secretion. A 77-year-old man developed massive bleeding after colon polypectomy. Coagulation testing revealed prolonged activated partial thromboplastin time (APTT), FXI activity of 4%, and FXI antigen levels of less than 1%. Genetic analysis identified novel compound heterozygous variants, p.Ser42Ile (S42I) and p.Trp519* (W519*). This study investigated the molecular pathogenic mechanisms underlying these variants.
Methods
HEK293 cells were transfected with expression vectors encoding wild-type (WT) FXI or the two FXI mutants. Cell lysates and culture supernatants were collected, and FXI antigen levels were evaluated by Western blotting. Non-reducing Western blot analysis was performed to evaluate dimerization. Cycloheximide (CHX) chase assays were used to determine the intracellular half-life, whereas proteasome inhibition experiments using MG132 were conducted to assess proteasome-dependent degradation. Immunofluorescence colocalization analyses with endoplasmic reticulum and Golgi markers were performed to evaluate abnormalities in intracellular trafficking.
Results
Both S42I and W519* variants exhibited reduced FXI secretion into culture supernatants. Intracellular FXI antigen levels were significantly increased in cells expressing S42I ($p<0.05$). In contrast, W519* was detected as a truncated protein with significantly reduced FXI antigen levels ($p<0.05$). Non-reducing Western blot analysis demonstrated preserved dimer formation ability in both variants. CHX chase assays revealed intracellular retention of S42I. Proteasome inhibition restored FXI antigen levels in W519*. Immunofluorescence analyses demonstrated reduced colocalization with endoplasmic reticulum and Golgi markers in both variants.
Discussion
Although S42I and W519* variants retained dimerization capacity, both may impair FXI secretion through abnormal intracellular trafficking and proteasome-dependent degradation. Further studies using co-expression systems of WT and mutant FXI are planned to clarify the effects of FXI variants on intracellular trafficking and secretion mechanisms of wild-type FXI.

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一般演題 Hematology

Atypical Lymphocytes Following Chimeric Antigen Receptor T-Cell Therapy

Morphological Findings and Temporal Kinetics Between Two CD19-Targeted Products in Patients Receiving CAR-T Therapy

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Background: Chimeric antigen receptor T-cell (CAR-T) therapy is an adoptive immunotherapy in which autologous T cells are genetically modified ex vivo to target tumor-associated antigens. Following infusion, circulating CAR-T cells may appear as atypical lymphocytes on peripheral blood smears and can influence morphologic interpretation. However, their morphological characteristics and temporal dynamics have not been fully characterized. This study aimed to characterize peripheral blood morphological findings after CAR-T therapy and to compare the timing and frequency of atypical lymphocyte appearance between two CD19-targeted CAR-T products.

Methods: We retrospectively analyzed 52 patients with mature B-cell malignancies who underwent CAR-T therapy at our hospital (tisagenlecleucel [tisa-cel], n=41; axicabtagene ciloleucel [axi-cel], n=11). Complete blood counts and peripheral blood smear findings after CAR-T infusion were compared.

Results: Atypical lymphocytes were defined as large lymphocytes with abundant basophilic cytoplasm and a low nuclear-to-cytoplasmic ratio. Within 15 days post-infusion, atypical lymphocytes were observed in 85.4% of the tisa-cel group and 100.0% in the axi-cel group. The peak proportion of atypical lymphocytes was 2.0% (1.0–4.0%) and 15.0% (10.5–42.5%) in the tisa-cel and axi-cel groups, respectively; the median time to peak was 4 days (3–7.5) and 7 days (6–7.5) post-infusion, respectively. The peak atypical lymphocyte counts were 42 (25–70) $\times 10^6$/L and 372 (186–840) $\times 10^6$/L in the tisa-cel and axi-cel groups, respectively ($p<0.001$ by Mann–Whitney U test). The peak atypical lymphocyte counts were correlated with soluble interleukin-2 receptor levels ($p=0.009$), and the temporal trends were generally consistent.

Conclusion: Differences were observed between CAR-T products in the timing and magnitude of atypical lymphocyte appearance. Further studies with larger cohorts and additional CAR-T products may improve our understanding of these morphological features and peripheral blood smear interpretation.

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一般演題 Hematology

Significance of TRBC1/TRBC2 expressions in the diagnosis of T-cell neoplasms

Multicolor flow cytometric analysis

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Flow cytometry (FCM) is useful for diagnosing hematologic malignancies. However, the diagnosis of T-cell neoplasms remains challenging due to the lack of a specific approach to detect clonality, such as the immunoglobulin light chain (kappa/lambda) analysis used for B-cell neoplasms. This study aimed to evaluate the clinical utility of FCM analysis of T-cell receptor constant β chain (TRBC) 1/TRBC2 expressions in the diagnosis of T-cell neoplasms. The TRBC is encoded by one of two mutually exclusive genes, *TRBC1* and *TRBC2*, which are randomly selected and expressed in normal T-cells during gene rearrangement. In contrast, neoplastic T-cells show restricted expression of either TRBC1 or TRBC2 (or absent for both). Therefore, FCM analysis of their expressions using anti-TRBC1 and anti-TRBC2 specific antibodies might provide a novel approach for detecting TCR αβ clonality.

We conducted multicolor FCM basic studies using anti-TRBC1 and anti-TRBC2 monoclocal antibodies (provided by Beckman Coulter) at Hyogo Prefectural Harima-Himeji General Medical Center and Hyogo Cancer Center, Japan. We developed an original TRBC panel for FCM and analyzed bone marrow, peripheral blood, lymph node, and other samples from 94 clinical cases. Among these, 58 patients without detectable neoplasms showed polyclonal TRBC1/TRBC2 expression patterns, whereas 36 patients showed restricted or absent expression. The TRBC2/TRBC1 ratio ranged 0.86-3.29 in normal $CD4^+$ T-cells and 0.80-5.75 in normal $CD8^+$ T-cells. The TRBC2/TRBC1 ratio significantly differed between normal and neoplastic T-cell populations for both $CD4^+$ and $CD8^+$ T-cells. Even in cases diagnostically challenging by conventional pathological and cytogenetic analyses, the TRBC2/TRBC1 ratio deviated from the normal range and provided useful information for diagnosis. In addition, small neoplastic T-cell population was detectable.

These results suggest that the multicolor FCM analysis using anti-TRBC1/TRBC2 antibodies provides a practical method for assessing T-cell clonality and has significant potential to improve the diagnosis of T-cell neoplasms. Phone: +81-79-289-5080

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一般演題 Hematology

In-House Flow Cytometry Improves Diagnostic Accuracy and Turnaround Time

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[Introduction] Flow cytometry (FCM) is essential for diagnosing hematological disorders, yet outsourced testing often limits diagnostic accuracy and clinical responsiveness because it relies on fixed panels and dual-color analysis. At the University of Tsukuba Hospital, outsourced CD45-based dual-color testing with eight fixed panels restricted analytical flexibility and frequently prolonged turnaround time (TAT).

[Objective] To evaluate the impact of transitioning from outsourced FCM testing to an in-house system, focusing on improvements in TAT, analytical performance, and clinical utility.

[Methods] In April 2025, we implemented an in-house FCM platform using 6- to 8-color multicolor analysis. Panel design followed protocols from the National Cancer Center Hospital, resulting in 12 panels: four for leukemia, six for lymphoma, and EuroFlow-compliant panels for multiple myeloma. A stepwise workflow was established to transition from screening panels to disease-specific panels, including AML, B-ALL, and T-ALL.

[Results] Testing began on the day of sample receipt or the following morning, and results were issued on the same day or the next morning, improving TAT. Multicolor analysis enabled more precise identification of abnormal cell populations and enhanced classification of leukemias and lymphomas. Subclassification of B-cell lymphomas—such as hairy cell leukemia, mantle cell lymphoma, and chronic lymphocytic leukemia—became feasible, contributing to improved diagnostic accuracy. Clinician-driven modifications to panel composition were rapidly incorporated, increasing responsiveness to evolving clinical needs.

[Conclusion] The introduction of in-house FCM testing effectively addressed the limitations of outsourced dual-color systems, achieving faster turnaround and higher diagnostic precision. This model provides a practical framework for improving the quality and timeliness of hematological diagnostics. Email: tanaka@tsukuba-i-lab.com

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一般演題 Hematology

Effects of Storage Time and Fixation on Neutrophil Antigens

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Background: Neutrophils play a central role in innate immunity, and the expression of surface antigens reflects their maturation and activation status. In flow cytometric analysis, surface antigen expression can be altered during sample storage. However quantitative evaluations of fixation effects on whole blood samples remain limited.
Objective: To evaluate the effects of 0.5% paraformaldehyde (PFA) fixation on storage time-dependent changes in neutrophil surface antigens (CD11b, CD16, CD45, CD62L, and CD172a), and to assess its validity as a pre-analytical stabilization method in whole blood flow cytometry.
Methods: Heparinized whole blood was collected from healthy volunteers and stained immediately using a direct staining method. Samples were divided into two groups: with and without 0.5% PFA fixation. After storage for defined time periods, fluorescence intensity (mean fluorescence intensity, MFI) was measured by flow cytometry, and temporal changes were compared between the groups.
Results: Under non-fixation conditions, CD62L expression markedly decreased over time, whereas CD172a showed an increasing trend. These temporal changes were largely abolished by PFA fixation. CD11b showed relatively minor changes, while CD16 demonstrated substantial inter-individual variability without a consistent trend. CD45 remained stable under non-fixation conditions but showed a slight decrease after fixation.
Conclusion: Neutrophil surface antigens exhibit molecule-specific ex vivo dynamics in whole-blood flow cytometry. PFA fixation suppresses these temporal changes, particularly in CD62L and CD172a, while potentially introducing measurement-related effects. These findings highlight the importance of optimizing pre-analytical conditions according to antigen characteristics.
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一般演題 Hematology

Mechanisms of Platelet Activation by *Helicobacter pylori* Lpp20

Potential Involvement of TXA_2- and ADP-Mediated Amplification Pathways

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Background: Lpp20, an outer membrane component of *Helicobacter pylori* (*H. pylori*), has been reported to activate and aggregate human platelets. We previously suggested the involvement of the arachidonic acid cascade in Lpp20-induced platelet aggregation. This study aimed to further investigate the mechanisms underlying Lpp20-induced platelet activation and aggregation.
Methods: Platelet-rich plasma (PRP) and platelet-poor plasma (PPP) were obtained from 10 healthy volunteers (5 males and 5 females in their 20s) after informed consent. Samples containing 5.0×10^7 platelets were prepared. Recombinant Lpp20 (rLpp20) protein was expressed in *Escherichia coli* transformed with an rLpp20-His-tag plasmid, followed by extraction and purification. Platelet aggregation assays were performed using rLpp20 (100 μg) and collagen (4 μg/mL) as agonists. In inhibition assays, SQ29,548 (2 μM) and ticagrelor (TCG, 100 μM) were used. Thromboxane B2 (TXB2) levels were measured, and platelet aggregates were microscopically evaluated.
Results: At 5 min after rLpp20 stimulation, one participant showed strong aggregation (≥70%), two showed moderate aggregation (25%–<70%), and seven showed weak aggregation (<25%), indicating marked interindividual variability. Platelet aggregation began several tens of seconds after rLpp20 stimulation. In the strong responder, the aggregation was markedly inhibited by SQ29,548 and/or TCG but not completely abolished. Microscopically, large platelet aggregates (≥20 μm) observed after rLpp20 stimulation were markedly reduced following inhibitor treatment. TXB2 levels markedly increased after rLpp20 stimulation and were reduced following treatment with SQ29,548, TCG, or both.
Conclusions: At least, rLpp20-induced platelet activation involves amplification pathways mediated by TXA2 and ADP. However, other signaling pathways independent of these receptors may also contribute to this phenomenon. The marked increase in TXB2 further supports the involvement of the arachidonic acid cascade.

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一般演題 Hematology

Delivering Amyloid Precursor Protein 770 to Platelets via Extracellular Vesicles

Secretion of Hypo-O-glycosylated Forms Through a Non-Golgi Dependent Pathway

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[Introduction] Amyloid precursor protein 770 (APP770), found in vascular endothelial cells, is abundant in platelets and linked to vascular injury and thrombotic disorders. However, its expression mechanism in anucleate platelets remains unclear. Given recent findings that platelets can take up biomolecules, we hypothesized that APP770 transfers to platelets via endothelial cell-derived extracellular vesicles (EVs). Since endothelial APP770 undergoes retrograde trafficking to the Golgi, where it acquires O-glycans, the glycan structure of APP770 in EVs and its association with intracellular trafficking were analyzed.

[Methods] Culture supernatant from human vascular endothelial cells was ultracentrifuged to isolate EVs. APP770 was quantified using ELISA, and its EV localization was analyzed using super-resolution microscopy. Fluorescently labeled EVs were incubated with platelets, and their uptake was assessed by flow cytometry. Halo-tagged APP770 expression in endothelial cells was achieved using an adenoviral vector. After platelets took up these EVs, they were activated with thrombin, and Halo-APP770 was analyzed. APP770-containing EV formation was investigated with Brefeldin A (BFA) treatment.

[Results] Super-resolution microscopy and analysis revealed APP770 in the EV fraction (~200 nm) from endothelial cells. The labeled EVs were efficiently taken up by the platelets. The stimulated platelets released Halo-APP770. Glycan analysis revealed highly O-glycosylated and hypo-O-glycosylated APP770 in endothelial cells, but only hypo-O-glycosylated APP770 in EVs. BFA treatment decreased APP770 levels in the culture supernatant but increased them in EVs.

[Conclusion] This study reveals a novel mechanism by which endothelial cell-derived EVs deliver APP770 to platelets, which is released upon activation. APP770 in EVs is hypo-O-glycosylated and APP770-containing EVs respond differently to BFA. The results suggest that APP770-containing EVs may be formed and secreted via a distinct pathway from the Golgi-dependent secretory pathway.

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一般演題 Hematology

Clinical Utility of Ret-He as a Functional Predictor

Targeting Erythrocyte Microcytosis in Maintenance Hemodialysis Patients

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Background

Functional iron deficiency(FID) is common in maintenance hemodialysis patients. Hemoglobin reflects long-term erythrocyte mass, whereas reticulocyte hemoglobin equivalent (Ret-He) reflects short-term iron availability during erythropoiesis. This study evaluates the relationship between Ret-He and early erythrocyte morphological changes.

Materials and Methods

A retrospective analysis was performed on 379 routine hemodialysis specimens in 2025. Ret-He, hemoglobin, and MCV were measured using a Sysmex XN analyzer. Correlation analysis and logistic regression were used to assess associations with microcytosis.

Results

The cohort mean Ret-He was 32.81±4.06 pg. Ret-He demonstrated a chronological mismatch with erythroid mass (Hb: $r = 0.20$, $p < 0.001$) but coupled robustly with cell morphology (MCV: $r = 0.79$, $p < 0.001$). Logistic regression validated Ret-He as a strong predictor of microcytosis ($p < 0.001$). Threshold dynamics identified Ret-He < 29 pg as the critical decompensation point. When Ret-He was Ret-He≧30 pg, microcytosis was < 4.1%; however, once Ret-He dropped below 29 pg, the microcytosis rate escalated to 56.6%, and reached 69.0% at Ret-He < 28 pg.

Conclusion

Ret-He is a sensitive marker of early erythropoietic iron restriction. A threshold of Ret-He <29 pg may be useful for early identification of functional iron deficiency. Integration into Laboratory Information Systems (LIS) may support real-time monitoring and guide iron and ESA therapy adjustment in dialysis patients.

Keywords

Maintenance hemodialysis, Ret-He, microcytosis

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一般演題 Hematology

Hematological analysis of captive beluga whales in Westman Islands, Iceland

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At the end of June 2019, two 12-year-old beluga whales (*Delphinapterus leucas*), Little Grey and Little White, arrived from a Shanghai water park to Westman Islands, Iceland. They reside at the Sea Life Trust (SLT) beluga whale sanctuary in an enclosed pool and have also been moved to a sea pen in Klettsvík bay, Westman Islands. Data has been gathered over a 7-year period, with more frequent sampling during disease periods. Sampling, handling, transfer of blood samples and interpretation of results were carried out by SLT and Dyralaeknathjonusta Sudurlands (DYSU). Samples were received by the department of pathology at Keldur for hematological analysis. White blood cell count (WBC) and hemoglobin were analyzed using HemoCue analyzers, while hematocrit and differential WBC count were done manually. Data analysis was done in RStudio for graphical visualization and descriptive statistics. A total of 78 samples were analyzed over this 7-year period, 34 from Little-White and 44 from Little Grey. Therefore, the repeated measurements were used to define animal-specific baseline values (median, minimum and maximum values). During bacterial infections in 2023 and 2026 there was a tendency for an increase in WBC count, neutrophils and stab neutrophils, while hematocrit and hemoglobin decreased. The range of hematocrit, hemoglobin and WBC count was comparable to previously reported values in belugas under managed care. Hematology analysis has been useful in detecting infections in the belugas and has helped with evaluating progression and success of the treatments used.

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一般演題 Hematology

Using Principal Components Analysis and Conditional Inference Tree

to Explore CBC Indicators as Predictive Models for Influenza

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【 Introduction 】During peak influenza seasons, using rapid screening tests on suspected patients in the emergency department (ED) is highly useful. Our study aims to utilize machine learning methods, specifically Principal Components Analysis (PCA) and Conditional Inference Tree algorithms, to analyze the blood test indicators of patients who underwent rapid influenza screening in the ED, thereby assisting clinicians in the judgment and evaluation of patient infection.【 Materials and Methods】A total of 6,779 individuals were collected, including 986 influenza-positive patients and 5,793 influenza-negative patients. PCA was used to reconstruct a new dimensionality-reduced 2D principal component plot. Finally, the indicators within the optimal model were imported into a Conditional Inference Tree to be transformed into a transparent and intuitive clinical decision flowchart. This study was approved by the Institutional Review Board of Kaohsiung Medical University Chung-Ho Memorial Hospital (KMUHIRB-E(II)-20250036). 【 Results 】The Conditional Inference Tree identified two highest-risk decision tree pathways for influenza,(a)：Clinically, patients showing signs of anemia (low RBC count, high RDW-CV) accompanied by an increase in basophils presents a strong positive signal. The model path is: RBC≦4x106/μL→RDW_CV > 16%→ Basophil_num > 29/μL.(b)：Clinically, an influenza patient with a normal RBC count exhibiting a simultaneous rise in neutrophils and drop in lymphocytes (high Neutrophil_num / Lymphocyte_num Ratio) is also a characteristic feature of the virus.The model path is RBC > 4x106/μL → Neutrophil_num ≦ 7811/μL→ Lymphocyte_num ＜ 143/μL. 【 Discussion 】The results of this study identified key independent predictive factors. Regression analysis confirmed that red blood cell count (RBC_count) and absolute basophil count (Basophil_num) were significant risk factors, while red cell distribution width (RDW-CV) and absolute lymphocyte count (Lymphocyte_num) were significant protective factors.

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一般演題 Hematology

Gut Microbiota Profiling in sCAEBV

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Systemic chronic active EBV disease (sCAEBV) is a rare and life-threatening disorder characterized by Epstein-Barr virus-infected T- or NK-cell proliferation accompanied by systemic inflammation. Although hematopoietic stem cell transplantation is currently the only curative treatment, biomarkers reflecting disease characteristics remain limited. Recent advances in microbiome research suggest that intestinal microbiota profiling may provide clinically useful biomarkers for immune-related diseases. To investigate the potential utility of gut microbiota as a biomarker in sCAEBV, fecal samples were collected from 10 patients with sCAEBV and 20 healthy controls. The intestinal microbiota was analyzed using 16S rRNA gene amplicon sequencing, and microbial diversity and taxonomic composition were compared between groups. Alpha diversity did not differ significantly between sCAEBV patients and healthy controls, whereas beta diversity revealed a distinct overall microbial community structure. Taxonomic analysis demonstrated an increased abundance of *Fusobacteriota* in sCAEBV patients, and OTU- and species-level analyses identified sCAEBV-associated bacterial taxa. Stratified analyses revealed that *Fusobacteriota* was significantly enriched in the T cell-type sCAEBV group compared with healthy controls, with unweighted beta-diversity indicating a distinct microbial community structure, whereas no significant differences were observed in the NK cell-type group. Age-based analyses showed a higher abundance of *Fusobacteriota* in sCAEBV patients aged <40 years, along with distinct beta-diversity profiles between age groups and between healthy controls and younger sCAEBV patients. These findings suggest that gut microbiota profiling may serve as a potential biomarker approach for sCAEBV and provide novel insights into disease-associated immune dysregulation. Microbiome-based laboratory testing may contribute to future diagnostic and therapeutic strategies for sCAEBV.

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一般演題 Hematology

Molecular Characterization of the Fibrinogen A-alpha R491C Variant

Functional and His-Tagged Secretion Analyses of the A-alpha R491C Variant

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Introduction: We identified a patient with heterozygous variant fibrinogen, AαArg491Cys (Yokkaichi II; Y-II), who had no history of bleeding or thrombosis and was suspected of having hypofibrinogenemia based on low fibrinogen levels (functional assay, 1.13 g/L; immunological assay, 1.31 g/L). The same mutation was previously reported in a German family (Bonn) with thrombotic dysfibrinogenemia. We investigated the molecular basis underlying the distinct phenotypes associated with AαR491C.

Materials and Methods: Patient plasma fibrinogen was purified, and protein characterization and thrombin-catalyzed fibrin polymerization assays were performed. The target mutation was introduced into a fibrinogen Aα-chain expression vector containing a C-terminal His tag by site-directed mutagenesis. Secretion dynamics were analyzed in the human hepatoma cell line HuH-7 transiently transfected with vectors expressing the wild-type (WT) or variant Aα-chain. Secreted variant fibrinogen in culture supernatants was analyzed by immunoblotting.

Results: Under non-reducing conditions, purified Y-II plasma fibrinogen showed additional high-molecular-weight bands that were larger than intact 340-kDa fibrinogen. In comparisons with fibrin polymerization from normal plasma fibrinogen, that from Y-II plasma fibrinogen was impaired. In Huh-7 cells, the secretion of AαR491C fibrinogen was markedly reduced to less than 10% of WT fibrinogen.

Conclusion: Y-II plasma fibrinogen showed impaired fibrin polymerization; however, the role of the high-molecular-weight bands in impaired fibrin polymerization and thrombogenicity remains unclear. Further studies using recombinant AαR491C fibrinogen are needed. In contrast, the secretion of AαR491C fibrinogen AαR491C from hepatocytes was markedly reduced, suggesting defective secretion associated with hypofibrinogenemia.

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一般演題 Hematology

Iron Deficiency Anemia Screening using Reticulocyte Hemoglobin Cellular Content (RHCC)

A Real-Time Monitoring Tool of Iron Status in a Previously Malaria-Endemic Area

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Anemia disproportionately affects developing nations that are plagued by poverty, malnutrition, and parasitism, with iron deficiency anemia seen as its leading form in the Philippines. While serum ferritin and transferrin are traditional biomarkers, Reticulocyte Hemoglobin Cellular Content (RHCC) provides a cost-effective, real-time assessment of iron availability. This study aimed to assess RHCC for detecting IDA in a previously malaria-endemic area, examine the relationship between prior malaria endemicity and IDA, and determine its prevalence in the region. With the use of a cross-sectional design, data were collected from Barangay San Miguel, Puerto Princesa City, Palawan, with a target population of 100 residents from age 18 to 59. Informed consent forms, questionnaires, and physician screening were provided to gather demographic information while blood samples were transported to the Ospital ng Palawan laboratory for RHCC determination using Horiba Yumizen H2500. To assess the data, central tendency and regression analysis were used for the statistical analysis. Findings revealed that RHCC remained within normal limits across genders (Males: RHCC = 33.92 pg; Females: RHCC = 31.25 pg), age groups (RHCC = 30.28 - 33.52 pg), and years of residency (RHCC = 30.88 - 32.28 pg). Participants with a history of malaria had normal RHCC levels (32.65 pg), indicating sufficient iron stores. Moreover, the regression analysis revealed a significant interaction between past malaria diagnosis, duration of residency, and RHCC ($F = 4.299$, $p = 0.007$), suggesting that RHCC is affected when malaria exposure is prolonged. As a sensitive diagnostic tool, RHCC testing can be integrated into public health strategies targeting highly susceptible populations to ensure early detection of nutritional deficiencies in vulnerable communities.

Keywords: *Iron deficiency anemia, reticulocyte hemoglobin cellular content, previous malaria endemicity, iron metabolism, biomarker*

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一般演題 Hematology

Multi-parameter Measurement Using Acridine Orange Fluorescence Staining.

Clinical Utility of Platelet Count and Immature Platelet Fraction Analysis.

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Purpose: Automated hematology analyzers are indispensable for routine clinical testing. Although increasing measurable parameters improves analytical quality and workflow efficiency, it generally requires additional reagents, complicating reagent management. We developed an analytical algorithm enabling simultaneous multiparametric measurement by detecting DNA and RNA fluorescence using acridine orange (AO) as a single fluorescent reagent. Its performance was evaluated using the CelltacG+ hematology analyzer (Nihon Kohden, Japan).

Methods: Reticulocytes (RET), nucleated red blood cells (NRBC), fluorescent platelet count (PLT-N; a proprietary parameter of Nihon Kohden), and immature platelet fraction (IPF) were simultaneously measured using an AO fluorescent reagent on the CelltacG+ hematology analyzer. The algorithm was evaluated against the XR-1000 analyzer (Sysmex, Japan) using 468 clinical samples.

Results: Strong correlations were observed between the two systems: RET ($r=0.96$), RET% ($r=0.96$), NRBC ($r=0.91$), NRBC% ($r=0.94$), PLT-N versus PLT-F ($r=0.99$), and IPF ($r=0.90$). In samples with platelet counts below $50\times10^3/\mu L$ ($n=36$), PLT-N also showed excellent correlation ($r=0.99$). Dual-wavelength fluorescence analysis using AO eliminated interference from fragmented red blood cells. IPF showed a slope of 1.13 and a correlation coefficient of 0.85, indicating clinically acceptable performance for evaluating thrombocytopenia and platelet production dynamics.

Conclusion: Simultaneous measurement of RET, NRBC, PLT-N, and IPF using a single AO fluorescent reagent was achieved. The developed algorithm demonstrated performance comparable to an existing commercial analyzer, including in thrombocytopenic samples, while simplifying reagent management and improving laboratory workflow.

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一般演題 Hematology

Novel *SERPINC1* c.204dup Frameshift Variant Associated with Inherited Antithrombin Deficiency

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Background
Inherited antithrombin (AT) deficiency is a thrombophilic disorder caused by abnormalities in the antithrombin gene (*SERPINC1*) and is a major risk factor for venous thromboembolism. We report two families carrying a novel *SERPINC1* variant, c.204dup (p.Glu69Argfs*36).
Cases
The proband in the first family was a 26-year-old woman who developed deep vein thrombosis (DVT) during pregnancy. She had a history of DVT and pulmonary embolism at 23 years of age, and several maternal relatives had experienced venous thrombosis. The proband showed reductions in both AT activity (45%) and AT antigen level (13.2 mg/dL), suggesting type I inherited AT deficiency. In the second family, a 70-year-old woman was suspected of having inherited thrombophilia because multiple family members were found to have thrombotic disease during a preoperative interview for lung cancer surgery. She had no history of thrombosis and showed normal AT activity (119%). In contrast, her two brothers and one sister, all of whom had histories of thrombosis, showed decreased AT activity levels of 39%, 72%, and 45%, respectively.
Genetic Analysis
After obtaining informed consent, *SERPINC1* genetic analysis was performed in both families. A heterozygous c.204dup (p.Glu69Argfs*36) variant was identified in the proband of the first family and in the two brothers and one sister of the second family. Family investigation was not performed in the first family. This frameshift variant was novel and had not been previously reported.
Discussion
The *SERPINC1* c.204dup variant introduces a premature termination codon through a frameshift, which may result in reduced AT antigen levels via nonsense-mediated mRNA decay or production of a truncated AT protein. In addition, the strong family histories of thrombosis in both families suggest that this variant may be responsible for type I AT deficiency.

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一般演題 Hematology

LIS Auto-Verification: Impact on Coagulation Workflow and Reliability

Enhancing PT and aPTT Reporting Efficiency

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【Objective】 Prothrombin Time (PT) is used to evaluate the impact of liver disease on coagulation function, diagnose congenital or acquired coagulation abnormalities, monitor oral anticoagulant dosage within the therapeutic range, and preoperative coagulation function to prevent intraoperative or postoperative bleeding risks. Activated Partial Thromboplastin Time (aPTT) is used to diagnose bleeding disorders, monitor anticoagulation therapy (such as heparin therapy), and evaluate preoperative coagulation status. Aa both tests are commonly performed and clinically important, our department has prioritized their inclusion in the Laboratory Information System (LIS) auto- verification system.

【 Methods 】 Auto-verification rules for blood coagulation analysis were developed based on the Clinical and Laboratory Standards Institute (CLSI) guideline. These rules included instrument flags, quality control criteria, critical values, delta checks, first-test parameters, auto- verification ranges, and previous values. Additionally, auto-verification rules from peer hospitals were collected. The final rules were determined through internal laboratory discussion, the average turnaround times (minutes) for PT and aPTT, as well as the percentage of auto-verification results, were collected and analyzed.

【Results】 Data collected after implementation in March 2025 showed that the average turnaround time for PT and aPTT decreased by 4.4 minutes (from 27.6 minutes to 23.2minutes) and 4.0 minutes (from 27.4 minutes to 23.4 minutes), respectively. Furthermore, the proportions of reports issued via auto-verification were 55.4% for PT and 92.8%for aPTT, respectively.

【Conclusion】 Implementing auto-verification eliminated the need for manual result validation and shortened turnaround time, and leverages LIS's auto-verification rules to provide reliable report quality.

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一般演題 Hematology

Management of Internal Quality Control in complete Blood Count

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Management of Internal Quality Control for the Beckman Coulter DxH800 Automated Analyzer in Complete Blood Count
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Introduction: In clinical pathology, quality control requires and necessitates the execution of several essential steps by the practitioner to guarantee the reliability of results, in compliance with their obligations toward both colleagues and patients. The aim of this study was to evaluate the trueness and precision of complete blood count (CBC) results in the hematology laboratory of the Farhat Hached Hospital in Sousse.

Methods: To achieve this, a study was conducted from December 2024 to February 2025 using the Beckman Coulter DxH800 analyzer. Particular emphasis was placed on the laboratory IQC for four hematological parameters: white blood cell count (WBC), red blood cell count (RBC), hemoglobin (Hb), and platelet count (Plt). IQC data were used for precision and trueness testing. The results obtained during this study period were recorded and utilized to plot Levey-Jennings charts and to calculate means, standard deviations (SD), coefficients of variation (CV), and biases.

Results: Specific documents for IQC management were developed to ensure standardized implementation and interpretation of IQC by all personnel. An Excel-based program was created to process the results on Levey-Jennings charts, thereby improving the monitoring of precision and trueness. The CV and bias for the three IQC levels were compared against the Ricos acceptable limits. Our results were compliant, with the exception of IQC Level 1 for WBC, where a constant systematic error was detected.

Conclusions: This study demonstrates that the statistical IQC results at the hematology laboratory of the Farhat Hached Hospital in Sousse show acceptable levels of precision and trueness, thus exhibiting good performance across the four parameters of the complete blood count analysis.

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一般演題 Hematology

Reference Intervals for Immature Platelet Fraction in Healthy Tunisians

Including Advanced Platelet Indices

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Background: Immature platelet fraction (IPF) and advanced platelet indices are increasingly used in routine hematology as indicators of thrombopoietic activity and platelet production. Their interpretation requires population-specific reference intervals because these parameters may vary according to ethnicity, geographic origin, age, and sex.

Aim: This study aimed to establish reference intervals for immature platelet fraction (IPF) and advanced platelet indices in a healthy Tunisian adult population.

Methods: A descriptive cross-sectional study was conducted at the blood bank of the La Rabta Hospital between April and May 2026. A total of 122 healthy voluntary blood donors aged 18–65 years were included for reference interval establishment (G1), while 20 additional healthy subjects were recruited for validation (G2). Complete blood count and platelet parameters were measured using the Sysmex XR-1000 automated hematology analyzer. The analyzed parameters included PLT-F, IPF%, absolute IPF, MPV, PDW, PCT, and P-LCR. The establishment of reference intervals was performed according to the general approach recommended by the Clinical and Laboratory Standards Institute (CLSI). Outliers were excluded using Tukey's method. Distribution normality was assessed using the Kolmogorov–Smirnov test. Reference intervals were established using a non-parametric percentile-based approach (2.5th–97.5th percentiles).

Results: The reference population included 94 males (77.0%) and 28 females (23.0%), with an overall median age of 40 years (Q1–Q3: 30–45.75). Before outlier exclusion, median values were 248×10³/µL for PLT-F, 3.3% for IPF, 9 ×10⁶/µL for absolute IPF, 10.7 fL for MPV, 12.55 fL for PDW, 0.27% for PCT, and 30.6% for P-LCR.

Outlier exclusion identified 6 aberrant values for IPF, 3 for PLT-F, MPV and PDW, 2 for P-LCR, and 1 for absolute IPF, while no outlier was detected for PCT. After exclusion, most platelet parameters showed normal distribution. However, IPF (%) remained non-Gaussian (Kolmogorov–Smirnov p = 0.014), supporting the use of non-parametric statistical analysis.

The established reference intervals were:

- PLT-F: 154–367 ×10³/µL
- IPF: 1.09–8.21%
- Absolute IPF: 3.4–18.9 ×10⁶/µL
- MPV: 9.2–12.51 fL
- PDW: 9.8–16.93 fL
- PCT: 0.18–0.39%
- P-LCR: 18.2–46.54%

Descriptive analysis according to age groups showed moderate variations of platelet indices across age categories without justification for age-specific reference intervals. Validation using the independent G2 cohort confirmed the reliability of the established intervals, with acceptable concordance according to CLSI recommendations.

Conclusion: This study established locally derived reference intervals for IPF and advanced platelet indices in a healthy Tunisian population using a robust non-parametric approach combined with Tukey outlier exclusion. These results may improve the interpretation of advanced platelet parameters in Tunisian laboratories and support their integration into routine hematological practice.

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一般演題 Hematology

Method comparison of iMOST-L and Sysmex XN-9100

Analytical agreement and feasibility of home-based monitoring in cancer patients

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The Norwegian Radium Hospital is a leading center for cancer treatment and research in Norway. Cancer patients often require frequent monitoring of hematological parameters, and repeated hospital visits for blood sampling may be burdensome and resource-intensive. This study evaluated the analytical agreement between the point-of-care hematology analyzer iMOST-L and the reference instrument Sysmex XN-9100, and explored its potential for home-based monitoring in cancer patients. A total of 100 patient samples were analyzed on both instruments. Prior to method comparison, analytical precision was evaluated using replicate measurements across multiple concentration levels. Agreement between methods was assessed using bias, regression, correlation, and Bland-Altman plots. Patient perceptions of home-based monitoring were collected using questionnaires and summarized using descriptive statistics. Hemoglobin and total leukocyte count demonstrated excellent agreement between methods ($r = 0.977$ and $r = 0.995$, respectively). Strong agreement was also observed for neutrophil ($r = 0.995$) and lymphocyte ($r = 0.998$) counts, whereas monocyte measurements demonstrated acceptable agreement. Reduced agreement was observed for eosinophils ($r = 0.697$) and basophils ($r = 0.541$), with basophils showing a statistically significant difference between methods ($p < 0.001$). Among questionnaire respondents ($n = 95$), 62% preferred self-testing using iMOST-L and 20% preferred testing using iMOST-L with nurse assistance, indicating positive attitudes toward home-based monitoring. The results indicate that iMOST-L provides comparable results to Sysmex XN-9100 for hemoglobin, total leukocyte count, and several differential count parameters. However, reduced agreement for eosinophils and basophils indicates that further evaluation is required prior to clinical implementation. Positive patient attitudes toward home-based monitoring support the potential role of point-of-care hematology testing in the follow-up of cancer patients. Contact information: Malin Myhre Olsson, Department of Medical Biochemistry, The Norwegian Radium Hospital, Oslo University Hospital, Norway. Email: malio3@ous-hf.no. Tel: +47 90881707

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一般演題 Hematology

Establishing CBC Reference Range Ages 20-29 Filipinos in Metro Manila

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In the Filipino setting, establishing locally derived Complete Blood Count (CBC) reference values is important for accurate clinical assessments as relying on foreign standards can lead to misdiagnosis due to genetic, environmental, and lifestyle variations. This study aimed to establish reference ranges for CBC parameters among healthy Filipinos aged 20–29 years in Metro Manila. Utilizing an analytical cross-sectional design, 120 healthy participants (60 males, 60 females) were screened through strict clinical criteria. Blood samples were collected and analyzed using the Maccura F-580 automatic hematology analyzer, with data evaluated adhering to CLSI EP28-A3c guidelines, applying the Harris and Boyd Method for sex partitioning and the Robust Method for percentile determination. Results revealed that sex-based partitioning was required for 55.6% of the parameters, including RBC count, HGB, HCT, PLT, and RDW-CV. Males presented significantly higher RBC profiles, specifically 12.8–16.2 g/dL for HGB and 4.4–5.6×10^{12}/L for RBC, while females ranged from 10.2–14.3 g/dL and 3.7–5.0×10^{12}/L, respectively. In contrast, females demonstrated a wider range and greater dispersion in PLT counts (150–326×10^{9}/L) compared to males (131–279×10^{9}/L). Parameters such as WBC count (4.7–10.8×10^{9}/L,) and red cell indices (MCV, MCH, and MCHC) showed no significant sex variations and utilized combined reference ranges. In conclusion, these localized values capture the unique biological profiles of the Filipino population more accurately than Western standards, providing a vital baseline for clinical laboratories in Metro Manila to enhance diagnostic accuracy and to prevent clinical misinterpretation.

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一般演題 Hematology

Diagnostic Performance of Immature Platelet Fraction for Differentiating Thrombocytopenia Mechanisms

Tunisian Cutt-off Values for Clinical Use

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Background: Thrombocytopenia is a common hematological abnormality resulting either from decreased platelet production (central thrombocytopenia) or increased peripheral destruction/consumption (peripheral thrombocytopenia). Distinguishing between these mechanisms is essential for patient management but often requires invasive bone marrow examination. The immature platelet fraction (IPF) has emerged as a potential non-invasive biomarker of thrombopoietic activity.
Aim: To evaluate the diagnostic performance of IPF (%) and absolute IPF in differentiating central from peripheral thrombocytopenia and to establish Tunisian diagnostic cut-off values.
Methods: This observational analytical study included 155 thrombocytopenic patients recruited from the Hematology Laboratory of La Rabta Hospital between April 2026 and May 2026. Patients were classified as having peripheral thrombocytopenia (n=113) or central thrombocytopenia (n=42) based on clinical, biological and bone marrow findings when available. Complete blood counts and IPF measurements were performed using the Sysmex XR-Series analyzer. Receiver operating characteristic (ROC) curve analysis was used to evaluate diagnostic performance and determine optimal cut-off values using the Youden index. To further investigate the independent association of IPF (%) and absolute IPF with peripheral thrombocytopenia, a multivariable logistic regression model incorporating both parameters was constructed.
Results: Peripheral thrombocytopenia patients exhibited significantly higher IPF values than central thrombocytopenia patients. Median IPF (%) was 7.7% (5.0–13.6) versus 5.3% (2.1–10.8) (p=0.017), while median absolute IPF was 6.5 $\times 10^6$/µL (4.0–10.7) versus 3.0 $\times 10^6$/µL (1.5–4.9) (p<0.001). ROC analysis showed that absolute IPF had superior diagnostic performance compared with IPF (%), with AUC values of 0.751 (95% CI: 0.661–0.836) and 0.625 (95% CI: 0.510–0.733), respectively. The optimal cut-off value for IPF (%) was 4.0%, yielding 85.0% sensitivity and 45.2% specificity. For absolute IPF, the optimal cut-off was 5.0 $\times 10^6$/µL, providing 69.0% sensitivity and 76.2% specificity. Multivariable analysis identified absolute IPF as the only independent predictor of peripheral thrombocytopenia (OR = 1.262, 95% CI: 1.119–1.423) (p < 0.001). The combined model did not improve diagnostic performance compared with absolute IPF alone (AUC = 0.751), indicating that absolute IPF is the most useful IPF-derived parameter for distinguishing peripheral from central thrombocytopenia in Tunisian patients.
Conclusion: Both IPF (%) and absolute IPF were significantly associated with the mechanism of thrombocytopenia. Absolute IPF demonstrated better overall diagnostic performance and may represent a valuable, rapid, and non-invasive biomarker for differentiating peripheral from central thrombocytopenia. The cut-off value of 5.0 $\times 10^6$/µL appears particularly relevant for the Tunisian population and could help reduce the need for invasive bone marrow investigations.

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一般演題 Hematology

Characteristics of morphometric parameters of platelets during myeloid neoplasms

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Introduction: Given the technological advancements, the automated hemogram could help establish the profile of myeloid neoplasms. The objective of this work was to study the morphometric profiles and platelet activation in myeloid hematopathies and to analyze their associations with other biological markers and prognostic scores.
Methods: A descriptive and analytical study was conducted in the hematology department of Rabta for a duration of two and a half months. Included in this study were: patients over 18 years old with a confirmed myeloid neoplasm (myeloproliferative neoplasms (MPN): chronic myeloid leukemia (CML), polycythemia vera (PV), essential thrombocythemia (ET), and primary myelofibrosis (PMF)), myelodysplastic syndromes (MDS), and acute myeloid leukemias. For each patient, extended blood counts performed on the Sysmex XR-10 analyzer at the time of diagnosis or during follow-up were recorded. A group of healthy individuals was formed.
Results: Sixty-six (n=66) patients followed for myeloid hematopathies and 61 apparently healthy individuals (control group) were included. in the myeloid hematopathy group, the median age was 69 years (interquartile range: 11) [35 years - 88 years]. The sex ratio = 0.86. the patients were classified into: MDS (n= 26), AML (n= 4), CML (n= 7), ET (n= 7), PV (n= 13), and MF (n= 9). The PLT-F was significantly higher than the count by PLT-O during myeloid hematopathies. (p ranging from 0.016 to 0.044). In total, 24/26 SMD patients had an IPF% >3. the parameters MPV, PDW, PLCR, and the MPV/P-LCR ratio were significantly higher during SMD (respectively=0.0016, 0.002, 0.017, 0.004). However, the IPF was elevated without statistical significance. Regarding the NMP, only the PCT was significantly higher than in healthy individuals. (p=0.034). only the platelet activation parameters (H-IPF, IPF%, and absolute IPF) were positively correlated with blastosis. (Rho between 0.8 and 0.83). no significant association was found between the IPSET-thrombosis score and platelet parameters due to the low power of the study.
Conclusion: Morphometric and activation parameters appear promising for guiding the diagnosis and prognosis of malignant hematological disorders. However, larger-scale studies should be conducted.

P-3-67

一般演題 Hematology

Bioinspired Nanoliposome Technology for Stabilization of Whole Blood Hematology Control

A Novel Preservation Platform for Long-Term Blood Control Stability

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Introduction: Whole blood hematology control materials are vital for laboratory quality assurance, but storage lesions compromise blood cell stability. Nanoliposome technology offers a biomimetic membrane shield that preserves erythrocyte, leukocyte, and platelet integrity during long-term storage, providing a promising strategy for developing ultra-stable hematology control materials in modern clinical laboratories. **Objective:** This study aimed to develop a nanoliposome-based nano-biomimetic membrane shielding system to produce ultra-stable whole blood hematology control materials capable of maintaining cellular integrity, homogeneity, and analytical accuracy during long-term storage. **Methods:** Bioinspired phospholipid–cholesterol–DCA nanoliposomes were prepared by thin-film hydration and sonication, then characterized by DLS, zeta potential, and TEM. Applied to whole blood, stability was evaluated during refrigerated storage using hematological, statistical, and ISO Guide 35:2017 analyses. **Results:** Nanoliposomes exhibited an average particle size of 158 nm and a zeta potential of −12.8 mV. TEM analysis showed predominantly spherical to quasi-spherical vesicles with well-defined membranes and no significant aggregation. During 11-day storage, linear regression indicated no significant changes in HGB, PLT, WBC, and RBC, while HCT increased significantly. According to ISO Guide 35 stability criteria, RBC, HGB, WBC, and PLT were stable, whereas HCT was unstable. Deviation analysis demonstrated acceptable changes for RBC (+6.18%), HGB (+0.72%), and PLT (−2.03%), while WBC (−19.50%) and HCT (+29.18%) exceeded the predefined ±10% acceptance limit. **Conclusion:** Nanoliposomes preserved RBC, HGB, and PLT stability during storage, showing promise for developing stable hematology control materials..

Keywords: nanoliposome, whole blood hematology control material, stability, quality control, blood preservation

P-3-68

Explainable Machine Learning Score for Thrombocytopenia Mechanism Classification

一般演題 Hematology

©MAHJOUB SONIA[1)]、SRAIRI Mayar、CHAKROUN Aya、NABLI Emna、GNOUMA Yosr、BACCOUCHE Hela、MAHJOUB Sonia RABTA HOSPITAL[1)]

Background : Differentiating peripheral from central thrombocytopenia remains a frequent diagnostic challenge in clinical practice. Although bone marrow examination is often considered the reference method for etiological diagnosis, it is invasive and not always readily available. Advanced hematological parameters generated by modern automated analyzers may provide valuable insights into the underlying mechanisms of thrombocytopenia and support non-invasive diagnostic approaches. **Objective :** To develop and validate an explainable machine learning model based on advanced hematological parameters for differentiating peripheral from central thrombocytopenia and to derive a simplified diagnostic score applicable in routine clinical practice.
Methods : This retrospective study included 155 consecutive patients with confirmed thrombocytopenia, comprising 113 cases of peripheral thrombocytopenia and 42 cases of central thrombocytopenia. Demographic characteristics and advanced platelet, erythroid, and leukocyte parameters obtained using a Sysmex XN/XR-series hematology analyzer were analyzed. Several Extreme Gradient Boosting (XGBoost) models were developed using different combinations of hematological parameters. Model performance was evaluated through 100 repeated Monte Carlo cross-validation iterations to assess robustness and reproducibility. Explainable artificial intelligence techniques based on SHAP (Shapley Additive Explanations) values were used to identify the most influential predictors. Based on these results, a simplified Tunisia Thrombocytopenia Differentiation Score (TTDS) was derived using the most informative parameters and their optimal diagnostic cut-offs.
Results : A total of 155 thrombocytopenic patients were included, of whom 72.9% had peripheral thrombocytopenia and 27.1% had central thrombocytopenia. Patients with peripheral thrombocytopenia exhibited significantly higher hemoglobin levels than those with central thrombocytopenia (10.7 vs 8.75 g/dL, $p = 0.006$). Total leukocyte and neutrophil counts were also significantly higher in the peripheral group (7.07 vs 4.00 $\times 10^3/\mu L$ and 4.47 vs 2.28 $\times 10^3/\mu L$, respectively; both $p < 0.001$). In contrast, RET-He values were significantly higher in central thrombocytopenia (32.35 vs 30.30 pg, $p = 0.015$). Among advanced platelet parameters, peripheral thrombocytopenia was associated with significantly higher PLT-F, IPF (%), absolute IPF, MPV, PDW, PCT, and P-LCR values (all $p < 0.05$), reflecting enhanced thrombopoietic activity and increased platelet turnover. No significant differences were observed for MCV, RDW indices, reticulocyte count, absolute reticulocyte count, IRF, or lymphocyte count. The best-performing model was the XGBoost model integrating platelet, erythroid, and leukocyte parameters, achieving excellent discrimination between peripheral and central thrombocytopenia. Repeated Monte Carlo cross-validation confirmed the stability and reproducibility of model performance across multiple training and validation datasets. SHAP analysis identified immature platelet fraction (IPF), absolute IPF, platelet large cell ratio (P-LCR), and platelet distribution width (PDW) as the most influential predictors. Higher values of these parameters were strongly associated with peripheral thrombocytopenia, consistent with increased bone marrow compensation in response to peripheral platelet destruction or consumption. Based on these findings, the Tunisia Thrombocytopenia Differentiation Score (TTDS) was developed. The score demonstrated a progressive increase in the probability of peripheral thrombocytopenia with increasing point values. ROC curve analysis showed good diagnostic performance, and a threshold of ≥3 points provided the optimal balance between sensitivity and specificity. Despite its simplicity, the TTDS achieved diagnostic accuracy comparable to that of the complete machine learning model while relying only on a limited number of routinely available hematological parameters.
Conclusion : Explainable machine learning applied to advanced hematological parameters allows accurate differentiation between peripheral and central thrombocytopenia. The proposed TTDS represents a practical, interpretable, and cost-effective diagnostic tool that may facilitate early etiological orientation of thrombocytopenic patients and reduce the need for invasive procedures such as bone marrow examination.

P-3-69

一般演題 Hematology

Interlaboratory trial of the complete blood count

contribution to the estimation of measurement uncertainty of a multiparametric test

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Introduction: Inter-laboratory comparison (ILC) is a focus addressed in the ISO 15189:2022 standard. The objectives of this work were to conduct an inter-laboratory comparison (ILC) on the automated complete blood count (CBC) and to estimate the measurement uncertainty (U(C)) of this test.

Methods: A CIL was organized by the hematology laboratory of La Rabta Hospital between 07/01/2024 and 07/04/2024, conducted among peers using Sysmex analyzers. The samples came from a homogenized whole blood donation and were distributed in EDTA tubes. All samples were sent to the participants and analyzed under repeatability conditions. Homogeneity and stability were verified. The raw results were transcribed onto Excel. The outlier data were discarded using the Cochran and Grubbs tests. The assigned value, its uncertainty, and the proficiency standard deviation were determined. The CLIA and Ricos reference ranges were used to determine precision, intermediate precision, and accuracy. Accuracy was assessed by calculating the Z-score. The expanded uncertainty of the measurements was estimated.

Results:17 participants were included. All measurements were within the acceptable limits of the assigned values. The reliability of the majority of the results was noted (except for the MCV (n=1) and Ht (n=2)). a problem of homogenization was noted. For intermediate fidelity (CVR): the method was not reliable for the counting of RBCs, MCV, Hct. A bias in accuracy was observed for all parameters except for the neutrophils (RBCs (n=8participants), Hb (n=4), MCV (n=3), Hct (n=2), PLq (n=2), WBCs (n=4)). The Mandel h and k statistics concluded to the intra-and inter-laboratory consistency for almost all participants. No participant had a Z-score≥3. On the other hand, questionable performances were observed in 06 cases. An estimate of the U(C) has been proposed for each parameter.

Conclusions: The non-conformities and deficiencies highlighted will incite to investigate the potential causes of the risks and to carry out corrective actions.

P-4-2

一般演題 Clinical Chemistry

Artificial Intelligence for Clinical Chemistry in Low-Resource Laboratory Settings

Implementing Edge AI for Real-Time Diagnostic Support in Connectivity-Challenged Environments

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Purpose: Clinical laboratories in developing regions face substantial diagnostic error rates, largely due to a critical shortage of specialists and unstable infrastructure. This study evaluates "Sudan Lab AI," an offline-capable artificial intelligence model designed to standardize diagnostics and enhance accuracy in limited-resource environments. The primary goal is to provide a resilient solution that overcomes connectivity challenges while maintaining high-quality diagnostic standards and reducing diagnostic delays.

Methods: We developed a dual-layer AI architecture to ensure continuous operation. The "Edge Layer" utilizes a lightweight, mobile-based image recognition algorithm to process and analyze laboratory data locally, functioning entirely without internet connectivity. This allows for real-time diagnostic support directly at the point of care. The "Cloud Layer" complements this by facilitating periodic, low-bandwidth data synchronization and remote quality control updates whenever a stable connection is established, ensuring the model's long-term accuracy and relevance.

Results: Preliminary field-testing in simulated low-connectivity settings demonstrated a significant 60% reduction in results turnaround time compared to traditional workflows requiring specialist review. The model maintained over 95% diagnostic accuracy when benchmarked against senior laboratory specialists, effectively mitigating common human interpretive errors. The system proved highly effective in zero-connectivity environments, showcasing its potential for immediate deployment in resource-limited settings.

Conclusion: Edge AI presents a transformative and resilient solution for biomedical laboratory science. By decentralizing analytical capabilities, it ensures that high-quality, reliable diagnostic standards are accessible even in areas where traditional infrastructure is unreliable or completely non-existent. This approach empowers local healthcare providers and strengthens the overall diagnostic framework in resource-constrained regions, ultimately improving patient outcomes.

P-4-3

一般演題 Clinical Chemistry

Long-term Stability of the Kappa Free Light Chain Index

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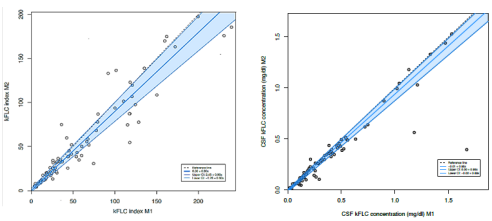
Background: Kappa free light chains (k-FLC) in the cerebrospinal fluid (CSF) are a novel biomarker for the assessment of intrathecal immunoglobulin synthesis. The impact of frozen storage duration on CSF k-FLC concentrations is unknown.

Objective: To investigate whether the duration of frozen storage influences CSF k-FLC concentrations and the k-FLC index.

Methods: CSF and serum samples from patients with multiple sclerosis (n = 70) and Lyme disease (n = 12), collected for routine diagnostic purposes, were stored at −20 °C. k-FLC and albumin concentrations were measured at two time points, i.e. before storage (M1) and after storage (M2). Agreement between measurements was analyzed using Passing–Bablok regression, and concordance of sample positivity was assessed using Cohen's kappa.

Results: A total of 82 patients with a median age of 33 years and a female predominance (61%) were included. The median time between measurements M1 and M2 was 2.3 years (75th percentile: 4.3 years; maximum: 7.4 years). Absolute concentrations of albumin and k-FLC in CSF and serum did not show meaningful changes over time, with percentage changes of less than 2% per year for all parameters. Consequently, the k-FLC index was not significantly affected by frozen storage duration (β = −0.012 per year, p = 0.327), showing comparable values at M1 (median 37, 25th–75th percentile: 23–89) and M2 (median 35, 20–77). Cohen's kappa for k-FLC index positivity between M1 and M2 was 0.85.

Conclusion: Frozen storage duration has no clinically relevant impact on CSF k-FLC concentrations or the k-FLC index.



P-4-4

一般演題 Clinical Chemistry

The Hidden Danger After Fever Subsides

A Rare Case Report and Laboratory Monitoring of Severe Rhabdomyolysis Complicating Influenza B

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Introduction: Influenza viruses typically present with respiratory manifestations; however, the risk of Influenza B-associated acute myositis progressing to rhabdomyolysis in pediatric patients remains a significant clinical concern. Evidence suggests that muscle-related complications often exacerbate within 24 to 48 hours post-defervescence (after fever subsides). If not identified and managed promptly, this condition can lead to acute kidney injury (AKI) and multi-organ failure. This report highlights the necessity of vigilant clinical observation and the pivotal role of laboratory critical value systems in preventing adverse outcomes.
Methods: Biochemical analyses were performed using the Abbott Alinity automated platform. Creatine kinase (CK) activity was determined via the IFCC-standardized kinetic method. Myoglobin and CK-MB levels were measured using chemiluminescent microparticle immunoassay (CMIA). All procedures followed the manufacturer's protocols, supported by stringent internal quality control and periodic calibration. Samples were processed under a STAT (emergency) workflow. The laboratory information system (LIS) was configured to trigger an automated critical value notification to the clinical team immediately upon CK levels exceeding institutional safety thresholds, in accordance with standard operating procedures (SOP).
Case Report: A 6-year-old male with no remarkable medical history presented with high fever and respiratory symptoms. He was diagnosed with Influenza B and commenced on oseltamivir therapy. Three days later, despite becoming afebrile, the patient developed severe bilateral lower extremity pain and a noticeable limping gait, prompting an emergency department visit.
Initial laboratory evaluation revealed leucopenia (WBC: 3,290/μL). Significant elevations in biochemical markers were noted: CK at 2,559 U/L and Myoglobin at 1,956.1 ng/mL, indicating acute muscle injury. The patient was admitted for observation. Within 24 hours of admission, the laboratory issued a critical value alert as CK surged to 8,228 U/L and CK-MB reached 72.8 ng/mL, confirming a progression to severe rhabdomyolysis.
In response to the alert, the medical team immediately initiated aggressive intravenous fluid resuscitation to mitigate the risk of renal tubular damage. Throughout the hospital stay, serial urinalysis and renal function panels remained stable, indicating no secondary AKI. Following three days of intensive hydration, the patient's myalgia resolved, and myoglobin levels declined to 516.4 ng/mL. He was subsequently discharged in stable condition for outpatient follow-up.
Discussion: This case underscores that clinical stability post-defervescence can be deceptive; persistent myalgia and gait disturbances are vital red flags for influenza-related complications. Literature indicates that Influenza B has a higher predilection for muscular involvement compared to Influenza A. This is attributed to the unique NB protein found in Influenza B, which alters cell membrane permeability, facilitating direct viral entry into myocytes. Furthermore, the virus triggers a robust immune response, characterized by a pro-inflammatory cytokine storm that compromises the sarcolemma, leading to the massive leakage of CK and myoglobin into the systemic circulation.
Conclusion: While influenza-induced severe rhabdomyolysis is relatively rare, its clinical course is often rapid and aggressive. Real-time monitoring of biochemical markers and the rigorous implementation of a laboratory-to-clinical critical value reporting system are essential. These mechanisms allow clinicians to adjust therapeutic strategies dynamically based on objective data. This case exemplifies the indispensable role of laboratory medicine in the management of acute pediatric conditions and its impact on improving patient prognosis.

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P-4-5

一般演題 Clinical Chemistry

MLS-Led ERAS Framework in Epilepsy-Induced Rhabdomyolysis

Four-Stage Dynamic Laboratory Monitoring with CK/UA Slope Stratification

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Background: Status epilepticus frequently triggers rhabdomyolysis, risking severe, rapidly progressive hyperuricemia, acute kidney injury (AKI), disseminated intravascular coagulation (DIC), and multiple organ dysfunction syndrome (MODS). Building on our 2025 report (Taiwan J Med Lab Sci 2025; 40:1), medical laboratory scientists (MLS) developed a comprehensive, scalable four-stage Enhanced Recovery After Surgery (ERAS)-inspired monitoring framework. This innovation addresses timeliness gaps in laboratory data tracking within Taiwan's intensive care units (ICUs), establishing MLS-generated biomarkers as essential clinical tools for time-sensitive interventions. **Methods:** IRB-approved case from southern Kaohsiung teaching hospital. The framework includes: Stage 1 (Screening): creatine kinase (CK)/uric acid (UA)/creatinine every 6 hours; CK slope >15%/6 h auto-escalates to q4h. Stage 2 (Validation): PT/aPTT/CRP/D-dimer; D-dimer >2 mg/L indicates coagulopathy risk. Stage 3 (Stratification): daily KDIGO-AKI/SOFA scoring; score >8 prompts ICU evaluation. Stage 4 (Decision): bootstrap-enhanced classification and regression tree (CART) analysis, based on time-series data, identifies key CK/UA slope predictors. **Results:** Admission: creatinine 3.09 mg/dL (eGFR 22.9 mL/min/1.73 m²). Day 1 post-seizure CK 5688 U/L surged to 18,751 U/L by Day 3, UA >30 mg/dL, ALT 784 U/L. Day 3: ALT 251 U/L, creatinine 6.94 mg/dL (eGFR 9.0), PT-INR 3.34. Day 5: myoglobin 12–15×10³ ng/mL. MLS real-time data improved diagnostic timeliness by 50%; Day 2 SOFA = 10 (respiratory 3, coagulation 2, liver 3, renal 2) triggered rasburicase/CRRT; length of stay 11 days, no MODS progression. **Conclusion:** This MLS-led ERAS-inspired framework validates serial CK/UA slopes as transformative biomarkers, shifting labs from reactive testing to proactive ICU risk stratification. Compared with historical ICU cases, it achieved 50% faster diagnosis without MODS progression. Ongoing multi-center validation studies are planned.

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P-4-6

一般演題 Clinical Chemistry

Impact of Taiwan's 2026 CKD-EPI Transition on Clinical Reimbursement

Navigating SGLT-2i Eligibility Risks and Staging Reclassification in Laboratory Medicine

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Estimated glomerular filtration rate (eGFR) is essential for chronic kidney disease (CKD) staging and treatment decisions. Differences between Modification of Diet in Renal Disease (MDRD) and Chronic Kidney Disease Epidemiology Collaboration (CKD-EPI) equations may alter CKD classification and affect eligibility for sodium-glucose cotransporter-2 inhibitors (SGLT-2 inhibitors). In Taiwan, following consensus between the Taiwan Society of Nephrology and the National Health Insurance Administration, laboratories are encouraged to report eGFR using the 2021 CKD-EPI equation. This study evaluated its impact on CKD staging and clinical implications.

We retrospectively analyzed data from 33,514 patients (October 2025–January 2026). eGFR was calculated using MDRD and the 2021 CKD-EPI equation. CKD stages (G1–G5) were assigned based on Kidney Disease: Improving Global Outcomes (KDIGO) criteria. In 4,133 patients, urinary albumin-to-creatinine ratio (UACR) was analyzed alongside eGFR.

CKD stage 3a–5 was identified in 5,844 patients using MDRD and 4,777 using CKD-EPI. Overall, 6,799 patients (20.3%) were reclassified, predominantly toward lower stages, including stage 2 to 1 (4,996 patients) and stage 3a to 2 (1,069 patients). CKD-EPI reduced cases with eGFR <60 but normal UACR (265 vs. 355), suggesting less overestimation of CKD. SGLT-2 inhibitors are indicated for selected populations (e.g., diabetes or high-risk CKD). Reclassification mainly affects patients meeting treatment indications: some may no longer meet eGFR thresholds, while others may avoid unnecessary therapy or inappropriate discontinuation. For patients without indications, staging differences primarily influence diagnosis and monitoring.

In Taiwan, adoption of the 2021 CKD-EPI equation significantly alters CKD staging and better aligns with albuminuria. The choice of eGFR equation influences SGLT-2 inhibitor eligibility in appropriate patients and improves clinical decision-making when combined with comorbidities and UACR.

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P-4-7

一般演題 Clinical Chemistry

Clinical Use of Beta-D-Glucan Testing in Rheumatology Outpatients

A Single-Center Retrospective Study

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Objective: To characterize how plasma 1,3-β-D-glucan (BDG) testing was used in rheumatology outpatients in Japan and to assess how BDG results were reflected in subsequent clinical management in routine single-center practice.

Methods: We retrospectively reviewed BDG test episodes in rheumatology outpatients between January 5, 2017 and February 4, 2026. BDG was measured using the Wako method, and ≥11 pg/mL was used as the clinical cutoff for positivity. BDG values were grouped as <6.0, 6-10, 11-29, 30-99, and ≥100 pg/mL. Anti-rheumatic medication exposure was defined as use of systemic corticosteroids, immunosuppressants, biologics, or targeted synthetic DMARDs at the time of BDG testing or within ±30 days. Repeated testing and oral or injectable antifungal use were assessed as measurable clinical responses. Antifungal use was classified as initiation or continuation according to treatment status before and after BDG testing.

Results: A total of 13,159 BDG tests were performed in 1,282 patients. The median number of tests per patient was 9 (IQR, 2-22), and repeated testing was observed in 78.9% of patients. Anti-rheumatic medication exposure was present in 11,036 tests (83.9%). BDG values were <6.0 pg/mL in 12,209 tests (92.8%), 6-10 pg/mL in 595 (4.5%), 11-29 pg/mL in 303 (2.3%), 30-99 pg/mL in 46 (0.3%), and ≥100 pg/mL in 6 (0.05%). Oral antifungal use was identified in 290 tests (2.2%), including 259 with BDG <6.0 pg/mL. Injectable antifungal use was identified in 2 tests.

Conclusion: BDG-positive results were few in rheumatology outpatients and were mainly observed in patients receiving anti-rheumatic medications. Oral antifungal agents were mostly administered in cases below the clinical cutoff value, indicating that treatment indications were not dependent on BDG levels. In addition, even with moderate to highly elevated BDG levels, injectable antifungal use was not frequent. These findings suggest that BDG testing may primarily be for surveillance purposes in this outpatient setting.

P-4-8

一般演題 Clinical Chemistry

Monitoring Metrological Traceability of Creatinine for Accurate Clinical Decision Making

Enhancing Estimated Glomerular Filtration Rate Reliability through Standardized Accuracy-based Proficiency Testing

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Background: Chronic Kidney Disease (CKD) staging (G1–G5) relies primarily on the Estimated Glomerular Filtration Rate (eGFR). This study evaluated the traceability of our creatinine results through the Taiwan Society of Laboratory Medicine (TSLM) accuracy-based proficiency testing (PT) program, which is metrologically traceable to the Reference Material Institute for Clinical Chemistry Standards (ReCCS) in Japan.
Methods: In 2025, our laboratory participated in the TSLM newly established accuracy-based PT program, utilizing three fresh, commutable human-based samples for each run. Target values are metrologically traceable to ReCCS, a JCTLM-listed and ISO 17034 accredited producer using Isotope Dilution Mass Spectrometry (ID-MS). We employed alkaline picrate kinetic creatinine assays on two Beckman Coulter AU5800 analyzers. Biases were evaluated biannually against TSLM's allowable errors criteria of 7.5% or ±0.114 mg/dL, whichever is greater.
Results: Data from six creatinine PT samples (with ID/LC-MS target values ranging from 0.95 to 3.49 mg/dL) demonstrated that all results were within the TSLM allowable range and were deemed "Acceptable". The mean biases for the two AU5800 analyzers were -0.032 mg/dL and -0.015 mg/dL, respectively. No proportional errors were found during the evaluation. These results confirm that our creatinine measurements maintained high accuracy and were successfully traceable to international standards via the ReCCS reference system.
Conclusions: Periodic analysis through accuracy-based PT is a vital tool for identifying systematic shifts, such as those caused by reagent lot variations, which can significantly impact eGFR-based CKD staging. When significant biases are detected, corrective actions—including adjusting calibration factors—ensure alignment with ReCCS-assigned reference values. Participation in the TSLM accuracy-based program guarantees the consistency and validity of laboratory data, directly improving the management and prognosis for individuals living with CKD.
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P-4-9

一般演題 Clinical Chemistry

Mind Map Guided Jaundice Analysis in Pancreatic Cancer

Clinical Case Study with Structured Causal Visualization

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Background: Pancreatic head cancer causes jaundice in approximately 65% of cases due to bile duct obstruction, frequently accompanied by weight loss and digestive disturbances that complicate early diagnosis. Although CA19-9 and endoscopic ultrasound (EUS) provide important diagnostic value, the causal relationships linking laboratory abnormalities—particularly conjugated hyperbilirubinemia observed in obstructive physiology—to underlying pancreatic malignancy remain insufficiently recognized in routine clinical practice. This gap may delay timely multidisciplinary intervention and adversely affect patient outcomes. Methods: We developed a comprehensive mind map for a stage IV pancreatic adenocarcinoma case presenting with progressive painless jaundice (TBIL 9.54 mg/dL; DBIL 6.39 mg/dL) and markedly elevated CA19-9 (>10,000 U/mL). Magnetic resonance imaging (MRI) revealed multiple pancreatic lesions with metastatic features. The mind map systematically integrated four domains: etiology, pathophysiology, diagnostic progression, and therapeutic management. Results: Three key causal insights were identified. First, pancreatic head mass compression explained disproportionate conjugated hyperbilirubinemia, distinguishing obstructive jaundice. Second, markedly elevated CA19-9 levels correlated with extensive metastatic burden, consistent with previous findings. Third, visual integration transformed fragmented clinical data into structured diagnostic reasoning, facilitating efficient communication among multidisciplinary teams and accelerating clinical decision-making. Conclusion: Mind mapping provides a structured, reproducible framework for visualizing causal pathways in jaundice evaluation. This approach enhances laboratory–clinical correlation, supports earlier recognition of pancreatic malignancy, and promotes more timely and coordinated multidisciplinary management.
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P-4-10

一般演題 Clinical Chemistry

Dynamic Changes of Sepsis Biomarkers in Polymorbid Cellulitis

A Collaborative Case Report by a Nurse Specialist and a Medical Laboratory Scientist

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Background: This case describes a 51-year-old male with cellulitis of the right lower limb triggered by tophus rupture, complicated by alcoholic hepatitis and septic shock. Alcoholic hepatitis impairs immunity and drug metabolism, increasing misdiagnosis and delayed treatment risk. Monitoring of WBC, CRP, and PCT, combined with left shift, may improve sepsis detection under Sepsis-3. The enhanced recovery after surgery (ERAS) model is rarely used in infectious emergencies and currently lacks a framework co-led by medical laboratory scientists and specialist nurses. **Methods:**We developed an ERAS-inspired four-stage decision framework. Stage 1 (infection alert): WBC >20×10³/μL with left shift indicates severe infection. Stage 2 (sepsis confirmation and initial treatment): PCT >2 ng/mL with clinical septic shock prompts antibiotic initiation; hydrocortisone is added for haemodynamic support, with central venous catheter placement for intensive care monitoring and fluid therapy. Stage 3 (treatment response): CRP decline and clinical improvement guide adjustment of colchicine and electrolytes to maintain internal homeostasis and control gout-related inflammation. Stage 4 (discharge): Monitoring of WBC, CRP, PCT, ProBNP, and blood gas, with qSOFA, clinical stability, oral tolerance, and wound healing, guides catheter removal and discharge planning. **Results:** On admission, WBC 29.4×10³/μL with left shift, CRP 502.8 mg/L, PCT 3.58 ng/mL, and qSOFA ≈1, matching stage 1 and prompting early antibiotic initiation. By day 10, vital signs stabilized, oxygenation recovered, inflammatory markers improved, and the wound healed; the patient was discharged after removing catheters and completing discharge education. **Conclusion:** This report shows that an ERAS-inspired framework co-led by laboratory scientists and specialist nurses is feasible in infectious emergencies, shortening decision-making time, enabling early antibiotic initiation and de-escalation, and avoiding prolonged ICU care.

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P-4-11

一般演題 Clinical Chemistry

Laboratory-Based Risk Stratification for Complicated Appendicitis

Prognostic Nutritional Index Enhances Risk Stratification in a Large Cohort

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Background: Early identification of complicated appendicitis is essential for appropriate management, yet reliable risk stratification remains challenging. Conventional inflammatory markers reflect inflammatory burden but may not capture host-related vulnerability. This study aimed to compare clinical, laboratory, and combined predictive models and to evaluate the incremental value of the prognostic nutritional index (PNI) as a marker of host immune–inflammatory status.

Methods: This retrospective study included 1,132 consecutive patients with acute appendicitis who underwent laboratory testing at initial presentation. Cases were classified as simple or complicated based on pathological findings and imaging, including ultrasonography and/or computed tomography. Three multivariable logistic regression models were constructed: a clinical model (Model A), a laboratory model (Model B), and a combined model (Model C). Model performance was assessed using the area under the receiver operating characteristic curve (AUC), with comparisons using DeLong's test.

Results: Complicated appendicitis was identified in 341 patients (30.1%). In multivariable analysis, higher C-reactive protein, higher neutrophil percentage, and lower PNI were independently associated with complicated appendicitis. The AUCs were 0.791 for Model A, 0.847 for Model B, and 0.857 for Model C. Model B significantly outperformed Model A ($p = 0.0020$), whereas no significant difference was observed between Models B and C ($p = 0.0816$). PNI remained an independent predictor after adjustment for conventional markers, suggesting additive value in capturing host vulnerability.

Conclusions: Laboratory-based models demonstrate strong discriminative performance comparable to combined models. PNI provides incremental value by reflecting host-related vulnerability and may enhance objective risk stratification in acute care settings.

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P-4-12

一般演題 Clinical Chemistry

Stability of lactate dehydrogenase activity during storage

-Relationship with its Subunit Structure-

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【Background】It is known that lactate dehydrogenase(LD) activity significantly decreases with refrigerated storage. That is believed to be due to the inactivation of the M-type subunit. However, in healthy samples, the proportion of M-type subunits is extremely low, and makes it difficult to explain by. We have previously reported that under conditions of the IFCC method, the H-type subunit has 6.24 times the activity of the M-type, and this suggests that LD5, which shows the same activity as LD1, contains more than six times the number of molecules. Therefore, we focused on the subunit structure and the number of molecules in order to elucidate the cause of the decrease in activity.

【Methods】A total of nine samples, including healthy, high LD1, and high LD5, were used, and they were refrigerated after sampling. LD activity measurement and LD isozyme testing were conducted weekly, and calculated inactivation rate based on the activity values of sampling.

【Results】It was confirmed that the activity levels gradually decreased from one week after measurement in all samples. After 4 weeks, the inactivation rates were less than 10% in samples with high LD1 (N=2), 10-20% in healthy samples (N=4), and 20-40% in samples with high LD5 (N=3). The inactivation rates by isozyme followed the order LD4 > LD5 > LD3 > LD2 > LD1, and marked decrease was observed in the fractionation pattern from LD3 to LD5.

【Conclusions】In this study, the inactivation rate with storage was highest in LD5-high samples, followed by healthy samples, and lowest in LD1-high samples. This suggesting that the decrease in LD activity depends on the proportion of the M-type present. On the other hand, the decrease in activity exceeded the activity of the M type, suggesting that the H type also became inactivated along with the inactivation of the M type. Additionally, the rate of inactivation for each isozyme was highest in LD4, which is presumed to be due to differences in the number of molecules between LD4 and LD5.

P-4-13

一般演題 Clinical Chemistry

Pseudo-Low Uric Acid

A Pre-analytical Pitfall in Acute Leukemia

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Purpose

To investigate the cause of unexpected uric acid (UA) decline in a pediatric acute leukemia patient treated with Rasburicase and to evaluate the impact of pre-analytical handling on laboratory results.

Methods

This is a single-case study of a 10-year-old female diagnosed with acute leukemia, hyperuricemia, and abnormal coagulation profile. Serial UA measurements were compared within the same day. Following an unexpected result, five repeated measurements were performed within 2 hours. Pre-analytical sample handling procedures were reviewed.

Results

UA level decreased from 11.1 mg/dL (8 hours prior) to 4.7 mg/dL initially. Repeated measurements within 2 hours further declined to 2.1, 1.1, 0.5, and 0.7 mg/dL, demonstrating a time-dependent downward trend. The patient had received rasburicase therapy, and samples were not processed under recommended cold conditions.

Conclusion

Rasburicase remains enzymatically active ex vivo and can degrade uric acid after blood collection. Inadequate cold handling leads to pseudohypouricemia and falsely decreasing UA levels. A progressive decline pattern should alert laboratory professionals to this pre-analytical error. Proper sample handling is essential to ensure accurate interpretation.

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P-4-14

一般演題 Clinical Chemistry

Correlation Between Plasma Catecholamines and Glycemic Fluctuations via Exercise Intensity

An Empirical Approach Using Heart Rate Reserve to Assess Physical Load

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[Purpose] Blood collection, the clinical starting point for specimen testing, is critical for ensuring the reliability of diagnostic data. However, associated stress triggers sympathetic activation and catecholamine secretion, which can induce transient pseudo-hyperglycemia by promoting gluconeogenesis and inhibiting glucose utilization. This study quantitatively evaluated the impact of physical stress on laboratory values using heart rate reserve (HRR) to account for individual variability. We aim to examine the correlation between plasma catecholamine dynamics and blood glucose levels to better understand stress-induced physiological changes. **[Methods]** The subjects were six healthy adults in their 20s (3 males, 3 females) without regular exercise habits. Following a fast of at least 10 hours and 30 minutes of supine rest, baseline blood samples were collected. Subsequently, exercise loads corresponding to 40% and 70% HRR were administered. Blood samples were collected immediately after exercise, as well as at 1, 2, and 5 minutes post-exercise. Plasma adrenaline, plasma noradrenaline, and blood glucose levels were measured at each time point to compare their respective dynamics. **[Results]** A significant increase in plasma catecholamine levels, particularly plasma noradrenaline, was observed in response to exercise load. Comparing intensities, high-intensity load (70% HRR) induced a more pronounced increase in plasma noradrenaline compared to moderate-intensity load (40% HRR). Blood glucose levels also demonstrated a significant increase immediately following exercise at the 70% HRR intensity. **[Conclusion]** This study demonstrated positive correlations between HRR, plasma catecholamines (adrenaline, noradrenaline), and blood glucose levels. Significant noradrenaline elevation at 70% HRR suggests stress-induced sympathetic activation directly impacts glucose metabolism. However, slight adrenaline and glucose increases indicate load conditions may have missed peak secretion. Future research must refine these conditions to further elucidate quantitative relationships between stress markers and metabolic fluctuations.

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P-4-15

一般演題 Clinical Chemistry

Association of CK-MB Inter-Reagent Variability with M/B Subunit Reactivity

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Introduction: Creatine kinase (CK)-MB activity is widely used as an indicator of myocardial injury. CK-MB activity is commonly measured using the immunoinhibition method, in which the M-type subunit is inhibited and the remaining B-type activity is doubled to estimate CK-MB activity. However, our recent study showed that the M-type subunit has approximately 1.3-fold higher activity than the B-type. Therefore, this study aimed to evaluate inter-reagent variability in CK-MB activity and to investigate its relationship with the relative reactivity of the M and B subunits.

Subjects and Methods: CK-MB assay reagents from three Japanese manufacturers—Kanto Chemical (Company K), FUJIFILM Wako Pure Chemical (Company F), and Sino-Test (Company S)—were evaluated. Seven samples, including CK-MB calibrators and control materials, were analyzed. CK and CK-MB activities were measured using each reagent system under routine conditions. Calibration was performed using both manufacturer-provided calibrators and K-factors. CK isoenzyme fractions in the calibrators were analyzed by electrophoresis.

Results: Total CK activity were comparable among the three manufacturers. In contrast, CK-MB activity was higher with Company S reagents than with the other two. The CK-MB/CK-B ratio ranged from 2.3 to 2.4 for Company S, whereas it ranged from 1.9 to 2.0 for Companies K and F. Electrophoretic analysis revealed that the calibrator from Company S consisted predominantly of a single CK-MB isozyme, whereas those from Companies K and F contained multiple isozyme components.

Discussion: Two manufacturers reported CK-MB values approximately twice as high as CK-B activity, which was consistent with previous expectations. However, one manufacturer reported a value approximately 2.3 times higher. These differences may be attributable to variations in subunit reactivity. The results suggest that differences between reagents can be corrected when the same calibrator is used.

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P-4-16

一般演題 Clinical Chemistry

Method Bias in CEA Measurement

Clinical Threshold Effects on Classification Discordance

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Purpose: Carcinoembryonic antigen (CEA) is widely used for tumor monitoring, and variability between analytical methods may influence clinical classification near the 5 ng/mL threshold. This study evaluated differences between chemiluminescent microparticle immunoassay (CMIA) and radioimmunoassay (RIA) and their impact on clinical classification.

Methods: A retrospective comparison was conducted using laboratory data collected between January 1, 2026 and April 20, 2026 at a regional teaching hospital. CEA results generated by the Abbott Alinity ci system for CMIA and the Packard COBRA II 5010 system for RIA were compared at the patient level. A total of 767 patient-level records were identified. Records with non-numeric results were excluded from quantitative analysis. Therefore, 654 analyzable records were included in the final classification analysis. Classification discordance was evaluated using a cut-off value of 5 ng/mL.

Results: Among the 654 analyzable records, 80 cases (12.23%) showed classification discordance, including 60 cases (9.17%) with CMIA >5 / RIA <5 and 20 cases (3.06%) with CMIA <5 / RIA >5. Classification discordance was predominantly unidirectional, with CMIA >5 / RIA <5 occurring three times more frequently than the opposite pattern. Classification discordance was mainly concentrated around the clinical threshold, approximately 3–8 ng/mL.

Conclusion: CMIA and RIA showed clinically relevant classification discordance in approximately 12% of analyzable records. These findings suggest method-related bias around the clinical threshold and support consistent use of the same assay for longitudinal follow-up and interpretation.

P-4-17

一般演題 Clinical Chemistry

%CDT and FIB-4 in ALD Diagnosis and Fibrosis Staging

Complementary Roles of %CDT and FIB-4 in Clinical Assessment

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Evaluation of the Association Between Carbohydrate-Deficient Transferrin (CDT), Routine Liver Enzymes, and Fibrosis-4 index (FIB-4) in the Diagnosis and Fibrosis Staging of Alcohol-associated liver disease.

Introduction: Early detection of chronic alcohol exposure and liver fibrosis is crucial for Alcohol-associated liver disease (ALD) management. This study evaluated the relationships between alcohol markers (%CDT, *r*-GT, MCV) and fibrosis predictors (FIB-4, AST/ALT), using FibroScan as a reference.

Methods: We retrospectively included 90 ALD patients (aged ≥20) with measurements of %CDT, liver enzymes, and liver stiffness. Patients with viral hepatitis or other confounding systemic illnesses were excluded. ROC analysis and multivariable logistic regression evaluated diagnostic performance and fibrosis associations.

Results: FIB-4 stratification identified 25 low-risk, 47 intermediate-risk, and 18 high-risk patients. High-risk groups showed strong correlation with F3–F4 stages (P<0.001). Age, AST, ALT, MCV, and r-GT increased with FIB-4 risk, while platelet count decreased. Median %CDT did not differ significantly between groups (P=0.257) but showed a modest correlation with FIB-4 (ρ=0.264), reflecting alcohol exposure rather than fibrosis severity. ROC analysis confirmed FIB-4 as the best serum predictor (AUC= 0.880), while %CDT had limited fibrosis diagnostic value (AUC= 0.565). Multivariable regression identified FIB-4 as an independent predictor (aOR=3.82, P<0.001).

Discussion: FIB-4 reliably identifies significant fibrosis in ALD, whereas %CDT reflects chronic alcohol consumption. Despite %CDT's limited predictive value for fibrosis severity , it remains clinically relevant for confirming alcohol intake. Our findings support using %CDT and FIB-4 as complementary markers: %CDT confirms consumption, while FIB-4 assesses liver injury. Combining both enables comprehensive, stratified evaluation to guide early intervention.

P-4-18

一般演題 Clinical Chemistry

Evaluation of Alternative Centrifugation Settings for Routine Chemistry Samples

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Centrifugation is a crucial pre-analytical step influencing sample quality and turnaround time (TAT). Manufacturers provide recommended parameters, but laboratories may optimize centrifugation settings to improve efficiency. This study compared a manufacturer-recommended protocol against a shorter, higher-speed protocol to assess equivalency and potential TAT reduction.

Blood samples from 20 volunteers were collected in duplicate sets of fluoride, plasma separator (PST) and serum tubes. One set was centrifuged at 1800 x *g* for 10 minutes using a swing-bucket centrifuge (manufacturer-recommended). The paired set was processed on the Roche cobas 8100 at 2250 x *g* for 8 minutes (laboratory-proposed). Post-centrifugation evaluation included inspection of plasma/serum separation, gel barrier integrity, fibrin/clot presence, and hemolysis. Hemolysis-sensitive analytes – Troponin T, potassium, lactate dehydrogenase (LDH), aspartate aminotransferase (AST) and alkaline phosphatase (ALP) – were measured to determine any clinical impact.

Among 40 paired sample sets, one PST tube showed fibrin presence at manufacturer-recommended setting; all others demonstrated adequate separation with intact gel barriers. No visible hemolysis was observed. Strong analytical concordance observed between both centrifugation protocols.

The laboratory-proposed centrifugation setting demonstrated equivalent performance to the manufacturer-recommended protocol. Adoption of this alternative setting can reduce TAT without compromising analytical quality.

This study evaluated a limited range of tube types and analytes. Broader validation across additional tube types, manufacturers, and biochemical parameters is required before general implementation.
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P-4-19

一般演題 Clinical Chemistry

Evaluation of Surfactants added to Automated Clinical Chemistry Reagents

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Background: The selection of surfactant type and concentration in reagents for automated clinical chemistry analyzers lacks clear criteria and is often empirical. Surfactants may also lyse contaminating blood cells, adversely affecting analytical results. This study aimed to evaluate whether contact angle and surface tension measurements can be used to assess surfactant performance and to establish a rational method for selecting suitable surfactants.
Methods: Eight nonionic surfactants were added to reagents for serum lactate dehydrogenase (LD) activity measurement. Contact angle, surface tension, and within-run precision were evaluated. Serial dilutions of each surfactant were mixed with whole blood to assess erythrocyte membrane damage. In addition, the effects of erythrocyte contamination on 25 routine biochemical test parameters were examined.
Results: Reagents containing Triton X-114 showed the lowest contact angle and surface tension, indicating superior wettability. Within-run precision of LD activity measurements showed coefficients of variation below the allowable CVA in all reagents tested. However, erythrocyte membrane damage was observed at a surfactant concentration of 0.01% for all surfactants. Erythrocyte contamination affected multiple parameters, with the most pronounced effect observed in LD activity.
Conclusions: Surfactants improve measurement stability by reducing interfacial energy and suppressing bubble formation and adhesion to the reaction cell wall. Although Triton X-114 showed high performance, phenyl-containing surfactants are listed as substances of very high concern (SVHC) under the REACH regulation in Europe and are restricted unless authorized. While not currently regulated in Japan, potential future restrictions highlight the need for environmentally friendly alternatives. In this study, Brij 35 demonstrated the best performance among low-environmental-impact surfactants and is considered suitable for use in clinical chemistry reagents. Contact angle and surface tension measurements were found to be useful indicators for evaluating surfactant performance.

P-4-20

一般演題 Clinical Chemistry

Short-chain fatty acids bias ion-selective electrode chloride measurements

Evidence from a method comparison with LC-MS/MS

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Background: Ion-selective electrodes (ISEs) are widely used for routine chloride measurement but are known to be susceptible to analytical interference from various substances. Such interference may lead to clinically misleading results, particularly in samples with complex biochemical composition. Unexpectedly elevated chloride concentrations are occasionally observed in decomposed biological fluids when measured using ISEs. Because decomposition leads to the accumulation of short-chain fatty acids (SCFAs), we hypothesized that these organic acids may interfere with chloride measurement and produce a positive analytical bias.
Methods: We analyzed pleural fluid samples obtained from autopsy cases (n = 36). Total SCFA concentrations were quantified, and chloride concentrations were measured using both routine ISE and reference liquid chromatography–tandem mass spectrometry (LC–MS/MS) methods. The discrepancy between the two methods (ΔCl) was evaluated using regression analyses, including models with interaction terms for decomposition status defined by β-phenethylamine detection. All statistical analyses were performed to assess the strength and independence of these associations.
Results: SCFA concentrations were markedly higher in decomposed samples. ISE-derived chloride measurements showed a strong positive bias in association with SCFA concentration ($B = 1.079$, $p < 0.001$; $R^2 = 0.912$). Furthermore, regression analysis identified a significant interaction effect ($p = 0.025$), indicating that the magnitude of this bias varied according to decomposition status. The interaction model accounted for 93.4% of the variability in ΔCl.
Conclusion: Elevated SCFA concentrations were strongly associated with positive bias in chloride measurements obtained by ISEs. These findings suggest that organic acids generated during decomposition can cause substantial analytical interference in chloride assays. Awareness of this effect may improve the interpretation of chloride measurements in complex biological samples.

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P-4-21

一般演題 Clinical Chemistry

Combined AFP, PIVKA-II, and GPC3 for Improved HCC Diagnosis.

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Background： Hepatocellular carcinoma (HCC) is a leading cause of cancer mortality, often diagnosed at advanced stages due to biological heterogeneity. While imaging and serum AFP are standard for surveillance, early detection via diverse biomarkers remains critical for improving prognosis. Promising circulating markers like PIVKA-II and GPC3 offer potential for more precise, individualized diagnostic strategies. **Methods：** The diagnostic performance of three circulating biomarkers - alpha-fetoprotein (AFP), protein induced by vitamin K absence-II (PIVKA-II), and glypican-3 (GPC3) was evaluated for the detection of hepatocellular carcinoma (HCC). Receiver Operating Characteristic (ROC) curves were constructed to determine the sensitivity and specificity of each individual marker. Furthermore, a logistic regression-based model was developed to integrate these three biomarkers into a combined diagnostic tool. Statistical analysis focused on comparing the Area Under the Curve (AUC) between the individual markers and the multi-marker combined model. **Results：** Among standalone markers, PIVKA-II showed the best performance (AUC 0.84), while the combined model (AFP 、 PIVKA-II and Glypican-3) achieved the highest accuracy (AUC 0.89). Although individual markers reached 100% specificity, their sensitivity was limited. The combined model significantly improved sensitivity to 81.1% while maintaining 97.2% specificity, proving the multi-marker approach superior for HCC screening. **Conclusion：** The integration of AFP, PIVKA-II, and GPC3 into a unified diagnostic model significantly improves the detection of HCC compared to conventional single-marker assays. This multi-biomarker approach facilitates earlier diagnosis and supports the implementation of more effective, personalized clinical interventions.

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一般演題 Clinical Chemistry

Novel ELISA Measuring sPTPRZ Using Glycan Standard for Glioma Diagnosis

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Glioma is one of the most common primary brain tumors and is associated with poor prognosis. Its diagnosis remains challenging due to the lack of reliable fluid biomarkers and the limited specificity of imaging, often necessitating invasive brain biopsy. We previously demonstrated that protein tyrosine phosphatase receptor type Z (PTPRZ) mRNA is significantly elevated in glioma tissues compared with normal brain tissue. Furthermore, soluble PTPRZ (sPTPRZ) levels are increased in the cerebrospinal fluid (CSF) of glioma patients. PTPRZ is heavily glycosylated, and the human natural killer-1 (HNK-1) epitope, characterized by a sulfated glucuronic acid–containing trisaccharide, is specifically expressed in neural tissues.

In this study, we developed a novel enzyme-linked immunosorbent assay (ELISA) to quantify sPTPRZ in CSF using a monoclonal IgG antibody targeting the HNK-1 glycan. The assay employed anti-HNK-1 antibodies for both capture and detection. Recombinant sPTPRZ was initially used as a standard and enabled differentiation between glioma and primary central nervous system lymphoma (PCNSL), but it exhibited significant lot-to-lot variability. To address this limitation, a synthetic HNK-1 glycan (propyl-biotin)–streptavidin (6:1) complex was adopted as a stable standard.

Analytical validation demonstrated good performance, including repeatability, intermediate precision, an appropriate measurement range, and no prozone effect. Clinical application revealed significantly elevated sPTPRZ levels in glioma patients compared with other disease groups, suggesting that this ELISA system is a promising minimally invasive diagnostic tool for glioma.

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P-4-23

一般演題 Clinical Chemistry

Investigation of Methotrexate-Induced Interference in Urinary NAG Measurement

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[Background] Methotrexate (MTX) is administered in high doses for the treatment of leukemia and osteosarcoma. Approximately 80–90% of MTX is excreted unchanged in the urine, and in cases of acidic urine, it may cause obstructive renal failure due to crystal deposition. We encountered a patient receiving MTX who exhibited an abnormal reaction curve in the urinary NAG assay, despite having alkaline urine. Therefore, we investigated the interference of MTX on the urinary NAG assay using the patient's urine and MTX solution. [Reagents and Methods] N-acetyl-β-D-glucosaminidase (NAG) levels were quantified using the N-Assay L NAG (Nittobo Medical Co., Ltd.) on a TBA-FX8 clinical chemistry analyzer (Canon Medical Systems Corporation). In the mixing tests, 1.5 mL of R1 reagent was added to 100 μL of pooled urine (normal control), patient urine (MTX: 43,560 μmol/L), or an MTX solution (55,016μmol/L), and the reaction process was visually monitored. In the addition test, MTX solution (55,016μmol/L) and patient urine (MTX: 43,560 μmol/L) were added to pooled urine at ratios ranging from 0.5:9.5 to 9:1, and their impact on the measurement was evaluated. [Results and Discussion] In the mixing test, crystal formation was observed in the patient urine and MTX solution, but not in the pooled urine. In the addition tests, NAG was measurable up to an added MTX solution concentration of 2,750μmol/L; however, at concentrations of 5,501μmol/L or higher, the measurements were inconsistent and considered unmeasurable. In the patient urine samples, NAG was measurable up to an added urinary MTX concentration of 8,712 μmol/L, whereas concentrations of 13,068 μmol/L or higher were not measurable. These findings suggest that MTX concentration-dependent interference exists in the measurement of urinary NAG. It is highly likely that the decrease in MTX solubility due to pH changes in Reagent R1 and the resulting crystallization of MTX caused the abnormal absorbance. Therefore, high MTX concentrations may affect urinary NAG results, and further investigation into the effects of reagent composition and pH is necessary.

P-4-24

一般演題 Clinical Chemistry

Glycan analysis of apoE, a risk factor for Alzheimer's disease.

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Alzheimer's disease (AD), the most common form of dementia, is characterized by the accumulation of amyloid-β (Aβ) aggregates in the brain, which trigger tau pathology, neuronal loss, and progressive cognitive decline from mild cognitive impairment (MCI) to dementia. Apolipoprotein E (apoE) exists as three major isoforms—apoE2, apoE3, and apoE4—with the apoE4 allele representing the strongest genetic risk factor for late-onset AD. In addition to its central role in lipid transport, apoE directly interacts with Aβ and influences its aggregation and clearance. Notably, individuals carrying the apoE4 allele show increased Aβ deposition and accelerated disease progression. Despite these insights, post-translational modifications of apoE, particularly glycosylation, remain insufficiently characterized, and isoform-specific glycosylation differences have not been systematically investigated.

In this study, we analyzed apoE glycosylation across isoforms using both recombinant expression systems and clinical samples. ApoE-His was expressed in HEK293FT cells and purified via nickel affinity chromatography. In parallel, viral vectors encoding apoE-His were produced in Plat-GP cells and used to infect U251 and HMC3 cells, enabling stable expression and secretion of apoE. Secreted proteins were collected from culture supernatants and purified for analysis. Furthermore, apoE was immunoprecipitated from serum and cerebrospinal fluid samples obtained from patients with normal pressure hydrocephalus. All samples were subjected to LC-MS/MS-based glycosylation analysis and classified by apoE isoform.

Our results revealed isoform-dependent differences in glycosylation patterns of apoE, particularly in recombinant proteins expressed in HEK293FT cells. These findings suggest that glycosylation may contribute to functional differences among apoE isoforms and may influence Aβ metabolism and AD pathogenesis, providing a potential basis for future biomarker and therapeutic studies.

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P-4-25

一般演題 Clinical Chemistry

Cardiac Biomarker Dynamics in Fabry Disease Myocardial Involvement

Clinical Implications of Biochemical Indicators for Early Detection of Cardiac Injury

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PURPOSE

To evaluate the dynamic changes in cardiac biomarkers associated with myocardial involvement in Fabry disease, and to assess their utility as sensitive indicators for early detection and disease monitoring.

METHODS

Serial cardiac biomarker data from a 64-year-old female patient with confirmed Fabry disease were retrospectively analyzed. Parameters included Troponin I, creatine kinase-MB (CK-MB), creatine phosphokinase (CPK), and N-terminal pro-B-type natriuretic peptide (NT-proBNP). Biochemical findings were correlated with histopathological results from endomyocardial biopsy, globotriaosylceramide (Gb3) immunostaining, and ultrastructural findings from electron microscopy.

RESULTS

Troponin I demonstrated marked dynamic fluctuation, rising from 0.018 ng/mL to a peak of 0.612 ng/mL before declining to 0.235 ng/mL, reflecting active myocardial injury. In contrast, CK-MB (11.9 → 6.5 ng/mL) and CPK (191 → 127 IU/L) exhibited a progressive downward trend. NT-proBNP was elevated at 526.3 pg/mL, indicating subclinical cardiac stress. Histopathological examination revealed vacuolation of cardiomyocytes and diffuse Gb3 deposition, while electron microscopy identified characteristic lamellar inclusions (zebra bodies), collectively confirming significant myocardial involvement.

CONCLUSION

Troponin I serves as a highly sensitive and dynamically responsive biomarker for myocardial injury in Fabry disease. The integration of serial biochemical monitoring with histopathological and ultrastructural findings provides a comprehensive approach for early diagnosis and longitudinal disease surveillance in this rare lysosomal storage disorder.

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P-4-26

一般演題 Clinical Chemistry

Hypercalcemia Differentiation in Lung Cancer with Concurrent Hyperparathyroidism

Biochemical Markers and Imaging Integration for Accurate Differential Diagnosis

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[PURPOSE]Hypercalcemia frequently occurs in patients with malignancy; however, its etiology may reflect either humoral hypercalcemia of malignancyor primary hyperparathyroidism—two conditions with distinct pathophysiological mechanisms and therapeutic implications. This study evaluates the diagnostic utility of serial biochemical markers in differentiating these etiologies in a patient with concurrent lung cancer and hypercalcemia.
[METHODS]Serial biochemical data were analyzed for a 54-year-old female with confirmed lung cancer presenting with hypercalcemia. Parameters included ionized calcium, intact parathyroid hormone (iPTH), serum electrolytes, and liver enzymes. Findings were correlated with Technetium-99m sestamibi (MIBI) scintigraphy to identify the anatomical source of parathyroid overactivity.
[RESULTS]Persistent hypercalcemia was documented across serial measurements (ionized Ca^{2+}: 6.54, 6.51, and 5.55 mg/dL). iPTHwas markedly elevated at 249.02 pg/mL, a finding inconsistent with HHM, in which PTH suppression is the expected hallmark. MIBI scintigraphy demonstrated intense focal uptake in the right inferior parathyroid region, consistent with parathyroid adenoma. Concurrent findings included hypokalemia (2.9–3.2 mmol/L), mild transaminitis (alanine aminotransferase: 49–73 IU/L), and normocytic anemia (hemoglobin: 9.3–9.9 g/dL), collectively reflecting systemic disease burden.
[CONCLUSION]In patients with malignancy-associated hypercalcemia, paradoxically elevated iPTH is a critical indicator of coexisting PHPT rather than HHM. The integration of serial biochemical markers with functional imaging enables accurate differential diagnosis, thereby preventing misattribution of hypercalcemia to tumor progression and guiding appropriate clinical intervention. This case highlights the indispensable role of biomedical laboratory science in navigating complex metabolic presentations.
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一般演題 Clinical Chemistry

Severe Hypocalcemia After Thyroidectomy

A Time-Series Laboratory Analysis of Postoperative Hypoparathyroidism

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PURPOSE
Post-thyroidectomy hypocalcemia is a life-threatening complication. This case report aims to clarify its pathophysiological mechanism through serial laboratory data and to highlight the diagnostic value of integrated time-series biochemical interpretation.
METHODS
A 30-year-old male with thyroid malignancy underwent total thyroidectomy and developed postoperative hypoparathyroidism. Serial laboratory data—including ionized calcium (Ca^{2+}), thyroid function tests (Free T4, TSH), parathyroid hormone (PTH), and thyroglobulin—were retrospectively analyzed.
RESULTS
Ionized calcium declined progressively (3.38 → 2.77 → 2.58 mg/dL), reaching a critically low threshold. Concurrently, PTH was inappropriately low (4.21 pg/mL), indicating severely impaired parathyroid function. Thyroid function tests remained stable, excluding thyroid hormone dysregulation as the primary etiology. Thyroglobulin was consistently suppressed (<0.3 ng/mL), consistent with postoperative thyroid ablation. The concordance of hypocalcemia and subnormal PTH strongly supports postoperative hypoparathyroidism due to parathyroid gland injury or devascularization. Reduced PTH further impairs renal calcium reabsorption, vitamin D activation, and intestinal calcium absorption, collectively exacerbating hypocalcemia.
CONCLUSION
Time-series interpretation of ionized calcium and PTH provides a robust diagnostic framework for postoperative hypoparathyroidism. Serial monitoring of these analytes enables early recognition and timely intervention. These findings underscore the essential role of laboratory medicine in assessing postoperative metabolic complications and guiding clinical decision-making.

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P-4-28

一般演題 Clinical Chemistry

Fasting Glucose and BMI in the Hong Kong Population

A Retrospective Cohort Study

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Abstract

Background: The global rise in diabetes and obesity presents significant health challenges. In Hong Kong, the relationship between fasting plasma glucose (FPG) and body mass index (BMI) remains insufficiently explored. Clarifying this association and identifying optimal BMI ranges for blood glucose changes may facilitate earlier intervention, reduce healthcare costs, and enhance public health outcomes in Hong Kong.
Methods: A total of 61,881 anonymous records collected from 2016 to 2023 at a HOKLAS-accredited laboratory in Hong Kong were analyzed. The dataset included age, gender, and collection date. Height, weight, and FPG were measured according to standard procedures, with FPG assessed using the ARCHITECT c8000 system. BMI was calculated as weight in kilograms divided by height in meters squared. Glycaemic status was determined using the 2025 American Diabetes Association (ADA) criteria, and World Health Organization (WHO) BMI cutoffs for Asians were applied. The association between FPG and BMI was examined using Pearson's correlation.

Results: The median BMI among participants was 23.06 kg/m^2, and the median FPG was 5.23 mmol/L. Diabetes was identified in 4.1% of the cohort. A significant positive association was observed between FPG and BMI ($r = 0.242$, $P < 0.005$). Individuals with obesity exhibited more than double the risk of diabetes compared to those with a BMI below 25 kg/m^2 (odds ratio 2.11, 95% CI 2.01–2.21). Receiver operating characteristic (ROC) analysis indicated optimal BMI cutoffs of 24.55 kg/m^2 for diabetes (AUC = 0.707) and 23.21 kg/m^2 for pre-diabetes (AUC = 0.670). Pearson's chi-square test further demonstrated a strong association between diabetes status and BMI categories ($\chi^2 = 3639.524$, $df = 3$, $N = 61,881$, $P < 0.005$).
Conclusion: This study identified a positive association between FPG and BMI. The BMI cutoffs determined are consistent with WHO guidelines for Hong Kong and may assist in assessing population health risks.

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一般演題 Clinical Chemistry

BMI and Uric Acid Levels in the Hong Kong Population

A Retrospective Cohort Study

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Abstract

Background: The gradual increase in the prevalence of obesity and hyperuricemia globally is remarkable. Some studies have found that the prevalence of overweight and obesity in males is significantly higher before the age of 45, and the rate of hyperuricemia is also higher in males. While research worldwide has found a positive correlation between body mass index (BMI) and serum uric acid (SUA) levels, there has been no specific research on this situation in Hong Kong. This study aimed to examine the correlation between BMI and SUA levels in the Hong Kong population.

Methodology: A total of 61,862 participants were selected from a Laboratory Information System (LIS) at a private laboratory in Hong Kong between 2016 and 2023. Five milliliters (ml) of fasting blood were collected and analysed for SUA levels after centrifugation. The ages, sexes, heights, and weights of all participants were also recorded. For the analysis of sex differences, data were categorised as female or male.

Results: The results showed that the prevalence of overweight, obesity, and SUA levels is significantly associated with sex in Hong Kong. Males had a significantly higher rate of overweight, obesity, and hyperuricemia. Interestingly, the positive correlation between BMI and SUA levels was considerably stronger in females than in males within the Hong Kong cohort.

Conclusion: Unhealthy eating habits, alcohol consumption, lack of physical activity, and hormonal disparities between genders correspond to a higher rate of overweight and obesity associated with elevated SUA levels in Hong Kong, especially in males. It is recommended that a more nutritious diet and regular exercise be maintained to help reduce obesity and hyperuricemia risks.

Keywords: *BMI; Dietary; Lifestyle pattern; Physical activity; Uric acid.*

P-4-30

一般演題 Clinical Chemistry

Analytical Evaluation of Roche Tina-quant Hemoglobin A1c Generation 4 Assay

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Hemoglobin A1c (HbA1c) measurement is a key parameter in monitoring long-term glycemic control. The Tina-quant Hemoglobin A1cDx Gen.4 (A1CX4) assay was developed with a change from polyclonal to monoclonal antibody technology, reflecting evolving regulatory considerations related to animal welfare. The assay remains standardized against IFCC and DCCT/NGSP reference systems. Evaluation of its analytical performance compared with the previous generation (A1CX3) is necessary to determine suitability for routine laboratory use.

This study evaluated the analytical performance of the A1CX4 assay compared with its predecessor (A1CX3) using CLSI-based protocols for precision, linearity and method comparison.

Precision was assessed using two levels of quality control. Linearity was evaluated using commercial linearity materials, and method comparison was performed using 46 patient specimens. Within-run and total CV were <1.0, meeting manufacturer's criteria. The assay demonstrated excellent linearity (4.3 – 20.3%) with deviations <6.5%. Method comparison showed strong correlation (R=0.9987; slope: 0.950; intercept: 0.390). Semi-quantitative analysis yielded 95.5% agreement and Cohen's Kappa of 92.6%, indicating good concordance.

The Roche Tina-quant HbA1cDx Gen.4 assay demonstrates excellent analytical performance and equivalence to its predecessor while integrating monoclonal antibody technology that supports ethical reagent development. It's precision, linearity and traceability confirm suitability for routine clinical use and continued standardization to IFCC and NGSP systems.

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P-4-31

一般演題 Clinical Chemistry

Implementing Artificial Intelligence in Clinical Chemistry

Concise Review and Recommendations

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Abstract: Artificial intelligence (AI) is transforming clinical chemistry and laboratory medicine, offering solutions across the total testing process (TTP). Machine learning, deep learning, and natural language processing applications now address pre-analytical error detection, analytical quality assurance, post-analytical interpretation, evidence-based laboratory management, and value-based laboratory medicine.

Research demonstrates impressive technical performance with an algorithm that could improve error detection for test recommendation systems. However, a significant translation gap persists between academic prototypes and clinical deployment.

This concise review examines current applications, practical implementation strategies, regulatory considerations, and future directions, emphasizing that successful AI adoption requires multicenter validation, workflow integration, robust data governance, and the indispensable role of the clinical scientist and chemical pathologist in maintaining human oversight in the risk management of patient care and safety.

Keywords: Artificial intelligence, clinical chemistry, laboratory medicine, machine learning, ISO 15189, total testing process, laboratory automation

P-4-32

一般演題 Clinical Chemistry

Serum Uric Acid and Fatty Liver Severity

A hospital-based cross-sectional study in Taiwan

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Purpose
Elevated serum uric acid is closely associated with metabolic dysfunction and may contribute to steatotic liver disease. However, its relationship with fatty liver severity remains incompletely characterized in real-world Asian populations. We aimed to evaluate the association between serum uric acid levels and ultrasonographic fatty liver severity in a hospital-based cohort.

Methods
This cross-sectional study used an institutional health database from southern Taiwan. Adults with available serum uric acid measurements and liver ultrasonographic grading were included. Fatty liver severity was classified as none, mild, moderate, or severe. Serum uric acid was analyzed in relation to fatty liver severity using trend analysis and ordinal logistic regression. Multivariable models were adjusted for demographic, glycemic, lipid, and renal parameters.

Results
A total of 3,722 participants were included in the preliminary analysis. Mean serum uric acid levels increased progressively with fatty liver severity, from 5.97 mg/dL in participants without fatty liver to 6.39 mg/dL in mild disease, 6.84 mg/dL in moderate disease, and 7.01 mg/dL in severe disease. Preliminary adjusted analyses also supported a positive association between higher serum uric acid levels and greater fatty liver severity.

Conclusion
Higher serum uric acid levels were associated with more severe ultrasonographic fatty liver disease in this hospital-based cohort. Serum uric acid may serve as an accessible clinical marker associated with steatotic liver severity. Further studies are needed to clarify the interplay among uric acid, adiposity, and metabolic dysfunction.

P-4-33

一般演題 Clinical Chemistry

Evaluating the performance of Apexbio Glucosure POC

Apexbio Glucosure POC

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Background
Point-of-Care Testing (POCT) for Glucose is typically performed by nurses in wards or clinical units, and the results have a direct impact on patient care. International standards, including ISO 15189 medical laboratory accreditation, CAP (College of American Pathologists) certification, and hospital accreditation standards, all maintain strict regulations regarding the quality management of POCT. This underscores the global emphasis on the quality of decentralized testing.
The purpose of this study was to analyze the performance of the Apexbio Glucosure POC Professional Glucose Monitoring System by comparing it with the Beckman AU5800 to determine if the system is suitable for clinical POCT Glucose testing.
Materials and Methods
1. Accuracy: Six CAP proficiency testing samples were collected and tested once each.
2. Precision:
· Within-Run Evaluation: Two different concentrations of quality control (QC) material were tested 20 consecutive times.
· Between-Day Evaluation: Samples were tested four times daily over five consecutive days.
3. Correlation: 40 patient samples were tested between the two instruments.
Results
1. Accuracy: The values for all six samples fell within the acceptable range defined by CAP standards.
2. Precision: In both Within-Run and Between-Day evaluations, the results for Level 1 (SD:1.5,1.6)and Level 3 (CV: 1.2%; 1.6%) met the acceptance criteria (L1: SD).
3. Correlation: The correlation coefficient (R2) between the different instruments was 0.98, which satisfies the acceptance standard of R2 >=0.95.
Conclusion
In accordance with ISO 15189 standards, the laboratory is responsible for the oversight of all POCT within the hospital; using this specific model facilitates more effective management. Since the results meet all laboratory validation and verification protocols, we have decided to adopt the Apexbio Glucosure POC Professional Glucose Monitoring System for POCT Glucose testing.

P-4-34

一般演題 Clinical Chemistry

Exploring Multiple Myeloma from a Laboratory Medicine Perspective

A Case Study of Laboratory Analysis in a Patient with Hyperglobulinemia

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Background
Multiple Myeloma (MM) frequently affects the elderly and often presents with non-specific clinical symptoms. This case study explores how laboratory professionals can identify abnormal protein data during preliminary biochemical screening and initiate protein electrophoresis. This process facilitates early diagnosis and assists clinicians in monitoring the progression of "CRAB" criteria (specifically anemia and bone lesions).
Case History
A 71-year-old female patient was admitted with back pain and multiple fractures of the thoracic and lumbar spine. Initial laboratory biochemical analysis revealed extreme abnormalities in protein metabolism:
· Total Protein (TP): 14.4 g/dL
· Albumin (Alb): 3.0 g/dL
· Globulin: 11.4 g/dL
· Hemoglobin (Hb): 6.2 g/dL (severe anemia)
· Urine ACR: 477.9 mg/g (abnormal microalbuminuria)
Laboratory Diagnosis
Given the extreme deviation of total protein and globulin levels, the following confirmatory tests were performed:
1.Serum Protein Electrophoresis (SPEP): A prominent monoclonal peak (M-peak) was detected in the Gamma region, with a fraction as high as 55.2% (Reference range: 9.8-24.4%).
2.Immunofixation Electrophoresis (IFE): Qualitative analysis confirmed IgG-Kappa type monoclonal immunoglobulin proliferation.
Final Assessment: Integrated laboratory data and imaging findings confirmed the diagnosis of MM accompanied by severe organ damage. Conclusion
This case demonstrates that laboratory sensitivity to "significantly elevated total protein" and "severe anemia" is a critical threshold for diagnosing MM. By employing standardized SPEP and IFE follow-up protocols, the laboratory does more than provide data; it actively guides the diagnostic direction, playing a central role in preventing the exacerbation of pathological fractures and evaluating patient prognosis.

P-4-35

一般演題 Clinical Chemistry

RISK FACTORS FOR ABNORMAL BIRTH WEIGHT, A RETROSPECTIVE STUDY

RISK FACTORS FOR ABNORMAL BIRTH WEIGHT, A RETROSPECTIVE STUDY

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Background: Abnormal birth weight (ABW), including low birth weight (LBW) and macrosomia, remains a critical challenge for neonatal health in developing countries. In Ghana, LBW prevalence is approximately 13.0%, yet data on localized risk factors remains sparse. This study compared risk factors for LBW and macrosomia at a hospital in the Ashanti Region, Ghana.
Methods: A retrospective cross-sectional study analyzed maternal register data for 619 newborns delivered between January and December 2022. Sociodemographic, obstetric, and labor-related variables were evaluated. Data were analyzed using SPSS v26.0 and GraphPad Prism v8.0. Multivariate logistic regression identified independent predictors for ABW.
Results: The overall prevalence of ABW was 12.4% (LBW: 8.4%; macrosomia: 4.0%; NBW: 84.2%). Most ABW cases occurred in mothers aged 20–29 years. Multivariate analysis showed that LBW was independently associated with nulliparity [aOR=2.635, 95% CI (1.162-5.975), p=0.020], multiparity [aOR=2.275, 95% CI (1.192-4.340), p=0.013], male sex [aOR=1.897, p=0.031], and a low 1-minute Apgar score [aOR=4.500, p=0.031]. Head circumference <33.0cm was protective against LBW. Macrosomia was independently associated with nulliparity [aOR=2.308, p=0.020] and male sex [aOR=3.113, p=0.030]. Conversely, neonatal length <55cm and Cesarean section delivery [cOR=0.382, p=0.021] were protective against macrosomia.
Conclusion: The 12.4% prevalence of ABW underscores a significant clinical burden. Nulliparity and male fetal sex were shared risk factors across the ABW spectrum. These findings suggest that targeted prenatal monitoring based on parity and fetal growth metrics could improve birth outcomes in low-resource settings.
Keywords:Abnormal Birth Weight, Low Birth Weight, Macrosomia, Neonatal Health, Ghana, Risk Factors.
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一般演題 Clinical Chemistry

Clinical, Biochemical, and Socioeconomic Profiles Correlating with Polycystic Ovary Syndrome

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With the rising prevalence of Polycystic Ovary Syndrome (PCOS) in the Philippines, women of reproductive age often face significant reproductive and metabolic abnormalities that serve as a substantial health burden. Consequently, women with PCOS, being affected by a complex endocrine and metabolic disorder, are constantly faced with varying clinical and biochemical manifestations, largely due to a connection between biological, environmental, and socioeconomic factors.

Thus, this study aimed to establish the relationship among the clinical features, biochemical parameters, and socioeconomic status of women diagnosed with PCOS in a clinical setting in Tarlac City.

Moreover, the researchers employed a quantitative descriptive-correlational approach with data gathered from women aged 18 to 49 at a specialized medical clinic in Tarlac. The data were collected through adapted survey questionnaires, including the Modified Kuppuswamy Socioeconomic Scale, and laboratory analysis, then analyzed using both descriptive and inferential statistics. Specifically, correlational analysis was utilized to examine the relationship between participants' socioeconomic status and their biochemical and clinical manifestations, such as glycated hemoglobin (HbA1c) and lipid profiles.

Clinical features, such as menstrual irregularities, hirsutism, and acne, were assessed alongside biochemical risks to show whether a significant relationship exists between socioeconomic status and the metabolic manifestations of PCOS. Specifically, the research focuses on how social determinants affect disease presentation and healthcare access within the selected population. Furthermore, this research is intended not only for women with PCOS but also for clinicians, public health authorities, and policymakers, for them to gain further knowledge and explore equitable health programs for women's reproductive and metabolic health.

Keywords: Polycystic Ovary Syndrome (PCOS), clinical features, biochemical profile, socioeconomic status, Filipino women

P-4-37

Unmasking the Pseudo-Stroke

一般演題 Clinical Chemistry

Laboratory Management of Aconitine-Induced Refractory Arrhythmia and Multi-Organ Dysfunction

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Introduction: Aconitine is a highly toxic alkaloid present in plants of the genus *Aconitum*, commonly found in traditional Chinese medicinal materials, possessing analgesic and anti-inflammatory efficacies. However, due to its extremely narrow therapeutic window, improper processing or excessive dosage can easily lead to cardiac and neurotoxicity. Furthermore, the clinical course of acute poisoning progresses rapidly and unpredictably; failure to achieve timely identification and management may lead to multiple organ failure or even death.

Case Presentation: The patient was a 69-year-old male with a medical history of hypertension, diabetes, and a prior stroke. After consuming a self-brewed unidentified herbal decoction, he experienced abdominal discomfort, nausea, and vomiting, followed by neurological symptoms mimicking an acute stroke, such as left-sided limb weakness and dysarthria. Upon arrival at the emergency department, his blood pressure dropped to 82/56 mmHg, indicating a state of shock. Initial biochemical data demonstrated only mild abnormalities, with a potassium (K) level of 3.4 mmol/L and creatinine of 1.46 mg/dL, while the EKG exhibited highly complex electrical chaos. His condition immediately deteriorated into cardiac arrest; following emergency resuscitation, Return of Spontaneous Circulation (ROSC) was achieved, and he was admitted to the ICU. During the ICU stay, early ABG analysis demonstrated metabolic acidosis, with a pH of 7.173 and bicarbonate HCO3- of 11.5 mmol/L, accompanied by a significantly elevated lactic acid level of 12.8 mmol/L. Troponin I and CK-MB exhibited marked fluctuations due to direct myocardial cell injury caused by aconitine, and echocardiography confirmed a decrease in left ventricular systolic function. From the third day of hospitalization, the WBC count surged to $26.59\times10^3/\mu L$ and CRP rose to 155 mg/L, reflecting a severe systemic inflammatory response. Lactic acid and ABG results remained persistently abnormal. Liquid Chromatography-Mass Spectrometry (LC/MS) analysis revealed a molecular mass suspected to be aconitine. Following aggressive treatment with Lidocaine, Amiodarone, and vasopressors, the relevant laboratory data gradually stabilized as the condition was brought under control. The patient was transferred to a general ward in the third week for continued observation and treatment.

Discussion: This case highlights the diagnostic challenges and potential dangers of acute aconitine poisoning. The patient's initial presentation of left-sided limb weakness and dysarthria can easily mislead clinical reasoning toward cerebrovascular disease. However, when neuroimaging excludes vascular lesions and the EKG shows highly diverse and abnormal findings, the possibility of poisoning should be considered immediately. In clinical practice, the fatal risk of aconitine poisoning depends not only on the toxin quantity; even if initial data are relatively normal, minor electrolyte imbalances under the influence of the toxin can significantly amplify myocardial instability, triggering a fatal "arrhythmic storm." Therefore, early identification and multidisciplinary team collaboration are essential to effectively shorten the diagnostic interval and improve patient prognosis and survival rates.

P-4-38

一般演題 Clinical Chemistry

The Future of Clinical Chemistry Global Innovations and Healthcare Impact

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clinical chemistry[1)]

The future of clinical chemistry will be driven by artificial intelligence, automation, personalized medicine, and advanced diagnostic technologies. Innovations such as molecular diagnostics, metabolomics, and point-of-care testing will improve disease detection, treatment monitoring, and patient care. Smart laboratories and digital systems will enhance efficiency and accuracy, while global efforts in standardization and sustainability will support better healthcare services worldwide.

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P-4-39

一般演題 Clinical Chemistry

Diabetes

DM

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Viral Hepatitis with Comorbid Diabetes Significantly Increases Risks of Vascular Stiffness and Hyperglycemia

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Purpose : To evaluate the independent and additive effects of viral hepatitis on vascular stiffness and hyperglycemia.
Methods : This cross-sectional study included 790 participants: healthy controls (n=123), hepatitis alone (n=48), diabetes alone (n=440), and hepatitis with diabetes (n=179). Vascular stiffness was measured by the vascular hardening index. Hyperglycemia was assessed by HbA1c. Insulin and HDL-C levels were also compared. Statistical analyses used ANOVA with post-hoc tests. Data are mean ± SD.
Results : The hepatitis-alone group showed no significant difference in vascular hardening index (p=0.139), but had significantly higher insulin (p=0.024) and lower HDL-C (p=0.003), indicating insulin resistance. The hepatitis-with-diabetes group exhibited a significantly elevated vascular hardening index (=0.012) and markedly higher HbA1c (p<0.001) compared to controls.
Conclusion :Viral hepatitis alone induces insulin resistance without overt vascular stiffening. However, when hepatitis coexists with diabetes, patients face significantly increased risks of both vascular stiffness and hyperglycemia. Screening for glucose metabolism and vascular function is essential in hepatitis patients.

Keywords: Viral hepatitis; vascular stiffness; hyperglycemia; insulin resistance; HbA1c

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一般演題 Clinical Chemistry

When Low Humidity Disrupts Automated Pipetting, A Real Life Example

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Our laboratory encountered issues with a UPLC–MS/MS method used for the analysis of immunosuppressants. Sample preparation was performed automatically using a Hamilton pipetting robot prior to analysis. Unexpected deviations were observed in standards and controls, and inspection of the analysis plate revealed abnormal phase separation.

The environmental conditions in the laboratory were extremely dry, with relative humidity as low as 6%. According to Hamilton Robotics, the recommended operating conditions for the robots include a humidity range of 15–85%. Could low humidity have affected the dispensing of the internal standard (IS), consisting of 100% methanol?

The method uses salting-out assisted liquid–liquid extraction, where NaCl, whole blood (samples/standards/controls), IS and acetonitrile are pipetted into an analysis plate prior to UPLC–MS/MS analysis. Originally, the salt solution, blood sample, and IS were added sequentially. The IS was dispensed into the air above the liquid.

To solve the problem, we modified the liquid class to dispense the IS using surface dispense rather than jet dispense. Also, the order of addition was changed so that the IS was dispensed directly into the salt solution already present in the well prior to the addition of the blood sample, thereby eliminating the need for changing tips. Parallel testing over a six-week period compared the modified procedure with the original routine. The modified pipetting strategy and updated liquid class settings produced satisfactory and reproducible results, resolving the issue.

These findings highlight the importance of pipetting strategy and environmental conditions, particularly humidity, when dispensing pure solvents in automated liquid handling systems. When adding an exact volume of a pure solvent, it is advantageous to dispense the liquid onto the surface of another liquid rather than into the air above the liquid — and we learned that this becomes even more important under low humidity conditions.

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一般演題 Clinical Chemistry

Development of a Highly Linear AST and ALT Activity Assay

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[Purpose] Recent automated biochemical analyzers have been designed for micro-volume analysis, and their optical path lengths are often around 5 mm. However, reagent formulations are based on the analytical conditions (1 cm path length) established when the recommended methods were formulated, making them unsuitable for current instruments. In particular, since the setting of the initial absorbance is critical for enzyme activity assays that utilize a decrease in absorbance, we investigated a method to improve linearity by doubling the NADH concentration in the AST (ALT) reagent, which had been producing abnormally high values.

[Methods] We used L-type Wako AST (ALT)・J2 (current method) reagents for AST and ALT activity measurements, and performed the measurements using the TBA-C4000 automated biochemical analyzer and the Hitachi 7012 clinical spectrometer. Additionally, we prepared AST and ALT reagents with NADH concentrations twice that of the current method (modified method) and compared them with the current method.

[Results] When the absorbance at 340 nm of the current method reagents for AST and ALT was measured, both values were found to be almost identical to the NADH concentration (0.16 mM) specified in the JSCC recommended method. The parallel precision of the modified method for both AST and ALT was 0.3–2.2% CV, which was nearly equivalent to that of the current method. Similarly, when the linearity of the modified method was evaluated, it was found to be 1.7–1.8 times better than that of the current method.

[Discussion] With the shift in enzyme activity measurement calibration from K-factors to enzyme calibrators, it has become possible to use reagents compatible with standardization. Based on this, we investigated an improved method for measuring AST and ALT activity using a NADH concentration twice that of the current method, optimized for an automated analyzer with a 5-mm path length. As a result, we were able to enhance linearity while maintaining the accuracy of the current method.

P-4-42

一般演題 Clinical Chemistry

Revisiting the Mediterranean Paradox: Correlation between sun exposure and VitD

Comparative study between populations in the Mediterranean area and Arctic regions

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Purpose: Despite high annual sunlight exposure, vitamin D deficiency remains common in Mediterranean countries, a phenomenon known as the “Mediterranean paradox.” The aim of this study was to evaluate whether this paradigm still holds true or if a shift is emerging, by comparing vitamin D levels in populations living at mid-low latitudes versus high-latitude countries. Methods: Serum 25(OH)D concentrations were analysed in two cohorts from Iceland (n=92,353) and Italy (n=27,028, Turin). Seasonal variation was assessed by monthly stratification and annual means calculated. Vit. D was measured using automated immunoassays: ECLIA in Iceland and CLIA in Italy, both based on competitive chemiluminescence. Despite methodological differences, both assays are CDC Vit. D Standardization-Certification Program (VDSCP) certified and traceable to LC-MS/MS reference methods, ensuring comparability. This standardization minimizes inter-assay bias and supports reliable cross-country comparisons of vit. D status. Summary: Vit. D concentrations showed broadly comparable mean values between Italy and Iceland, with Iceland remaining relatively stable between 2020 and 2025, while Italy showed an increase over the same period. Median values were close to mean values, suggesting balanced distributions despite occasional high outliers. In Italy, seasonal variation was evident, with higher values during summer and early autumn and lower during winter. Females generally showed slightly higher values than males. Under-18 tended to present lower or more variable concentrations. The Italian 2020 pattern may reflect an association with COVID-19 lockdown-related reduced outdoor exposure. Conclusion: Contrary to popular belief, the results show no significant differences in vitamin D levels between countries with higher or lower sunlight exposure. This suggests that lifestyle, rather than geographical location, is the primary determinant. In support of this, studies in Nordic countries show second-generation Asian, Middle Eastern, African immigrants have significantly higher vit. D levels than first-generation immigrants of the same ethnicity.
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P-4-43

一般演題 Clinical Chemistry

Biochemical Signature of Academic Stress

Comparative Assessment of Serum Cortisol and Perceived Academic Stress among Selected Medical Technology Students

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In an increasingly demanding academic environment, stress remains a growing concern for student well-being, and cortisol serves as a key physiological marker of the body’s stress response. This study assessed morning serum cortisol and perceived academic stress to provide a more comprehensive understanding of academic stress among Medical Technology students. A descriptive-comparative, cross-sectional design was used involving 101 first- to third-year Medical Technology students at the University of Santo Tomas, Philippines. Blood samples were collected between 8:00 AM and 10:00 AM to minimize diurnal variation and were analyzed using the MAGLUMI® Cortisol chemiluminescence immunoassay. Perceived academic stress was measured using the Perceived Academic Stress (PAS) Scale. Data were analyzed using descriptive statistics, independent-samples t-test, one-way ANOVA with post hoc comparisons, and Pearson’s r correlation. Results showed a mean serum cortisol level of 129.13 ± 38.44 ng/mL, which was within the manufacturer-indicated reference interval of 45.5–208.2 ng/mL. Most students reported moderate academic stress (85.1%), followed by high (10.9%) and low (4.0%) stress, with perception of workload emerging as the highest stress-related category. No significant difference in cortisol levels was found across year levels, $F(2, 98) = 2.373$, $p = 0.099$. Pearson’s correlation also showed no significant relationship between serum cortisol and perceived academic stress, $r = -0.175$, $p = 0.080$. Overall, perceived academic stress was common among the students, but single morning serum cortisol measurements did not significantly vary by year level or correlate with perceived stress. These findings suggest that academic stress is multifactorial and may not be fully captured by a single basal cortisol measurement.

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一般演題 Clinical Chemistry

Association Between Fatty Liver Index and Renal Function Indice

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Background

The fatty liver index (FLI) is a surrogate marker for assessing fatty liver risk, calculated from body mass index, waist circumference, triglycerides, and γ-glutamyltransferase. Fatty liver is associated with metabolic risk factors, whereas evidence regarding the association between FLI and renal function indices remains limited, particularly for cystatin C–based estimated glomerular filtration rate (eGFR). This study aimed to examine whether the FLI is associated with renal function.

Methods

We analyzed data from 6,115 individuals undergoing health checkup at Kyushu Central Hospital, excluding those with eGFR <30 mL/min/1.73 m². Participants were classified into low (<30), intermediate (30–59), and high FLI groups (≥60). Receiver operating characteristic (ROC) curve analysis was performed to assess the diagnostic accuracy of the FLI for detecting fatty liver on abdominal ultrasonography. Associations between FLI and renal function indices were examined using FLI and multivariable linear regression analyses adjusted for age and sex. Approved by the institutional REC (approval no. 22124).

Results

Fatty liver on abdominal ultrasonography was observed in 1,733 participants (28.3%), and the AUC of FLI was 0.895. The mean values of creatinine-based on eGFR (eGFRcr) in the low, intermediate, and high FLI groups were 80.69, 76.01, and 75.31 mL/min/1.73 m², respectively; and those of cystatin C-based on eGFR (eGFRcys) were 109.02, 98.85, and 93.91 mL/min/1.73 m², respectively. In multivariable linear regression analyses, higher FLI was significantly associated with lower eGFRcys ($p < 0.001$), whereas no significant association was observed with eGFRcr ($p = 0.821$).

Conclusions

These findings suggest that cystatin C–based assessment may provide additional information for evaluating renal function in individuals at high risk of fatty liver.

P-4-45

一般演題 Clinical Chemistry

Palmitic Acid-Induced Acinar-to-Ductal Metaplasia in Pancreatic Steatosis

Marine Natural Products as Candidate Inhibitors of Pancreatic Steatosis Progression

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[Purpose]Non-alcoholic fatty pancreas disease (NAFPD) is strongly associated with pancreatic precancerous lesions. Acinar-to-ductal metaplasia (ADM), a transdifferentiation process in which acinar cells acquire ductal characteristics, is considered a pivotal early pathological event in pancreatic carcinogenesis. This study aimed to establish an in vitro model of NAFPD-induced ADM and to evaluate the inhibitory potential of marine natural products against pancreatic steatosis and its downstream progression.

[Methods]The mouse pancreatic acinar cell line 266-6 and primary murine acinar cells were treated with palmitic acid (PA) to induce intracellular lipid accumulation and ADM transformation. Morphological alterations were assessed by phase-contrast microscopy. Intracellular lipid content was quantified by Oil Red O staining. Expression of the acinar cell marker amylase 2b and the ductal progenitor marker pancreatic and duodenal homeobox-1 (Pdx-1) was analyzed by Western blotting to validate model establishment.

[Results]PA treatment induced significant intracellular lipid accumulation in both 266-6 cells and primary acinar cells. Time-course microscopy revealed a progressive morphological transition from the characteristic cobblestone epithelial phenotype to elongated, duct-like spindle-shaped cells. Consistent with ADM, Western blot analysis demonstrated a marked decrease in amylase 2b expression concurrent with a significant upregulation of Pdx-1, confirming successful acinar-to-ductal transdifferentiation. These findings establish a reproducible in vitro NAFPD-induced ADM model.

[Conclusion]The established NAFPD-ADM model provides a reliable platform for mechanistic investigation of pancreatic steatosis and early pancreatic carcinogenesis. This model is amenable to high-throughput screening of marine natural products, facilitating the identification of bioactive compounds capable of suppressing lipid accumulation and attenuating disease progression toward pancreatic malignancy.

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P-4-46

一般演題 Clinical Chemistry

Development of an ELISA Assay for Apolipoprotein C-II Transfer Rate

Toward Assessment of Individual TG Metabolism

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【 Introduction 】 To grasp the risk of atherosclerotic cardiovascular disease, triglyceride (TG) concentrations have been measured in clinical laboratories. However, due to the limitation of relying on TG quantification to understand individual TG metabolism, a surrogate marker is required. TG is hydrolyzed by lipoprotein lipase, whose activity is enhanced by apolipoprotein （apo）C-II. ApoC-II is transferred bidirectionally between very low-density lipoprotein (VLDL) and high-density lipoprotein (HDL). We developed and validated a method to measure the apoC-II transfer rate and investigated its dynamics in healthy individuals.

【Methods】We collected VLDL and HDL samples from four healthy volunteers (Ethical approval: M2015-546). To trace apoC-II transfer, each lipoprotein was labeled with biotin. Biotin-labeled VLDL was incubated with unlabeled HDL to induce the apoC-II transfer, which was then re-isolated by ultracentrifugation. The amount of apoC-II transferred to HDL was measured by ELISA using an anti-apoC-II antibody and peroxidase-conjugated streptavidin to calculate the transfer rates. The reverse apoC-II transfer (HDL to VLDL) was also analyzed.

【 Results 】 The developed ELISA assay showed good repeatability, with intra- and inter-assay coefficients of variation of 5-16% and 10-17%, respectively. The recovery rates were 89-106%. In the transfer from VLDL to HDL, the apoC-II transfer rate was 40-65%, and a lower transfer rate was observed in individuals with a higher TG/protein ratio in VLDL. In contrast, in the reverse transfer, the transfer rate was 55-72%, and no clear association with lipids or protein compositions was observed.

【Conclusions】We successfully developed an assay with good performance. The lipid content of VLDL may regulate the efficiency of apoC-II transfer to HDL, thereby indirectly regulating TG metabolism. This method may be useful for understanding the mechanism of hypertriglyceridemia and for the precise evaluation of individual lipid metabolism; however, further studies are needed.

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P-4-47

一般演題 Clinical Chemistry

Exosomal Markers Associated with Lipoprotein(a) and Cardiovascular Risk

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Objective: Cardiovascular disease (CVD) remains a leading cause of mortality worldwide. Patients with elevated lipoprotein(a) [Lp(a)] continue to exhibit substantial residual cardiovascular risk despite effective conventional low-density lipoprotein cholesterol (LDL-C) reduction. Circulating exosomes and exosomal microRNAs (miRNAs) have emerged as potential biomarkers of vascular inflammation and endothelial dysfunction. Therefore, this study aimed to further investigate associations between serum exosomal molecular markers, Lp(a) levels, and cardiovascular-related clinical parameters.

Methods: With Institutional Review Board approval, residual serum samples from routine testing were collected and divided into high Lp(a) (n = 25) and low Lp(a) (n = 25) groups. Exosomes were isolated using a precipitation-based method and characterized by CD9 and CD63 expression. Exosomal RNA was extracted, and miR-92a and miR-146a expression was assessed by RT-qPCR. Lipid profiles, glucose metabolism, renal function, and inflammatory markers were compared between groups.

Results: Preliminary results demonstrated a significant difference in Lp(a) concentrations between groups ($p < 0.001$). High-sensitivity C-reactive protein (hs-CRP) levels were markedly elevated in the high Lp(a) group ($p = 0.041$), whereas LDL-C, HDL-C, triglycerides, total cholesterol, HbA1c, BMI, and renal function parameters showed no significant differences. Analyses of exosomal miRNA expression are ongoing.

Conclusion: Elevated Lp(a) was associated with increased inflammatory activity independent of conventional lipid parameters, supporting the concept of residual cardiovascular risk. Further analyses of exosomal miRNAs may provide additional insights into the molecular mechanisms linking Lp(a), vascular inflammation, and cardiovascular risk.

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P-4-48

一般演題 Clinical Chemistry

Critical Low Glucose Workflow Optimization

Enhancing Pseudo-Hypoglycemia Identification and Laboratory Reporting Efficiency Through Quality Improvement Strategies

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Background: Critical low glucose is a common emergency laboratory alert, but extremely low results may represent pseudo-hypoglycemia caused by delayed centrifugation, leukocyte glycolysis, or discrepancies between point-of-care testing (POCT) and central laboratory analyzers. Misinterpretation may lead to unnecessary clinical interventions.

Objective: To establish a standardized workflow for interpretation and report release of critical low glucose results in emergency laboratory settings.

Methods: A five-level workflow was developed, including repeat analysis with quality control verification, evaluation of pre-analytical factors, comparison between POCT and central laboratory glucose results, integration of clinical information, and comprehensive assessment for report release or repeat specimen collection.

Results: The workflow improved the consistency and accuracy of critical low glucose interpretation. Pseudo-hypoglycemia was frequently associated with markedly low central laboratory glucose results accompanied by normal POCT values or significant inter-method discrepancies, particularly in delayed-processing specimens or patients with leukocytosis. After implementation, unnecessary clinical alerts and repeat blood collections were reduced, while interpretation confidence, report consistency, and traceability improved.

Conclusion: Accurate interpretation of critical low glucose results requires combined evaluation of analytical, pre-analytical, and clinical factors. The proposed workflow effectively differentiates true hypoglycemia from pseudo-hypoglycemia, reduces erroneous reporting, and enhances patient safety in emergency laboratory practice.

P-4-49

一般演題 Clinical Chemistry

Urine Microalbumin QC Optimization

Improving Analytical Stability Through Open-Vial Calibrator Management

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Background: Urine microalbumin is a sensitive biomarker for early renal impairment. During routine quality control (QC) monitoring, persistent systematic drift was observed in Levey-Jennings charts after prolonged calibrator use, potentially affecting low-concentration sample accuracy.

Objective: To investigate the relationship between QC drift and calibrator open-vial duration and to optimize calibrator replacement strategy.

Methods: A before-and-after quality improvement study was conducted using an automated chemistry analyzer with daily two-level QC monitoring. Before intervention, calibrators were used until manufacturer expiration dates. After intervention, calibrators were mandatorily replaced within two weeks after opening. QC drift patterns, systematic deviation frequency, and QC distribution within target ranges were evaluated.

Results: Before intervention, gradual unidirectional QC shifts and trend warnings were observed during prolonged calibrator use. After implementation of the two-week replacement policy, QC distributions became more stable, systematic drift decreased, and recalibration events caused by QC failure were reduced.

Conclusion: QC drift in urine microalbumin measurement was closely associated with prolonged calibrator open-vial duration. Implementing a two-week replacement policy improved analytical stability and result consistency. Assay-specific open-vial management and trend monitoring are important for early detection of systematic analytical error.

Keywords: Urine microalbumin, Quality control, Levey-Jennings chart, Calibration drift, Open-vial stability, Quality improvement

P-4-50

一般演題 Clinical Chemistry

Integrated NADH Chelate Assay Using a NADH Oxidase

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Background

Conventional NADH assays rely on UV absorbance at 340 nm, which often suffers from sample interference and limited sensitivity. To overcome these issues, we aimed to develop a visible-range, high-sensitivity NADH quantification system by combining a hydrogen peroxide–producing NADH oxidase reaction with a metal-chelate–based chromogenic method.

Methods

A lactic acid bacterium–derived gene was cloned into an expression vector and expressed in engineered *E. coli*. Soluble fractions were analyzed by SDS-PAGE and Western blotting, and the recombinant enzyme was purified using affinity and size-exclusion chromatography. The metal-chelate chromogenic system was incorporated into the reaction, and absorbance changes in the visible range were monitored using dual-wavelength detection.

Results

SDS-PAGE confirmed IPTG-induced expression of the target protein, and purification yielded high-purity enzyme at roughly 800 mg per liter of culture. The enzyme showed NADH-dependent absorbance decreases with K_m = 0.38 mmol/L and V_{max} = 1.54 ΔAbs /min. Incorporation of the chromogenic system produced clear, concentration-dependent absorbance changes, demonstrating reliable detection of the enzymatic reaction.

Conclusions

We successfully expressed and purified a recombinant oxidoreductase and quantified its NADH-oxidizing activity. The kinetic properties indicate strong reactivity toward NADH, supporting its compatibility with a metal-chelate–based visible detection system. Further optimization and validation will advance development of a practical, high-sensitivity NADH assay.

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一般演題 Clinical Chemistry

Measurement method for NAD^+ and NADH as an aging biomarker

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Background

As Japan enters a super-aged society, interest in biomarkers that objectively assess biological aging is expected to grow further. Nicotinamide adenine dinucleotide (NAD^+) levels decrease with aging and are considered to be implicated in the pathogenesis of age-related diseases such as obesity, diabetes, and Alzheimer's disease. Consequently, it is garnering attention as a novel aging biomarker. Existing measurement methods based on spectroscopic analysis face challenges regarding sensitivity and the influence of coexisting substances. Therefore, this study aimed to develop a method for measuring NAD^+ and NADH in blood that is highly sensitive, resistant to the influence of coexisting substances, and easily measurable using automated biochemical analyzers. We developed a method using a metal chelator "A". In this report, we describe the basic performance evaluation of this method in aqueous solution samples.

Methods

1. Reagents

Reagent 1 (R-1) : 0.2 mol/L HEPES buffer (pH 7.0), 1.8 mmol/L metal chelator "A", 0.1% Triton X-100, 2.7 U/mL Ascorbate Oxidase. Reagent 2 (R-2) : 10 mmol/L Formic Acid buffer (pH 3.0), 1.5 mmol/L $FeCl_3 \cdot 6H_2O$, 11.5 µmol/L 1-Methoxy PMS, 0.1% Triton X-100.

2. Measurement method

Analytical instrument : Hitachi Biochemical Automatic Analyzer LABOSPECT 008. Analytical conditions : 15 µL sample, 100 µL R-1, 65 µL R-2. Single-wavelength 2-point end-point assay.

Results

We confirmed linearity in the range of 0~100 µmol/L NADH aqueous solution. Repeatability (n=20) was 3.67% or less for all concentrations of 10, 50, and 100 µmol/L NADH aqueous solutions. Quantitation limit was 1.56 µmol/L at a CV of 10%.

Conclusion

We have successfully developed a highly sensitive measurement system that can detect low concentrations by using metal chelator "A".

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P-4-52

一般演題 Clinical Chemistry

Electronic Display Board

the Biochemical Analyzer Track System

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Alarms in biochemical analyzer track systems are often caused by specimen blockage, sensor abnormalities, or equipment issues. Due to the lack of obvious audible alerts, alarms may be overlooked in busy laboratory environments, resulting in delayed specimen processing and instrument downtime.

To improve alarm recognition and response efficiency, an electronic display board system was implemented by connecting the track system to a large-screen monitor. Different operational statuses were displayed using color-coded indicators: green for normal operation, yellow for warning conditions, half-red/half-green for critical alarms or instrument stoppage, and gray for power-off status.

Before implementation, the average time for staff to recognize alarms exceeded 30 minutes. After implementation, the response time was reduced to within 5–10 minutes. The electronic display board significantly improved alarm visibility and accelerated abnormal event handling.

This visual management system effectively reduced instrument downtime, improved laboratory report turnaround time, and enhanced patient safety. In addition, the system is low-cost, simple to operate, and suitable for expansion to other automated laboratory sections.

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P-4-53

一般演題 Clinical Chemistry

Real-World Verification of CYFRA 21-1 Reference Intervals: Pandemic Partitioning?

A 10-Year, 7-Hospital Longitudinal Real-World Evidence Study of 10,046 Asian Health Examinees

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CYFRA 21-1, a cytokeratin 19 fragment from epithelial cell apoptosis, is used as a biomarker for lung malignancies (particularly non-small cell lung cancer) and benign pulmonary conditions. However, the manufacturer's cut-off (3.3 ng/mL) for serum CYFRA 21-1 was established decades ago in pre-pandemic Caucasian populations, and may not reflect real-world demographic shifts or the post-COVID-19 epidemiological landscape. Whether the COVID-19 pandemic constitutes a required partitioning factor for serum CYFRA 21-1 reference intervals (RIs) remains unanswered. This study applied CLSI EP28-A3c partitioning criteria to a multi-center real-world database spanning a decade to address this question. We retrospectively analyzed 16,241 serum CYFRA 21-1 measurements from 10,046 healthy employees across seven Chang Gung Memorial Hospital branches in Taiwan (2014-2023). Subjects with malignancy or 14 pre-defined benign conditions within 90 days were excluded. Multivariable regression assessed contributions of age, sex, hospital site, and pandemic period. Age-specific 95th percentile RIs were derived using three R-based validations: refineR algorithm with Box-Cox transformation; Fokkema log-normal asymmetric RCV; and Monte Carlo simulation. Contrary to initial concerns about pandemic-related effects, multivariable analysis identified age, not the pandemic period, as the dominant determinant of serum CYFRA 21-1 levels (β=1.043 for ≥60 vs. 20-29 years, $p<0.001$; pandemic β=0.040, $p=0.007$). Age-stratified P50/P95 values progressively increased: 1.15/2.64 (20-39y), 1.53/3.05 (40-49y), 1.88/3.69 (50-59y), and 2.16/4.20 ng/mL (≥60y), substantially exceeding the manufacturer's 3.3 ng/mL cut-off. The COVID-19 pandemic was not an independent partitioning factor for CYFRA 21-1 RIs; rising positivity reflected population aging. We proposed and re-evaluated an age-stratified RI for CYFRA 21-1 to reduce false-positive results and unnecessary follow-up. Our three-track validated framework, anchored in real-world data and CLSI EP28-A3c criteria, offers a robust approach for tumor marker RI verification in the post-COVID-19 era.

P-4-54

一般演題 Clinical Chemistry

FT4 and FT3 measurement using Equilibrium-Dialysis-LC-MS/MS as a complementary method

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Measurement of free thyroxine (FT4) and free triiodothyronine (FT3) are critical for diagnosing thyroid diseases. Immunoassays are commonly used in clinical laboratories and provide clinically useful results but are vulnerable to interference caused by e.g. cross-reaction, heterophile antibodies, biotin and anti-analyte antibodies. Direct measurement of FT4 and FT3 using Equilibrium Dialysis (ED) combined with Liquid Chromatography-Tandem Mass Spectrometry (LC-MS/MS) is regarded as the most accurate method. This technique separates protein bound T4 and T3 from their unbound fractions and directly quantitates the free concentration of hormones and is least affected by analytical interferences or patient-derived substances (e.g. some medication, supplements or endogenous antibodies). Interference can lead to patients showing discordant thyroid results not aligning with patients' clinical status. We compared results using immunoassay with Abbott Alinity i and our newly developed ED-LC-MS/MS method that measures FT4, FT3 and free Testosterone (FT) simultaneously, with primary focus here on the former two. Samples were dialyzed overnight. The dialysate was purified and extracted by using solid-phase extraction (SPE) and chromatographically separated by using LC-MS/MS in positive ion and multiple reaction monitoring (MRM) mode. The ED-LC-MS/MS method was able to detect FT4 within reference range and demonstrated better reproducibility in some samples that presumably showed falsely elevated FT4 or discordant thyroid results with immunoassay. Indicating that the suspected samples may be affected by interferences or other analytical factors. Implementation of this method yields more accurate results compared to automated immunoassay because it can overcome most interferences and instrument-dependent challenges that occur in clinical routine measurements by directly measuring the amount of analyte in samples. We believe that the ED-LC-MS/MS, despite being more expensive and complex to perform, is a useful complementary clinical method allowing for improved medical assessments.
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P-4-55

一般演題 Clinical Chemistry

Thyroid Dysfunction in Lithium-Treated Bipolar Patients

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Introduction
Bipolar disorder is a common chronic psychiatric condition. Lithium remains the gold-standard mood stabilizer; however, its use is associated with adverse effects, particularly thyroid dysfunction. The aim of this study was to comparatively evaluate the frequency and biological characteristics of thyroid function abnormalities in bipolar patients treated with lithium versus healthy controls.
Material sand Methods
A retrospective case-control study was conducted at Razi Hospital Manouba from January to June 2022. Patients with bipolar disorder treated with lithium for at least one year were compared with healthy controls. TSH, FT4, and plasma lithium levels were collected. Biological hypothyroidism was defined as TSH > 4.2 µIU/mL with FT4 < 12 pmol/L.
Results
The total population included 100 subjects, comprising 50 bipolar patients and 50 controls. The mean age of patients was 44.92 ± 11.21 years, with a sex ratio of 1.08. The mean plasma lithium level in patients was 0.58 ± 0.15 mmol/L.Median FT4 concentrations were significantly lower in patients compared to controls (14.44 [13.25–16.85] vs 15.77 [14.48–17.12] pmol/L; p = 0.039). Conversely, median TSH concentrations were significantly higher in patients (2.20 [1.37–3.10] vs 1.53 [1.20–2.31] µIU/mL; p = 0.018). Biological hypothyroidism was observed in 4 patients versus 1 control, with no statistically significant difference (p = 0.678).
Conclusion
Lithium-treated bipolar patients showed a tendency toward hypothyroidism. Although overt biological hypothyroidism was not significantly different, lithium may still affect thyroid function, supporting the need for regular monitoring.
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P-4-56

一般演題 Clinical Chemistry

Serum Beta-2 Microglobulin as a Biomarker of Severe Psychoses

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Introduction

Schizophrenia and bipolar disorder are severe psychotic disorders associated with immune activation. Beta-2 microglobulin (B2M) is a potential marker of this process. This study aimed to compare serum B2M levels in patients with severe psychoses and healthy controls. **Material sand Methods**

A cross-sectional case-control study was conducted at Razi Hospital over a six-month period. Patients with schizophrenia, patients with bipolar disorder diagnosed according to DSM-5 criteria, and age- and sex-matched healthy controls were included. Sociodemographic and clinical data were collected, and serum beta-2 microglobulin levels were measured in all participants.

Results

Serum B2M levels were measured in 60 patients with severe psychoses (30 schizophrenia, 30 bipolar disorder) and 30 healthy controls. The median B2M level among patients was 1.68 mg/L (IQR: 1.38–1.97). Patients with bipolar disorder exhibited the highest concentrations (2.25 mg/L; IQR: 1.95–3.10), followed by patients with schizophrenia (1.94 mg/L; IQR: 1.70–2.10). B2M levels were significantly higher in patients than in controls ($p < 0.05$). Furthermore, bipolar patients had significantly higher levels than schizophrenic patients ($p < 0.05$). A B2M threshold of 1.96 mg/L was associated with an increased risk of severe psychosis (OR = 5.93; 95% CI: 2.05–17.20; $p < 0.001$). A significant negative correlation was observed between B2M levels and parental age at birth. In addition, patients receiving lithium or risperidone treatment exhibited significantly higher B2M concentrations ($p < 0.05$).

Conclusion

Lithium-treated bipolar patients showed a tendency toward hypothyroidism. Although overt biological hypothyroidism was not significantly different, lithium may still affect thyroid function, supporting the need for regular monitoring.

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P-4-57

一般演題 Clinical Chemistry

Association Between VPA and Hyperammonemia: A Retrospective Cross-Sectional Study

Evaluation of Serum Valproic Acid Concentration, Ammonia Level, Age, and Sex

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Valproic acid (VPA) is a widely used antiepileptic and mood-stabilizing agent. Hyperammonemia is a known but potentially underrecognized adverse effect of VPA therapy, which can occur even with therapeutic drug levels. Understanding the relationship between VPA serum concentrations and ammonia levels is crucial for clinical monitoring and patient safety. This study investigated the association between serum VPA concentration and ammonia level and further examined the influence of age and sex.

Data on VPA and ammonia concentrations from blood samples collected on the same day in 2025 were collected.This retrospective cross-sectional study included 1,038 valid cases, comprising 600 male and 438 female patients. Statistical analyses included independent-samples t tests, chi-square tests, Pearson correlation, and Cohen's d effect size estimation. Ammonia levels were categorized as <80ug/dl, 80–99ug/dl, 100–119ug/dl, and ≥120ug/dl.

Male patients had significantly higher mean VPA concentrations than female patients (65.24 vs. 61.98 μg/dL, p=0.0361), although the effect size was small (d=0.132). Ammonia levels were also significantly higher in male patients (70.26 vs. 64.67 ug/dl, p=0.0005; d=0.219), whereas female patients were older on average than male patients (50.51 vs. 44.82 years, p<0.001). The proportion of male patients increased with higher ammonia categories and was significantly elevated in the <80 ug/dl, 80–99 ug/dl, and 100–119 ug/dl groups, with the highest proportion observed in the 100–119 group (73.1%, p=0.0008). Sex-specific differences in VPA concentration within ammonia strata were not statistically significant. Overall, the correlation between serum VPA concentration and ammonia level was weak (r=0.099). Serum VPA concentration was weakly associated with hyperammonemia and did not independently determine risk. Male and younger age appeared to be associated with increased susceptibility to VPA-related hyperammonemia. These findings support closer ammonia monitoring during VPA therapy, particularly in male and younger patients.

P-4-58

一般演題 Clinical Chemistry

Evaluation of True versus suspected pseudohyponatremia in tertiary care setting

Lab based pilot study on pseudohyponatremia reassessment and diagnostic corelation adjusted for patient setting

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Background
Hyponatremia is a common electrolyte abnormality associated with significant morbidity and mortality. However, laboratory-reported hyponatremia may not always reflect a true reduction in plasma sodium concentration, as abnormal plasma constituents can cause pseudohyponatremia. Identifying pseudohyponatremia is important for appropriate management.
Objectives
To determine the proportion and severity distribution of laboratory-reported hyponatremia over a two-month period and estimate the proportions of true hyponatremia and suspected pseudohyponatremia.
Methods
This retrospective observational study was conducted in a tertiary care biochemistry laboratory over two months. All serum sodium measurements were screened for hyponatremia. Cases with available clinical and biochemical data underwent detailed evaluation. Suspected pseudohyponatremia was identified based on hyperproteinemia and hyperlipidemia.
Results
Among 38,633 serum sodium measurements, 12,389 (32.1%) were hyponatremic, of which 60.7% were mild. Of 847 cases analyzed, 350 (41.3%) were classified as true hyponatremia, 480 (56.7%) as suspected pseudohyponatremia, and 17 (2.0%) as indeterminate. Hyperproteinemia was significantly associated with lower sodium values (p=0.01). Clinical–laboratory agreement was poor (κ=0.02; agreement 38%). Distribution of true and suspected pseudohyponatremia differed significantly across care settings (p=0.021).
Conclusion
A substantial proportion of laboratory-reported hyponatremia may represent suspected pseudohyponatremia. Poor clinical–laboratory concordance highlights the need to integrate biochemical findings with clinical assessment. Serum osmolality may improve diagnostic accuracy and guide patient management.

P-4-59

一般演題 Clinical Chemistry

Risk-Based Management of Pre-Analytical Non-Conformities In Biochemistry Laboratory

According to ISO 15189:2022

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Background and aims:
The pre-analytical phase is crucial in immunoassays due to analyte instability and method sensitivity. In accordance with ISO 15189:2022, this study aimed to identify and analyze pre-analytical non-conformities in the immunoassay section of Sahloul University Hospital.
Methods and materials:
A prospective study was conducted in April 2025 using NC records and the SanteLab Laboratory Information System. NCs were classified and analyzed using Pareto charts, Ishikawa diagrams, and Failure Mode and Effects Analysis (FMEA) within a PDCA framework.
Results:
Among 2,455 laboratory requests, 104 NCs (4.23%) were identified. Sample collection errors were the most frequent (47.1%), followed by LIS-related errors (33.6%) and patient identification defects (8.6%). Pareto analysis revealed that unpaid requests (24%), unreceived samples (19%), hemolyzed samples (15%), missing clinical information (13%), and insufficient sample volume (5.7%) accounted for nearly 80% of NCs. FMEA identified eight major risks (criticality index ≥8), leading to corrective actions including staff training, document revision, information system enhancement, and logistical reorganization.
Conclusion:
Risk-based management of pre-analytical NCs in accordance with ISO 15189 improves laboratory performance and enhances patient safety.
Keywords:
Pre-analytical phase, Non-conformities, Immunoassay, GLPG, ISO 15189

P-4-60

一般演題 Clinical Chemistry

Sigma Metric-Based Internal Quality Control in Clinical Biochemistry

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Background and aims:
Internal quality control (IQC) is a regulatory and normative requirement in medical biology laboratories. As IQC practices vary among laboratories, control procedures should be adapted to analytical performance of the method and clinical requirements of the parameter assessed. This study aimed to describe the IQC management process implemented in the Clinical Biochemistry Laboratory of Sahloul University Hospital and establish parameter-specific approach for IQC sample processing.

Methods:
This prospective study evaluated IQC management for four serum analytes (urea, sodium, aspartate aminotransferase [AST], and calcium) measured on the Beckman DxC 700 AU® analyzer. Two control materials were used. Total Allowable Error (TEa) specifications were obtained from the Ricos biological variation database. IQC procedures were defined according to Sigma Metrics: Sigma >6, one control level daily with the $1_{3.5}s$ rule; Sigma 4–6, two control levels daily with the $1_{2.5}s$ rule; Sigma 3–4, two control levels twice daily using Westgard multirules ; and Sigma <3, three control levels three times daily with the full set of Westgard rules. An IQC management strategy based on Sigma Metrics and Westgard rules was established.

Results:
Sigma Metric evaluation identified three categories of analytical performance, determining the number of control levels and IQC frequency. Urea showed excellent performance (Sigma = 8.55), while AST demonstrated acceptable performance for routine use (Sigma = 4.82). Sodium and calcium exhibited poor performance (Sigma = −1.37 and 1.61, respectively). Based on these results, an IQC management procedure was developed and submitted to the laboratory quality management unit.

Conclusion:
The Sigma approach should be combined with complementary quality management tools, particularly patient-based moving averages, for analytes exhibiting low Sigma performance levels.

P-4-61

一般演題 Clinical Chemistry

Comparative Analysis of Semaglutide, Liraglutide, and Tirzepatide Cardiometabolic Outcomes

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Background:
Cardiometabolic disorders such as type 2 diabetes mellitus (T2DM), obesity, and cardiovascular disease (CVD) remain major global health challenges. Incretin-based therapies, including the GLP-1 receptor agonists semaglutide and liraglutide, and the dual GIP/GLP-1 receptor agonist tirzepatide, are increasingly used to address hyperglycaemia and obesity, and have been evaluated for both cardiometabolic risk markers and selected cardiovascular and renal outcomes.

Objective:
This review summarizes and contrasts the pharmacology of semaglutide, liraglutide, and tirzepatide, distinguishing between surrogate cardiometabolic risk markers (e.g., glycaemic control, body weight, and lipid parameters) and confirmed clinical outcomes, including major adverse cardiovascular events (MACE) and renal endpoints.

Methods:
Recent data were synthesized from pivotal randomized clinical trial programs, SUSTAIN and PIONEER (semaglutide), LEADER (liraglutide), and SURPASS and SURMOUNT (tirzepatide), as well as meta-analyses, post hoc analyses, and observational studies addressing mechanistic and long-term cardiometabolic outcomes.

Results:
All three agents improved HbA1c, weight, and cardiometabolic outcomes, with tirzepatide generally showing larger reductions across clinical trials. Semaglutide and liraglutide consistently benefited BMI, lipids, and cardiovascular risk, while tirzepatide shows promise pending CVOT data. Renal outcomes were favorable across the class, though results varied by baseline characteristics and trial design.

Conclusion:
Semaglutide, liraglutide, and tirzepatide are key therapies for type 2 diabetes and cardiometabolic disease. Tirzepatide's dual activity may enhance metabolic and lipid outcomes, while semaglutide and liraglutide have strong evidence for cardiovascular and renal safety. However, comparisons are based on indirect evidence and should be interpreted cautiously.

P-4-62

一般演題 Clinical Chemistry

Association of hs-CRP and Lipid Profile among Filipino Tobacco Users

Evaluation of Biomarkers for Cardiovascular Disease Risk Among Smokers and Heated Tobacco Users

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Tobacco combustion from conventional cigarette smoking induces systemic inflammation and oxidative stress, causing a heightened risk of developing cardiovascular diseases (CVD). This health crisis led to the emergence of smoking alternatives such as heated tobacco products (HTPs) (Hatsukami & Carroll, 2020). These devices heat tobacco at lower temperatures than conventional cigarettes, creating non-chemical-containing smoke (Znyk et al., 2021). The study aims to assess and compare high-sensitive C-reactive protein (hs-CRP) levels and lipid profiles among Conventional Cigarette Smokers (CCS), Switchers to HTPs, and Never-Smokers (NS) to evaluate comparative cardiovascular disease risk. Serum samples were collected from fifteen systematically categorized adult participants (n=15). The serum hs-CRP levels were quantitatively determined via latex-enhanced immunoturbidimetric assay (LETIA), utilizing latex particles sensitized with anti-CRP antibodies, measured in milligrams per liter (mg/L). Concurrently, total cholesterol, triglycerides, and high-density lipoprotein (HDL) levels were analyzed using colorimetric methods, measured in milligrams per deciliter (mg/dL). The serum samples were processed using semi-automated machines, namely Pentra C400 for hs-CRP and NT 300 for lipid profile. Low-density lipoprotein (LDL) and very-low-density lipoprotein (VLDL) concentrations were derived using the Friedewald equation. The post-hoc pairwise comparison showed that the CCS group had significantly higher hs-CRP levels than the Switchers group (p=0.017), while there was no significant difference between the Switchers and the NS group (p=1.000). In contrast, the lipid profile values among the participant groups were found to be not significantly different. These findings indicate that while lipid metrics remain unchanged, switching to HTPs significantly mitigates systemic inflammation, thereby lowering overall cardiovascular disease risk compared to conventional smoking.

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一般演題 Clinical Chemistry

Urinary Vanin-1 Improves a Multimarker Diagnostic Model for CKD

Association With Albuminuria and Enhanced Diagnostic Performance

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Background: Chronic kidney disease (CKD) biomarkers primarily reflect glomerular dysfunction, while biomarkers of tubular injury may provide complementary information. Vanin-1, a pantetheinase expressed in renal tubular cells and involved in oxidative stress pathways, has emerged as a potential marker of tubular injury. This study evaluated the association of urinary Vanin-1 with conventional renal biomarkers and its diagnostic value in CKD.

Methods: This cross-sectional study enrolled 190 participants, including 175 patients with CKD stages 1-5 and 15 non-CKD controls. Urinary Vanin-1 concentrations were measured using ELISA. Pearson correlation, multivariable linear regression, binary logistic regression, and receiver operating characteristic (ROC) analyses were performed. A multimarker logistic regression model incorporating urinary Vanin-1, UACR, and UPCR was constructed.

Results: Urinary Vanin-1 was significantly correlated with UACR (r = 0.393), UPCR (r = 0.360), serum creatinine (r = 0.255), and eGFR (r = -0.223) (all $p < 0.001$). In multivariable linear regression, UACR remained the only independent factor associated with urinary Vanin-1. Urinary Vanin-1 levels were higher in advanced CKD (stages 4-5) than in early-stage CKD (stages 1-3). ROC analysis showed modest diagnostic performance for urinary Vanin-1 alone (AUC=0.667, 95% CI 0.527–0.808, p=0.032). UACR, UPCR, and serum creatinine yielded AUCs of 0.769, 0.756, and 0.925, respectively. The multimarker model improved diagnostic performance (AUC=0.806, 95% CI 0.729–0.883, p<0.001).

Conclusion: Urinary Vanin-1 is associated with albuminuria and proteinuria and may reflect proteinuria-related tubular injury. Although its standalone diagnostic performance is modest, incorporation into a multimarker model with UACR and UPCR improved diagnostic accuracy, supporting its role as a complementary biomarker for CKD evaluation.

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一般演題 Clinical Chemistry

Verification of venous blood collection tubes with new separating gel

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Introduction Greiner Bio-One has introduced a new polyacrylate-based separating gel (Gel 2.0) for Vacuette serum and lithium heparin tubes, replacing the current polyolefin oligomer gel. As these tubes are widely used in routine laboratory testing, this study aimed to assess whether the new gel affects analytical results.

Methods 36 routine clinical chemistry analytes were evaluated using samples from ten apparently healthy laboratory staff (men and women). After standard pre-analytical handling, serum from each tube type was pooled, frozen, thawed, and analyzed x 10 per analyte. Patients attending routine phlebotomy were also invited to donate an additional sample that was collected in new gel tubes. Paired samples from conventional and new tubes were analyzed for eight tumour markers and three therapeutic drug monitoring (TDM) assays x 6 per analyte. Mean differences between tube types were calculated for all analytes.

Results No clinically significant differences in mean values were observed between the tube types. The evaluated analytes included a broad range of routine parameters: ***hormones*** **(**17-hydroksyprogesterone, AMH**,** estradiol**,** FSH**,** FT4**,** FT3**,** hCG/β-hCG**,** hGH**,** LH**,** progesterone**,** PRL**,** SHBG**,** testosterone**,** TSH**),** ***vitamins/metabolites*** (Active B12, homocysteine, MMA, Vitamin A, Vitamin E, 25-OH Vitamin D), ***enzymes*** (ALP, amylase AST, LDH), ***electrolytes*** (chloride, magnesium, osmolality, phosphate, sodium), ***proteins*** (ceruloplasmin, Cystatin C, haptoglobin, IgM, transferrin), ***cardiac markers/lipids*** (cTnT, LDL-cholesterol), ***tumour markers*** (AFP, beta-2-macroglobulin, CA125, CEA, chromogranin A, free light chains (kappa/lambda), neuron specific enolase, PSA) and ***TDM*** (gentamicin, tobramycin, vancomycin).

Conclusion The introduction of polyacrylate-based separating gel in serum and lithium heparin tubes did not significantly affect analytical results for the analytes studied. The new tubes can therefore be considered interchangeable with current tubes in routine laboratory practice.

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一般演題 Clinical Chemistry

Coronary Heart Disease Risk Analysis Utilizing Serum Cystatin C

A Quantitative Assessment of Filipino Compliant Type 2 Diabetes Mellitus with Chronic Kidney Disease

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Type 2 Diabetes Mellitus (T2DM) significantly increases susceptibility to Chronic Kidney Disease (CKD) and Coronary Heart Disease (CHD), forming a critical cardio-renal-metabolic triad. Traditional biomarkers, such as HbA1c, are unreliable in T2DM with concurrent CKD, necessitating alternative risk-stratification tools. Serum Cystatin C was assessed as a predictive biomarker of CHD risk across different CKD stages (Stages 3, 4, and 5), and its cutoff values for CHD risk stratification were determined.

This study employed a quantitative, diagnostic research design in tertiary hospitals in Manila, Philippines, which enabled the assessment of the association between cystatin C levels and the risk of coronary heart disease in patients with CKD as a complication of T2DM. Serum Cystatin C was quantitatively measured using Lateral Flow Immunoassay. Additionally, Total Cholesterol, LDL, HDL, and hs-CRP were measured to corroborate the predictive capacity of Cystatin C for CHD risk.

ROC curve analysis showed that Cystatin C could be a predictive biomarker for CKD Stage 3 (AUC = 0.979, p=0.001), Stage 4 (AUC=1.000, p=0.001), and Stage 5 (AUC=1.000, p=0.001) in patients with T2DM. Cystatin C cutoffs were 0.0930 mg/dL (0.930 mg/L), 0.0975 mg/dL (0.975 mg/L), and 0.1005 mg/dL (1.005 mg/L) for moderate CHD risk in stage 3, stage 4, and stage 5, respectively. While Cystatin-C cutoffs were 0.1005 mg/dL (1.005 mg/L), 0.1245 mg/dL (1.245 mg/L), and 0.2375 mg/dL (2.375 mg/L) for high CHD risk for stages 3, 4, and 5, respectively. Serum Cystatin C levels were significantly associated with increased CHD risk among elderly compliant T2DM patients with CKD.

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一般演題 Clinical Chemistry

Quality Improvement of Quantitative FIT Screening in Taiwan

A Nationwide Total Quality Management Program for Colorectal Cancer

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Colorectal cancer (CRC) remains one of the most prevalent malignancies in Taiwan. The fecal immunochemical test (FIT) is globally recognized as the most cost-effective modality for population-based CRC screening. Since 2010, the Health Promotion Administration (HPA) of Taiwan has implemented a nationwide quantitative FIT screening program targeting adults aged 45–74 years, with biennial free testing. The Taiwan Society of Laboratory Medicine (TSLM) has shouldered central responsibility for quality oversight of this program for nearly two decades. A comprehensive total quality management (TQM) framework was established across 169 participating testing institutions. Five core strategies were implemented: (1) institutional qualification and onboarding criteria; (2) two cycles of annual external quality assessment (EQA); (3) on-site expert visits for newly enrolled laboratories or those demonstrating performance deficiencies; (4) structured questionnaire surveys evaluating the complete analytical process from pre-analytical specimen collection through post-analytical report generation; and (5) targeted CRC screening education and training programs for laboratory professionals. Over 80% of participating institutions have achieved accreditation through the Taiwan Accreditation Foundation (TAF) or the College of American Pathologists (CAP). EQA accuracy rates consistently reached 97–99%. The national screening positivity rate is projected at approximately 6% by 2025, with confirmed positive cases proceeding to free colonoscopy for definitive polyp or cancer detection. This multicomponent quality improvement program demonstrates that sustained institutional engagement, rigorous EQA, and targeted education can achieve high analytical accuracy across a large-scale national FIT screening network. The model offers a replicable framework for improving laboratory quality in population-based CRC screening programs, with direct implications for early cancer detection and reduction of CRC mortality.

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一般演題 Clinical Chemistry

Are ovarian reserve hormonal markers always concordant?

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Are Ovarian Reserve Hormonal Markers Always Concordant?
Introduction: Ovarian reserve can be assessed using hormonal markers such as follicle-stimulating hormone (FSH) and anti-Müllerian hormone (AMH). FSH reflects the pituitary regulation of developing follicles, whereas AMH, produced by pre-antral and antral follicles, is a direct indicator of the follicular pool. There is a negative correlation between these two parameters; however, biological discordances may complicate clinical interpretation.
Objective: The aim of our study was to describe the frequency and characteristics of discordances between AMH and FSH in the evaluation of ovarian reserve.
Materials and Methods: This retrospective study included patients who underwent simultaneous FSH and AMH testing at the Clinical Biochemistry Laboratory of the Pasteur Institute of Tunis (March 2025 – March 2026). Hormone assays were performed using electrochemiluminescence (ECLIA) on the Cobas e411 analyzer, between the 3rd and 5th day of the menstrual cycle. Discordances were defined as low AMH associated with normal FSH, or normal AMH associated with elevated FSH. Statistical analysis used Jamovi software (v2.6).
Results: A total of 166 patients, with a mean age of 32.5 ±8.4 years, were included. The median AMH level was 2.08 ng/mL [0.31–4.25], and the median FSH level was 6.81 IU/L [5.34–9.67]. According to age, decreased AMH was observed in 28.9% (n=48) of patients. A negative correlation was found between AMH and FSH ($r = -0.438$; $p < 0.001$). Among patients with low AMH, 60.4% (n=29) had normal FSH levels, highlighting the frequency of discordances. No patient had normal AMH associated with elevated FSH.
Conclusion: A significant proportion of patients showed decreased AMH despite normal FSH, confirming AMH as a more sensitive marker for early ovarian reserve decline. Combined FSH–AMH assessment remains relevant, but AMH should be prioritized to guide infertility management and reproductive planning.

P-4-68

一般演題 Clinical Chemistry

Risks assessment in medical laboratories using Failure Effects Analysis

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Introduction: The aim of this study was to introduce the failure mode and effect analysis (FMEA) as a method used for risk assessment and improving Occupational Health and Safety in a public medical laboratory. This qualitative-quantitative study was performed in the Laboratory of Biochemistry and Hormonology at Pasteur Institute of Tunis.

Methods: The study included staff who are familiar with the diagnostic process in the laboratory. A process map was designed to show key steps in the clinical diagnostic testing process and FMEA method was used for risks determination and analysis.

This study was performed in the following order:

- Setting up a multi-disciplinary working group
- Functional analysis: detailed description of each operation
- Risks analysis: standard FMEA worksheet for determination of the failures and their occurrence (O), severity (S) and detectability (D)
- Data analysis: RPN Calculation
- Corrective measures

Results: Results of FMEA has shown that medical staff, patients and contractor personnel are exposed to various hazards (12 identified hazards). A total of 61 risks were identified: 3 high risks (RPN ≥ 240), 24 moderate risks (RPN≥120) and 34 low risks (RPN < 120).

Based on our findings, we implemented actions that included elaboration of standard operating procedures SOP, staff education and training, workplace up grading in accordance with security standards, purchasing of individual and collective protection equipment and emergency exercises.

Conclusion: FMEA method helped us to systematically identify and prioritize risks to staff, patient, suppliers and facilities. Our findings directed changes, which, in turn, reduced potential hazards. We recommend this method of evaluation to other health care structures interested in improving safety and security.

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一般演題 Clinical Chemistry

Validated UPLC-MS/MS Assay for Monitoring ADHD Medications in Pediatric Urine

©Ching-Mei Chen、Liang-Jen Wang、Huey-Ling You、Wan-Ting Huang

INTRODUCTION: Attention-Deficit/Hyperactivity Disorder (ADHD) treatments, including methylphenidate, atomoxetine, and aripiprazole, require precise therapeutic drug monitoring (TDM) due to significant inter-individual pharmacokinetic variability and potential psychiatric adverse effects. Given their short half-lives and primary urinary excretion, a non-invasive monitoring approach is highly desirable, particularly for vulnerable pediatric populations.

OBJECTIVE: To develop and validate a rapid, non-invasive UPLC-MS/MS method for quantifying methylphenidate, atomoxetine, aripiprazole, and their metabolites in urine, and to evaluate the correlation between urinary and plasma drug concentrations.

METHODS: Urine samples (100 µL) underwent glucuronidase hydrolysis followed by Oasis HLB solid-phase extraction (SPE). Analytes were quantified via UPLC-MS/MS using positive electrospray ionization (ESI+) in multiple reaction monitoring (MRM) mode. The total analytical run time was optimized to 2.5 minutes per sample.

RESULTS: Validated per CLSI C62-A guidelines, the assay achieved a limit of detection (LOD) of 1 ng/mL and excellent linearity (1–1000 ng/mL, $r > 0.999$). Intra- and inter-assay coefficients of variation (CV) were <2.9% and <5.2% (n=40), respectively. Mean recoveries ranged from 96.6% to 103.7%. Crucially, no significant matrix effects were observed, and assay performance remained robust despite the presence of proteinuria or hematuria. Clinical application in 417 ADHD patients confirmed significant inter-individual concentration variability among patients receiving identical dosages.

CONCLUSION: We established a robust, high-throughput, and non-invasive UPLC-MS/MS assay for ADHD medication monitoring. This method facilitates precise dosage adjustments and personalized treatment strategies, ensuring optimal clinical outcomes for pediatric patients.

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P-4-70

一般演題 Clinical Chemistry

Kidney Injury Molecule-1 Outperforms Conventional Markers for Early Diabetic Nephropathy

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BACKGROUND: Diabetic nephropathy is a common microvascular complication of Diabetes Mellitus (DM) and a leading cause of chronic kidney disease. Conventional biomarkers, including proteinuria and serum creatinine, have limited sensitivity for detecting early renal injury. Kidney Injury Molecule-1 (KIM-1) has emerged as a promising biomarker for the early detection of kidney damage before abnormalities in traditional renal function markers become apparent.

OBJECTIVE: This study aimed to evaluate the association between KIM-1 levels and clinical characteristics among DM patients without proteinuria and with normal serum creatinine levels.

METHODS: A cross-sectional analytical study was conducted involving 52 DM patients selected through purposive sampling. The study was performed at the Laboratory of Dadi Regional Special Hospital, South Sulawesi, Indonesia, from June to October 2025. KIM-1 levels were analyzed according to sex, age, duration of DM, and glycemic control status. Statistical analyses included the Kruskal–Wallis test and post hoc Mann–Whitney test.

RESULTS: Significant associations were found between KIM-1 levels and duration of DM ($p<0.001$) as well as glycemic control status ($p<0.001$). No significant associations were observed between KIM-1 levels and sex ($p=0.579$) or age group ($p=0.779$). KIM-1 levels differed significantly across duration-of-DM groups ($p=0.001$). Patients with uncontrolled DM exhibited significantly higher KIM-1 levels than those with controlled DM (0.91 ng/mL vs. 0.76 ng/mL; $p<0.001$). Elevated KIM-1 levels were detected in patients with DM duration of at least one year despite normal serum creatinine levels and absence of proteinuria.

CONCLUSION: KIM-1 is positively associated with disease duration and glycemic control status in DM patients. Elevated KIM-1 levels in the absence of proteinuria and serum creatinine abnormalities suggest that KIM-1 may serve as a sensitive biomarker for the early detection of diabetic kidney injury.

KEYWORDS: Diabetes Mellitus; Kidney Injury Molecule-1; Serum Creatinine; Proteinuria; Diabetic Nephropathy.

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P-4-71

一般演題 Clinical Chemistry

Vitamin D status and thyroid profile in tunisian population

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INTRODUCTION: Vitamin D is a hormone that may be involved in various thyroid diseases. Recent studies have shown an association between vitamin D status and plasma levels of thyroid hormones. However, this relationship has not been investigated in Tunisia. The aim of our study was to describe the relationship between vitamin D status and thyroid profile in an adult Tunisian population.

METHODS: This was a descriptive study with retrospective data collection including all adult patients who underwent simultaneous measurement of 25-hydroxyvitamin D (25[OH]D), thyroid-stimulating hormone (TSH), and free thyroxine (FT4) at the Clinical Biochemistry and Hormone Laboratory of the Pasteur Institute of Tunis over a 6-year period. According to the Institute of Medicine, a 25[OH]D level < 20 ng/mL was considered insufficient, while a level > 20 ng/mL was considered normal. Statistical analysis was performed using SPSS software version 26.

RESULTS: A total of 897 patients were included in this study. The mean age of the study population was 46.49±14.96 years, with a female-to-male ratio of 6.06. Vitamin D insufficiency was significantly more frequent in women than in men (59.1% vs 41.7%, $p < 0.001$). No significant difference was found in serum FT4 and TSH levels between the group with vitamin D insufficiency and the group with normal vitamin D levels. We observed a correlation only between age and vitamin D levels ($r = 0.24$, $p < 0.001$).

CONCLUSION: Despite the absence of an association between vitamin D levels and thyroid hormones, the role of vitamin D in inflammatory processes justifies its assessment in thyroid disorders, particularly those of autoimmune origin.

P-4-72

一般演題 Clinical Chemistry

Preanalytical Practices Among Healthcare Professionals

Knowledge gaps and training needs in blood sampling

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Introduction: Preanalytical errors are a major source of nonconformities in medical laboratory testing and may affect the reliability of biological results. This study evaluated preanalytical practices among healthcare professionals at Farhat Hached University Hospital, Sousse, Tunisia, to identify gaps and propose improvement measures.

Materials and Methods: A descriptive cross-sectional study was conducted among staff involved in blood sampling. Data were collected using an anonymous questionnaire exploring patient identification, tube selection, labeling, transport and storage conditions, access to written procedures, use of the laboratory manual, and training needs.

Results: Forty-nine healthcare professionals participated. Most were nurses (69%) or laboratory technicians (16%). Mean age was 35 +/- 8 years, and 89% were female. More than one third had over 10 years of experience, but only 24% had received recent training in preanalytical procedures. Systematic patient identity verification before sampling was reported by 85.7% of participants, and 61.2% used computerized labels before blood collection. However, only 61.2% knew the rule requiring a separate tube for some tests, and 26.5% were unaware of the time constraint for samples collected after 10:30 a.m. Sample transport was mainly performed by a courier (61.2%), often under non-standardized conditions. When uncertain about tube selection, 42.9% consulted the laboratory manual, and 77.6% expressed a need for continuing education.

Conclusion: Although several good practices are applied, gaps remain in tube selection, sampling time constraints, and transport conditions. Targeted training, improved access to procedures, and harmonization of preanalytical practices are needed to reduce errors and improve result reliability.

Keywords: Preanalytical phase; Blood sampling; Healthcare professionals; Quality improvement; Training needs

P-4-73

一般演題 Clinical Chemistry

Reproducibility of Routine Chemistry Assays

Internal quality control data from a Tunisian university hospital

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Introduction: Analytical reproducibility is essential for reliable medical laboratory testing. When manufacturer reproducibility data are unavailable, internal quality control (IQC) can verify assay performance under routine local conditions. This study evaluated the reproducibility of enzymatic creatinine, urea, total bilirubin, and direct bilirubin assays at Farhat Hached University Hospital, Sousse, Tunisia.

Materials and Methods: A prospective analytical study was conducted over 30 days, from 18 January to 18 February 2026. Bio-Rad IQC materials, lot 89780, were analyzed on a Beckman Coulter DxC 700 AU analyzer at two concentration levels. For each analyte and level, the mean, standard deviation, and coefficient of variation (CV%) were calculated and compared with SFBC and EFLM analytical performance specifications.

Results: The observed CVs were satisfactory for all parameters. Urea showed CVs of 2.23% and 2.25% at levels 1 and 2, respectively. Enzymatic creatinine showed a CV of 1.71% at both levels. Direct bilirubin showed CVs of 1.95% and 4.61%, while total bilirubin showed CVs of 0.98% and 2.48%. All CVs were below the acceptable limits, indicating good reproducibility of the evaluated methods.

Conclusion: Enzymatic creatinine, urea, total bilirubin, and direct bilirubin assays showed satisfactory analytical reproducibility. IQC data provide a useful local reference for performance verification and support continuous monitoring of analytical quality.

Keywords: Analytical reproducibility; Internal quality control; Clinical chemistry; Creatinine; Urea; Bilirubin

P-4-74

一般演題 Clinical Chemistry

Reference Intervals for Lipid Profile in Healthy Adults

Reference Intervals for Lipid Profile in Healthy Adults in Cameroon

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Introduction. Lipid profile parameters (total cholesterol (TC), triglycerides (TG), high-density lipoprotein cholesterol (HDL), and low-density lipoprotein cholesterol (LDL)) are important biomarkers for assessing cardiovascular disease risk. It is essential to establish local reference intervals (RIs) to improve client management and research. These RIs are influenced by factors such as sex and age.

Objectives: To determine the mean, standard deviation, median, 95th percentile RIs for lipid profile parameters, and the difference between sex and age groups.

Method: This cross-sectional study was conducted between March 2026 and May 2026 at the Regional Hospital Bamenda, Cameroon. Participants were healthy voluntary blood donors aged 18 to 60 years. The Kruskal-Wallis test and the Mann-Whitney U test were used to assess differences by sex and by age group, respectively. Statistical significance was set at $p \leq 0.05$.

Results: A total of 256 participants (141 males and 124 females) were recruited for the study. The median TC was 175 mg/dl, TG was 72.8 mg/dl, HDL was 59.7 mg/dl, and LDL was 57.8 mg/dl. There were significant sex differences in TC (higher in males, $p < 0.001$) and HDL (higher in females, $p < 0.001$). The < 30-year age group showed prominent differences, with significantly lower TC, TG, and LDL compared with the older groups ($p < 0.05$).

Conclusion: This study provides locally derived RIs for lipid profiles by sex and age group. These findings can be used to enhance clinical decision-making in patient management and to inform research within the population.

Key Words: Cholesterol, cardiovascular disease, Triglycerides, lipoprotein, Reference intervals, Triglycerides, Healthy Adults,

P-5-1

一般演題 Pathology

Emerin, SUN1, and SUN2 Expression Decreased in Poorly-differentiated Lung Adenocarcinoma

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Background and Objectives: SUN1 and SUN2 are nuclear envelope proteins that directly bind to Emerin and interact with the cytoskeleton. This study aimed to examine the expression of Emerin, SUN1, and SUN2 in invasive lung adenocarcinoma using computer-assisted image analysis (CAIA) of immunohistochemically stained specimens. Correlations among these proteins and their associations with histological subtype and differentiation grade were investigated. Expression levels of these proteins were compared between primary tumors and lymph node metastases.

Material and methods: Sixty cases of invasive lung adenocarcinoma were examined, including ten cases with lymph node metastases. Formalin-fixed, paraffin-embedded sections were immunohistochemically stained for Emerin, SUN1, and SUN2 and visualized digitally using whole slide images (WSIs). Five representative areas were selected from each WSI, and cells were counted using CAIA to calculate positive cell rates (%).

Results: Emerin expression levels showed weak correlations with SUN1 and SUN2 (R = 0.3820 and 0.2192, respectively), whereas SUN1 expression moderately correlated with SUN2 expression (R = 0.4668). The expression levels of Emerin, SUN1, and SUN2 were significantly lower in solid adenocarcinoma than in papillary adenocarcinoma (p = 0.0312, 0.0027, and 0.0079, respectively). Furthermore, expression levels of all three proteins were significantly decreased in poorly differentiated adenocarcinoma compared with well- and moderately differentiated adenocarcinoma (p = 0.0027, 0.0035, and 0.0009, respectively). No significant differences were observed in the expression levels between primary tumors and lymph node metastases.

Conclusions: Similar to Emerin, SUN1 and SUN2 are involved in the tumor differentiation and histological architecture in invasive lung adenocarcinoma. However, their expression levels are not associated with lymph node metastases.

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一般演題 Pathology

Immunohistochemical Analysis of Hepatocellular Carcinoma After Immunotherapy

Spatial Distribution of Cytotoxic T Cells and Tumor Associated Macrophages

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Purpose: The spatial interplay between cytotoxic T cells and the immunosuppressive microenvironment after immune checkpoint inhibitor (ICI) therapy in hepatocellular carcinoma (HCC) remains highly heterogeneous and requires precise tissue-level evaluation.

Methods: We conducted a comparative pathological analysis on representative post-ICI HCC resection tissues. Immunohistochemical stainings for CD8, CD163, and PD-1 were performed. Histological architectures, tumor border infiltration, and tertiary lymphoid structures (TLS) were independently evaluated via visual, semi-quantitative microscopic assessment by pathologists.

Results: Pathologists identified two distinct microenvironment phenotypes. Case 1 exhibited high tumor heterogeneity, featuring a dense fibrous capsule border with prominent band-like CD8+ infiltrates and focal PD-1 expression, alongside low background inflammation. Conversely, Case 2 displayed a homogenous immune profile with borderless infiltrative growth, severe background cirrhosis, and abundant, highly active TLS heavily populated by PD-1+ lymphocytes, indicating functional immune reservoirs. Crucially, micro-spatial evaluation in both cases revealed that despite dense aggregates of immunosuppressive CD163+ macrophage nests, CD8+ T cells successfully infiltrated directly into these clusters, breaking the traditional "immune-excluded" barrier.

Conclusions: Post-immunotherapy HCC tissues demonstrate highly divergent macro-architectures, where PD-1 profiling validates background TLS as active immune engines. However, at the micro-environmental level, ICI therapy drives CD8+ T cells into CD163+ macrophage aggregates regardless of gross tumor borders. This striking spatial co-infiltration highlights the potent dynamic of immunotherapy to break through M2 macrophage-mediated immune exclusion, demonstrating a critical potential to overcome localized M2 macrophage suppression.

P-5-3

一般演題 Pathology

Digital Control of Formalin Bottles

Barcode-based management using SafeCheck in pathology

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Formalin-filled bottles used in pathology laboratories require strict control because they contain toxic and regulated chemicals. Loss, misplacement, or inventory discrepancies can cause safety, administrative, and compliance issues. We evaluated whether SafeCheck, a barcode-based management system for formalin bottles, could improve routine bottle control in the pathology department of a hospital. SafeCheck was developed and commercialized by Sansho MEC Co., Ltd. under the supervision of the Department of Pathology, Toyama University Hospital. Each bottle was assigned an individual barcode to enable digital tracking of the inventory status and bottle movement. Workflows before and after implementation were compared for monthly reconciliation time, recording completeness, traceability, usability, and safety. The formaldehyde vapor concentration near the bottles was measured during routine handling to assess potential exposure. Before implementation, monthly reconciliation depended on handwritten ledgers and manual checking and required approximately 10 min. After implementation, inventory data could be exported directly to Excel, and reconciliation was completed in approximately 1 min, representing a 90% reduction in time. No recording omissions have been identified since the introduction of the system. The barcode-based workflow simplifies bottle tracking, improves traceability, reduces administrative burden, and strengthens accountability in hazardous chemical container management. Formaldehyde vapor measurements confirmed that routine use did not increase detectable workplace exposure under the evaluated conditions of this study. These findings indicate that SafeCheck is a practical and efficient system for formalin bottle management. Barcode-based digital control may improve efficiency, documentation reliability, traceability, and operational safety, and may also be applicable to other hazardous chemical containers in laboratory settings.

Acknowledgement / Funding: This work was supported by research funding from Sansho MEC Co. Ltd.

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P-5-4

一般演題 Pathology

A Novel Formalin Container for Safer Pathology Practice

Development and refinement of exposure source control during tissue fixation

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Aims:Formalin is essential for tissue fixation, yet formaldehyde exposure remains a safety concern. We developed a novel reduced-exposure formalin container and evaluated it as an engineering source-control device.

Methods:Prototypes were refined with feedback from pathologists, medical technologists, and nurses, resulting in 10-mL and 30-mL formats. Airborne formaldehyde was compared with a conventional container under closed-space conditions by solid sorbent-high-performance liquid chromatography. The lid was opened for 10 s, and air was sampled for 10 min including the opening period. Five paired measurements were obtained: two at 30 mL, two at 10 mL, and one larger tupper-size condition. Usability impressions from 25 endoscopy staff were also reviewed.

Results:The developed container showed lower concentrations in all five pairs. Developed versus conventional values were 0.03 vs 1.41 and 0.03 vs 0.95 ppm at 30 mL, 0.15 vs 1.12 and 0.06 vs 0.13 ppm at 10 mL, and 0.14 vs 14.1 ppm in the larger condition. Pooled mean concentrations were 0.082 ± 0.059 ppm and 3.542 ± 5.921 ppm, respectively. Exploratory analysis of log-transformed paired values showed significant reduction ($p = 0.013$). Staff feedback was generally favorable regarding safety and reassurance.

Conclusions:The developed container markedly reduced airborne formaldehyde under standardized test conditions and showed good practical acceptability. It may complement ventilation, local exhaust, and exposure monitoring in pathology practice.

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一般演題 Pathology

Insights into Tenascin-C in MAPK inhibitor resistance in melanoma

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Targeted therapies against the MAPK signaling pathway have improved outcomes for patients with BRAFV600-mutant melanoma. However, rapid resistance to MAPK inhibitors (MAPKi) remains a major challenge driving disease progression. Beyond tumor-intrinsic mechanisms, the tumor microenvironment is increasingly recognized as a key regulator of adaptive resistance. Proteomic profiling identified the extracellular matrix glycoprotein Tenascin-C (TNC) as strongly upregulated in MAPKi-resistant melanoma cells. To investigate its functional relevance, TNC was knocked out in primary BRAFV600-mutant melanoma cells using CRISPR/Cas9. Real-time live-cell imaging showed that TNC deficiency significantly altered proliferation dynamics and migratory behavior, suggesting a role for TNC in regulating cellular programs linked to aggressiveness and adaptation. Phosphoproteomic analyses revealed distinct changes between TNC-knockout and control cells, indicating broad remodeling of intracellular signaling networks. Enrichment analyses linked these changes to, among others, cell adhesion, extracellular matrix organization, and focal adhesion signaling, implicating TNC in both proliferative and microenvironmental adaptation. Kinase-substrate enrichment analysis further showed altered kinase activity, reinforcing the role of TNC in signaling pathways associated with melanoma plasticity and therapeutic adaptation. Ongoing integration with RNA sequencing data aims to identify convergent pathways and refine the mechanistic basis of TNC-mediated resistance. Together, these findings identify TNC as a potential mediator linking extracellular matrix dynamics to intracellular signaling programs that promote therapy resistance, highlighting TNC-associated pathways as potential targets to improve the durability of targeted therapies in BRAFV600-mutant melanoma.

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一般演題 Pathology

Transforming Surgical Pathology Grossing: Digital Frameworks to AI Integration

Leveraging System Success Models for Scalable Training and Future AI Adoption

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Purpose: Grossing complex surgical specimens (breast, colorectal, and lung) traditionally relies heavily on individualized pathologist experience. This study evaluates the clinical impact of a standardized digital training workflow designed to empower medical technologists (MTs) to independently perform complex grossing. Grounded in the Information System Success (ISS) and Theory of Planned Behavior (TPB) models, it also outlines a roadmap for future Artificial Intelligence (AI) integration.

Methods: A consensus-based grossing protocol was implemented and tracked across approximately 1,000 monthly specimens. To scale this, a Moodle-based learning platform was designed. Analyzing institutional data from 234 healthcare professionals, the study utilized ISS and TPB models to evaluate how system quality and organizational support drive user adoption. Building upon this, an AI-integration framework is proposed to assess future user acceptance of AI-assisted lesion measurement.

Results: Clinical implementation successfully reduced and maintained pathologist-requested re-cut rates at 2-3% across high-volume cases. Crucially, this high-level MT competency enables attending pathologists to completely transition away from macroscopic grossing, allowing them to focus exclusively on microscopic slide review and diagnosis. Furthermore, structural evaluations confirm that technical quality and administrative assistance are core predictors of platform adoption, pre-establishing the organizational support needed to mitigate future technological resistance toward AI tools.

Conclusion: Combining clinically validated workflows with ISS and TPB frameworks creates a sustainable educational pathway. This digital foundation standardizes complex tissue sampling, optimizes physician workload, and minimizes diagnostic delays. Furthermore, it cultivates a receptive environment for integrating AI-assisted pathology tools, ultimately elevating overall laboratory quality control and patient care.

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一般演題 Pathology

Assessment of Fungal Staining with Chromic Acid-Free Methenamine Silver

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Grocott methenamine silver (GMS) staining is widely used for detecting fungal organisms in tissue sections. However, conventional protocols rely on 5% chromic acid as the primary oxidizing agent. Chromic acid is highly corrosive, toxic, and classified as a human carcinogen, germ cell mutagen, and environmental hazard, posing significant health and safety risks to laboratory personnel. This study evaluated a safer oxidizing strategy for GMS staining that eliminates chromic acid while preserving staining performance.

A modified GMS protocol was developed using heat pretreatment combined with periodic acid oxidation in place of chromic acid. Tissue sections were immersed in distilled water and incubated at 80 °C for 20 minutes, followed by oxidation with 1% periodic acid at room temperature for 15 minutes. Standard methenamine silver staining was subsequently performed and compared with the conventional protocol.

Heat pretreatment significantly enhanced the oxidative efficiency of periodic acid. Fungal organisms, including *Pneumocystis jirovecii*, *Cryptococcus neoformans*, *Aspergillus* spp., and *Candida* spp., were clearly demonstrated as sharply defined black structures. Staining quality and tissue morphology were comparable to those obtained with the chromic acid–based method. Importantly, the modified protocol eliminated exposure to hazardous hexavalent chromium, thereby improving laboratory safety.

Heat pretreatment combined with periodic acid oxidation provides a stable, reproducible, and effective chromic acid–free alternative to conventional GMS staining. This modified method maintains excellent diagnostic performance while offering a safer and more practical approach for routine histopathological detection of fungal organisms. +886 933556877

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一般演題 Pathology

Comparative Evaluation of Different Methods of Double Immunohistochemical Staining

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Background: Immunohistochemistry (IHC) is an essential diagnostic tool in pathology for detecting specific antigens in tumor cells. Conventional IHC visualizes only one antigen per tissue section, limiting interpretation. Double IHC staining allows simultaneous detection of two antigens with different chromogens, improving contrast and facilitating evaluation of marker relationships. However, most protocols use time-consuming sequential staining. This study evaluated a parallel double-staining approach using a dual-color detection system and compared it with the conventional sequential method.

Methods: Two antibody combinations were selected for diagnostic applications: SOX2/GFAP for distinguishing neoplastic gliomas from non-neoplastic gliosis, and Ki-67/Synaptophysin for assessing proliferative activity in neuroendocrine tumors. Double IHC staining was performed on formalin-fixed, paraffin-embedded tissue sections using a Leica BOND III automated immunostainer. Sequential staining used separate HRP/DAB and AP/Fast Red detection systems, whereas parallel staining employed a dual-detection system (ChromoPlex 1 Dual Detection) with simultaneous incubation of premixed primary antibodies. Staining quality and processing time were compared.

Results: The parallel staining approach demonstrated superior staining quality and contrast compared with the sequential method, enabling clearer visualization of marker distribution and spatial relationships. Moreover, without increasing reagent costs, the total staining time was reduced by approximately 2 hours.

Conclusions: Parallel double IHC staining provides improved visual presentation while substantially reducing processing time. This approach enhances diagnostic efficiency and represents a practical and effective alternative to conventional sequential double staining in routine clinical pathology. +886 933556877

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一般演題 Pathology

A Study of Rapid Silver Staining Method

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In the case of pituitary neuroendocrine tumors (PitNETs), intraoperative rapid examination requires determining whether the resected tissue is a PitNET or non-neoplastic anterior pituitary tissue; however, this determination is difficult based solely on rapid hematoxylin and eosin (HE) stains. In normal adenohypophysis, the reticulin fiber network preserves the microacinar architecture, whereas it is typically disrupted in PitNETs. Based on this property, we developed a "rapid silver staining method" that enables reticulin staining within a shorter time for intraoperative diagnosis, while conventional methods typically require about an hour. For this study, we used FFPE liver specimens and reacted them with 0.5%potassium permanganate solution, 2%oxalic acid solution, silver ammonia solution, and 0.2%gold chloride solution at 50℃ to determine the shortest time required to achieve staining intensity equivalent to that of standard silver staining. We evaluated the usefulness of the staining for diagnosis in collaboration with a pathologist. Heating accelerated the reactions of each reagent, and by performing certain steps of the silver staining protocol at 50℃. The total staining time was approximately 10 minutes, a result that is sufficiently practical for rapid diagnosis. However, in specimens where fibrosis is insufficient or excessive due to the small size of the sample, the advantages of silver staining cannot be fully utilized, thereby limiting its diagnostic utility. It is essential to thoroughly discuss the procedure with the operating surgeon in advance and ensure that sufficient tissue samples are available in order to effectively utilize this rapid silver staining method. This method enables the accurate diagnosis of PitNET within the limited timeframe available during intraoperative rapid testing. Furthermore, this method has been validated in numerous cases at other institutions. We hope that it will be adopted by more institutions in the future to improve the accuracy of PitNET diagnosis. (Kobe University Hospital: 078-382-6474)

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一般演題 Pathology

Consistent Membranous Staining of Pancreatic Islets in IGF2BP3/IMP3 Immunohistochemistry:

A Clone Specific and Unexpected Immunoreactivity with Potential Diagnostic Pitfalls

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[Background] Insulin-like Growth Factor 2 mRNA Binding Protein 3 (IGF2BP3/IMP3) is an oncofetal protein widely used as an immunohistochemical marker of malignancy, including pancreatic cancer. While optimizing IGF2BP3 immunohistochemistry (IHC) using clone 69.1 on pancreatic tissues, unexpected membranous staining was observed in the pancreatic islet cells. This staining pattern was discordant with the known cytoplasmic localization of IGF2BP3, prompting a systematic evaluation of its reproducibility and specificity. **[Methods]** Formalin-fixed, paraffin-embedded pancreatic tissue samples were analyzed using IHC with a focus on non-neoplastic pancreatic islets. Pancreatic neuroendocrine tumors (NETs) and pancreatic ductal adenocarcinomas were examined for comparison and assay validation. IGF2BP3 IHC and RNA in situ hybridization were performed using automated protocols. Multiple IGF2BP3 antibody clones were compared. Multiplex IHC with pancreatic endocrine cell markers was performed to identify the cellular lineage. **[Results and Discussion]** Clone 69.1 consistently exhibited a distinct membranous staining pattern corresponding to pancreatic β-cells, despite the absence of IGF2BP3 mRNA. Similarly, NET specimens also exhibited clear membranous immunoreactivity with 69.1; however, this staining was independent of insulin production and IGF2BP3 mRNA expression. In contrast, other IGF2BP3 antibodies did not display membranous staining, indicating that this feature is unique to 69.1. **[Conclusion]** This study highlights a robust and reproducible clone-specific membranous staining produced by the IGF2BP3 antibody clone 69.1 in pancreatic islets and NETs. This distinct localization suggests that 69.1 may interact with uncharacterized membrane-associated structures rather than exhibiting the canonical cytoplasmic localization of IGF2BP3. Recognition of this unique immunoreactivity is essential to avoid diagnostic misinterpretation in pancreatic pathology, and further studies are warranted to elucidate the underlying molecular mechanisms of this phenomenon.
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一般演題 Pathology

Digital Pathology Implementation in Remote Canadian Regions

A summary of unique opportunities and challenges

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ABSTRACT:

Background/Objectives: Digital pathology has the potential to revolutionize pathology diagnostics, especially in geographically isolated and underserved regions. By leveraging technology, telepathology, and integration with computer-aided diagnostic tools, digital pathology can improve access to prompt and accurate diagnostics. **Methods:** Our key steps to implementing digital pathology and transitioning operations to a digital network are assessing existing infrastructure, identifying gaps in connectivity and resources, and creating a workflow tailored to the needs of the healthcare system. **Results:** We present an approach of implementing digital pathology in Timmins, Northern Ontario, Canada, focusing on addressing regional disparities and the improvements that come alongside utilizing digital pathology. Our results show that digital pathology can provide prompt, efficient and better-quality diagnostic services to rural and un-deserved areas, improving patient care and outcomes. It also represents a cost-effective option with savings from eliminating travel costs, courier costs and additional operational efficiencies. **Conclusions:** Implementing digital pathology in rural settings presented with challenges related to infrastructure, technical abilities, workforce readiness, cost and other aspects involved in transitioning from traditional microscopy to a fully digital pathway. Digital pathology systems can help ensuring seamless data flow and improving overall healthcare delivery. Telepathology also allows pathologists to provide diagnostic services from a distance, which is particularly beneficial in areas with a shortage of pathologists.

Keywords: artificial intelligence; digital health; digital pathology; digital pathology implementation; remote diagnosis; telepathology; whole slide imaging.

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一般演題 Pathology

Frozen section aids ocular sebaceous gland carcinoma diagnosis & management.

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Introduction: Sebaceous gland carcinoma is a malignant tumour of the eyelid that often mimics benign conditions, therefore making early and accurate diagnosis is important. Frozen section examination is a useful intraoperative technique to assess tumour margins and guide further surgical management.

Purpose: To evaluate the role of frozen section in the management of Sebaceous gland carcinoma of the eyelid.

Methods: This retrospective study included 72 cases of Sebaceous gland carcinoma over the period of three years (Jan23-Dec25). Clinical details such as age, gender, laterality, and site of involvement were recorded. Frozen section was performed in 29 cases using a rapid intraoperative technique where clinically fresh tumour free tissue margins are sent from the OT immediately for frozen section and sectioned using a cryostat (SLEE MNT) (-20°C), stained by H&E, and then examined under a microscope by reporting pathologist to assess presence of tumour at surgical margins. Frozen report is released within half an hour.

Results: The mean age of patients was 60.73 years. There were 27 (37.5%) males and 45(62.5%) females (3:5 ratio). The left eye was involved in 32(44.4%) cases and right eye 40 (55.5%) cases. The upper eyelid was more commonly affected in 48 cases (66.6 %). Frozen section was performed in 29/72 (40.28%) cases, out of which only 4 cases (13.79%) showed one of the margins involved by tumour. After the frozen specimen the margins are processed for FFPE sections. Histopathological examination of the main tumour showed 29 poorly differentiated, 20 moderately differentiated, and 23 well-differentiated tumours. On histopathology correlation there was 100% Concordance between Frozen section and histopathology reports.

Conclusion: It helps the surgeon to detect margin involvement intraoperatively. It aids in achieving complete tumour excision and reducing recurrence. Frozen section is a valuable tool in the surgical management of eyelid Sebaceous gland carcinoma.

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一般演題 Pathology

Clinicopathological significance of Nectin-4 in urothelial carcinoma

Nectin-4 expression is associated with favorable clinicopathological features

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Background: Nectin-4 is a therapeutic target in advanced urothelial carcinoma (UC), and enfortumab vedotin (EV) is widely used in clinical practice. However, the clinicopathological significance of Nectin-4 expression in UC remains controversial. We aimed to characterize the expression patterns and clinical relevance of Nectin-4 in both upper and lower tract UC.
Methods: Immunohistochemical analysis of Nectin-4 was performed in 147 upper tract UC (UTUC) and 93 bladder UC (BLCA) surgical specimens. We also conducted complementary analyses using publicly available RNA-seq datasets.
Results: Nectin-4 was mainly expressed in tumor cells with membranous and cytoplasmic localization. High expression was detected in 84% of UTUC and 83% of BLCA cases. Increased Nectin-4 expression was associated with papillary architecture, lower tumor grade, earlier pathological T stage, and favorable clinical outcomes. Cytoplasmic staining was more frequent in advanced-stage tumors. In UTUC, Nectin-4 expression positively correlated with UPK3 and GATA3, and negatively with PD-L1 and CK5/6. A combined marker model showed strong prognostic value. Consistent with these findings, in silico analyses using public datasets confirmed that higher *NECTIN4* expression was associated with improved survival in both UTUC and BLCA. Pathway analysis showed enrichment of oxidative phosphorylation, lipid metabolism, and chemical carcinogenesis pathways in NECTIN4-high tumors, whereas EMT-related pathways were enriched in NECTIN4-low tumors.
Conclusion: Our findings highlight the clinical relevance of evaluating Nectin-4 expression and its subcellular localization in UC. IHC-based assessment of Nectin-4 may provide useful information for prognostic stratification and could contribute to optimizing therapeutic strategies in UTUC and BLCA.
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P-5-14

一般演題 Pathology

Evaluation of reaction endpoint in periodic acid methenamine silver staining

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Introduction: Periodic acid–methenamine silver (PAM) staining is indispensable for evaluating renal glomeruli. The methenamine silver reaction is a critical step that determines staining quality and often introduces variability among technologists. We previously reported a method using the color development in the glomerular basement membrane (GBM) and renal tubular brush border (RTBB) as indicators. However, observation of RTBB becomes difficult with tubular atrophy, making subtle color changes challenging to detect, and criteria for endpoint remain ambiguous. In the present study, we aimed to identify more objective and reproducible indicators for the reaction endpoint using autopsy and biopsy specimens.
Materials and Methods: Sections were cut at 1 µm thickness; autopsy specimens were prepared as 15 serial sections and biopsy specimens as 3 serial sections, subjected to PAM staining. **[Study 1]** Using autopsy kidneys, the time point at which RTBB turned brown was used as a reference. Reactions were stopped at 1-minute intervals for 5 minutes before and after this, and were compared with fully stained specimens to determine the optimal endpoint. **[Study 2]** In 30 biopsy specimens, PAM-stained sections prepared using the conventional endpoint (GBM turned black) were compared with those prepared using the endpoint identified in Study 1.
Results: [Study 1] In addition to GBM and RTBB, favorable results were obtained by using (i) the reaction point at which the mesangial matrix became indistinct due to intense blackening, and (ii) the reaction point at which nuclear outlines became clearly visible, as indicators. **[Study 2]** Favorable staining results were similarly obtained in biopsy specimens when the endpoint identified in Study 1 was applied.
Conclusion: Favorable PAM staining results were obtained by using the degree of color development derived from nonspecific reactions in peri-glomerular tissue as a criterion for the reaction endpoint of the methenamine silver reaction.
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P-5-15

一般演題 Pathology

HEQUALYZER: What do you see when you look at H&E?

Empowering Biomedical Laboratory Scientists through an integrated colorimetric and artefact framework

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Background. Digital pathology demands rigorous quality control of whole slide images (WSI), traditionally performed manually by BLS (biomedical laboratory scientists) — qualitative, prone to intra- and inter-observer bias, time-consuming, and irreconcilable with sustainable high-throughput operation.
Objective. To develop and assess the pilot operational feasibility of HEQUALYZER for quantitative haematoxylin and eosin (H&E) staining assessment, integrated with adapted GrandQC for artefact quantification, as a unified quality control framework.
Methods. 544 WSI from heterogeneous biopsies were digitised at 40× on an Aperio GT450DX (CAPGS, Coimbra). HEQUALYZER applied a multi-step pipeline — tissue detection, stain deconvolution, nuclear segmentation, patch-based dual-resolution sampling — extracting optical density and CIE L*a*b* lightness for haematoxylin and eosin, classified against literature-derived thresholds (*OPTIMUM*, *ACCEPTUM*, *REVISIO*). GrandQC detected five artefact types: folded tissue, air/edges, out-of-focus, dark spots/foreign bodies and pen markings. A rule-based system mapped outputs to five corrective tiers: release (*OPTIMUM* or *ACCEPTUM*, ≤10% total artefact); re-stain (*REVISIO*); and, when total artefact >10%, re-coverslip (air/edge), re-digitise (out-of-focus), or re-cut (folded tissue or dark spots), assigned by dominant artefact type.
Results. HEQUALYZER approved 93.9% (511/544), median 10 s/WSI. The integrated framework released 83.8% (456/544), mean processing time 34 s/WSI, and flagged 88 (16.2%) for BLS review; 55 (10.1%) flagged on artefact burden alone, folded tissue predominant in 32 (5.9%). Tiers: re-stain 6.1% (n=33, REVISIO), re-cut 7.9% (n=43), re-digitise 3.7% (n=20), re-coverslip 0.4% (n=2); 9 WSI required ≥2 actions. Convergent agreement with H&E L* ratio: κ=0.283; OR=16.0; χ^2=41.4; p<0.001.
Conclusion. The HEQUALYZER + GrandQC framework offers a robust, scalable WSI quality control solution aligned with the leading laboratory accreditation and certification standards, empowering BLS to evolve from manual reviewers to data-driven quality stewards with traceable corrective actions.

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一般演題 Pathology

Analysis of CEACAM6 expression in intrahepatic cholangiocarcinoma

Analysis of CEACAM6 expression in relation to the progression of intrahepatic cholangiocarcinoma

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Intrahepatic cholangiocarcinoma (iCCA) is a malignant tumor arising above the second-order bile ducts and has a poor prognosis. Therefore, the development of novel early diagnostic markers and therapeutic strategies is urgently needed. We previously reported that integrin αvβ6 (β6), a cell adhesion molecule, may be a pathological diagnostic marker and therapeutic target molecule for iCCA. However, the mechanisms of activating integrin molecules remain unclear. In this study, we focused on CEACAM6, which was identified as a differentially expressed gene in RNA- sequencing analysis of ITGB6-knockout iCCA cell lines, and investigated CEACAM6 expression and its relationship with integrin β6 in iCCA. First, we analyzed CEACAM6 expression and its association with clinicopathological features in 67 surgically resected iCCA tissue samples. CEACAM6 showed little expression in non-tumor bile ducts but was strongly expressed in tumors, and its expression in tumors was classified into high (in 34 cases) and negative to low (in 33 cases). High CEACAM6 expression was associated with large duct type in localization, periductal infiltrating type and intraductal-growth type in macroscopic type, well differentiation type, and bile duct invasion, and was positively correlated with integrin β6 expression. In vitro analysis demonstrated that CEACAM6 mRNA expression varied among iCCA cell lines in the following order: HuCCT1 > SSP-25 > RBE > HuH28. Furthermore, ITGB6 expression suppression using siRNA in HuCCT1 and SSP-25 cells resulted in decreased CEACAM6 expression at both the mRNA and protein levels. Immunofluorescence staining revealed the partial colocalization of CEACAM6 and integrin β6. In the future, we will analyze the effects of CEACAM6 suppression on integrin β6 expression, downstream signaling pathways, and protein-protein interaction between CEACAM6 and integrin β6 to clarify their roles in iCCA progression.

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一般演題 Pathology

Implementation of MacroPATH MX SK C-Scan

Image-Based Macroscopic Biopsy Documentation

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In the laboratory of histology, the MacroPATH MX SK camera with integrated C-scan software has been purchased and implemented for the routine handling of various types of biopsies specimens. The purpose of the C-Scan system is to optimize the process and workflow when handling biopsies by replacing dictated macroscopic description of the histological material with standardized image-based documentation, thereby reducing the workload across different professional groups.

Commissioning of the MacroPATH MX SK C-Scan required an approved acceptance test, for which a set of acceptance criteria was established to ensure that the performance and quality of the equipment met both the laboratory's requirements and the supplier specifications. The criteria included successful QR-code reading on cassettes, image acquisition time, image quality, as well as requirements to the software which included integration with the laboratory information system (LIS), and transfer of image files to the image management system (IMS).

The acceptance test was conducted over a two-week period and included 220 requisition numbers comprising 516 patient samples from gastrointestinal pathology. The process involved continuous evaluation and optimization. System performance and equipment was primarily assessed based on feedback from the pathologists and biomedical laboratory scientists involved. The MacroPATH MX SK C-Scan fulfilled all predefined acceptance criteria and was therefore approved for routine clinical use.

The implementation of MacroPATH MX SK C-scan resulted in increased uniformity, improved traceability, and more detailed macroscopic descriptions, all of which is beneficial to the diagnostic quality. In addition, the workflow related to handling biopsies has been reassessed to ensure internal quality and traceability which contributes to optimal patient safety.

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一般演題 Pathology

Rapid Fresh Pathology for Breast Core Biopsies

A section-free workflow preserving tissue for downstream testing

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Purpose

Breast core needle biopsy plays a critical role in tumor diagnosis and biomarker evaluation. However, limited specimen volume often restricts tissue availability for downstream immunohistochemical and molecular analyses. Conventional frozen section examination is generally unsuitable for small core specimens because of tissue loss and freezing artifacts. This study evaluated a rapid fresh pathology (RFP) workflow for real-time imaging of fresh breast core biopsy specimens while preserving tissue integrity.

Methods

Fresh breast core biopsy specimens obtained from outpatient patients were processed using a rapid whole-mount hematoxylin and eosin staining protocol followed by nonlinear optical mesoscale imaging via PATHOscope PS100 system. H&E-contrast images were generated without tissue sectioning or freezing. The images were compared with corresponding formalin-fixed paraffin-embedded (FFPE) histology for evaluation of tissue architecture, tumor cellularity, and specimen preservation.

Results

RFP successfully generated high-resolution H&E-contrast images from fresh breast core specimens within minutes. Histologic structures including invasive tumor nests, stromal components, adipose tissue, and glandular architecture were identifiable on RFP images. The section-free workflow minimized tissue consumption from limited core specimens and preserved tissue integrity for subsequent ancillary testing. Rapid imaging also demonstrated feasibility for immediate specimen adequacy assessment during biopsy workflows.

Conclusion

RFP provides a rapid and tissue-preserving imaging approach for fresh breast core biopsy evaluation. This workflow may support real-time biopsy assessment while preserving valuable tissue for downstream diagnostic and molecular analyses.

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一般演題 Pathology

ARIA-Like Mouse Model Based on Cerebral Amyloid Angiopathy

Crossing endothelial APP770 mice with a conventional AD model

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Alzheimer's disease (AD) is often accompanied by Cerebral Amyloid Angiopathy (CAA), which is characterized by the accumulation of amyloid-β (Aβ) in cerebral blood vessels. In recent years, anti-Aβ antibodies have been used as therapeutic agents for AD; however, treatment-related adverse events observed on MRI, known as amyloid-related imaging abnormalities (ARIA), have become a major concern. The molecular mechanisms underlying ARIA remain unclear, partly due to the lack of animal models that faithfully recapitulate ARIA pathology. We previously generated an AD mouse model with prominent CAA pathology, characterized by Aβ accumulation in both the brain parenchyma and cerebral vasculature, by crossing endothelial cell–specific APP770-expressing mice (EC-APP770^{+}) with a conventional AD model (Tachida *et al.,* ***J Biol Chem***, 298, 101880 (2022)). In the present study, we used this model to establish and characterize an ARIA-like mouse model. Twelve-month-old EC-APP770^{+} : *App* $^{NLGF/wt}$ mice and *App* $^{NLGF/wt}$ mice were administered aducanumab (100 mg/kg) intraperitoneally once weekly for 4 weeks, after which the model was evaluated by assessing Aβ clearance and the presence or absence of microbleeds. In both EC-APP770^{+} : *App* $^{NLGF/wt}$ mice and *App* $^{NLGF/wt}$ mice, the number of $A\beta_{42}$-positive parenchymal plaques was significantly reduced following aducanumab treatment, confirming the efficacy. Furthermore, Berlin blue staining revealed a significant signal exclusively in the aducanumab-treated EC-APP770^{+} : *App* $^{NLGF/wt}$ mice. Clusters of CD68-positive cells were observed in and around hemosiderin-positive areas, particularly surrounding blood vessels, and their phenotypic characterization is currently underway. These results demonstrate that this novel AD model recapitulates both AD and CAA pathology and serves as a useful model for ARIA, contributing to a better understanding of its pathogenesis.

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P-5-20

一般演題 Pathology

Rapid immunohistochemistry using an alternating current electric field

for intraoperative frozen-section diagnosis

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Application of immunohistochemistry (IHC) as an objective method for intraoperative rapid tissue diagnosis, considered to be a source of stress for pathologists, has recently been attempted in Japan. Although frozen sections are routinely used for intraoperative rapid tissue evaluation, diagnosis based solely on rapid hematoxylin-eosin staining is often difficult because of artifacts introduced during section preparation. In this presentation, we introduce a rapid IHC method that utilizes an alternating current electric field developed for this purpose, together with thermal treatment of frozen sections. Electric field mixing (EFM) is a non-contact mixing technique in which a stationary microdroplet is positioned between upper and lower electrodes and exposed to a low-frequency electric field, which induces movement of water molecules within the droplet without the need for mechanical stirring or an agitation device. Because this method is effective for mixing minute amounts of liquid on the microliter scale, it is expected to shorten reaction times during immunohistochemical staining. Using rapid IHC, staining can be completed within approximately 10-15 minutes. Furthermore, it was found that addition of heat-induced antigen retrieval before staining enabled the use of many antibodies commonly employed in routine pathological diagnosis. In addition, use of a fixative composed of equal parts 100% formalin and 100% ethanol supplemented with 5% acetic acid improved staining quality in frozen tissue sections. We consider that combining immunohistochemistry with intraoperative rapid tissue biopsy can improve diagnostic accuracy, thereby contributing not only to improved patient care but also to reduced diagnostic stress on pathologists.

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一般演題 Pathology

Evaluation of lead-induced ROS *in vitro* and *in vivo*

Implication for molecular mechanisms of heavy metal toxicity and antioxidant intervention authors affiliation

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Lead (Pb) is a ubiquitous environmental pollutant that poses severe risks to human health by inducing multi-organ toxicity mediated through reactive oxygen species (ROS) generation. This study investigates the cytotoxic and oxidative pathways of lead acetate ($Pb(C_2H_3O_2)_2$) utilizing an integrated framework that bridges an in vitro human cell model with an in vivo invertebrate model to establish a comprehensive evaluation platform for heavy metal toxicity. For the in vitro model, human embryonic kidney cells (HEK293T) were exposed to lead acetate (0~100 μM). Cell viability was evaluated via MTT assay after 24 and 48 hours to determine half-maximal inhibitory concentrations (IC_{50}), while intracellular ROS accumulation was quantified utilizing the CM-H_2DCFDA fluorescent probe via flow cytometry. Concurrently, for the in vivo model, age-synchronized Caenorhabditis elegans were exposed to identical concentrations to record chronological mortality and evaluate systemic ROS accumulation within the intestinal tract via in vivo fluorescence staining. The in vitro results demonstrated that lead acetate significantly reduced HEK293T viability in a clear dose- and time-dependent manner, yielding IC_{50} values of approximately 50 μM at 24 hours ($p < 0.01$) and decreasing to 25 μM at 48 hours ($p < 0.001$). Flow cytometric analysis revealed a marked, concentration-dependent increase in CM-H_2DCFDA fluorescence intensity, confirming severe intracellular ROS accumulation that overwhelmed innate cellular defenses. Parallel in vivo data indicated a significant, dose-dependent reduction in C. elegans lifespan, with ongoing staining anticipated to reveal a corresponding surge in systemic oxidative stress within the nematode gut. In conclusion, this study demonstrates a strong correlation between in vitro cellular damage and initial in vivo organismal survival decline. This dual-model approach provides a reliable framework for evaluating environmental toxins and facilitating future screening of protective natural antioxidants.
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一般演題 Pathology

Anti-Lung Cancer Activities of Curcuminoids via Multi-Target Mechanisms

Insights from Molecular Docking, Cell Culture, and *C. elegans* Models

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Lung cancer remains a leading cause of global mortality, with non-small cell lung cancer (NSCLC) accounting for 85% of cases. Developing multi-target, low-toxicity agents that precisely reactivate apoptosis is of paramount clinical importance. This study utilizes an integrated platform to evaluate active derivatives from Curcuma longa. Initially, molecular docking via SwissTargetPrediction screened compound-target binding affinities against key NSCLC proteins (Caspase-3, EGFR, Bax, Bcl-2). MTT assays determined the IC_{50} on A549 lung adenocarcinoma cells and HEK 293T cells. Flow cytometry with Annexin V/PI staining, Clonogenic, and Wound Healing assays evaluated apoptotic, long-term anti-proliferative, and anti-metastatic potentials. Mechanistic pathways were elucidated using RT-qPCR and Western Blotting for intrinsic mitochondrial apoptosis markers. Finally, a Caenorhabditis elegans model evaluated in vivo bio-safety and physiological protection. In silico analysis demonstrated outstanding binding affinities; notably, α-turmerone (1), 4-(1',5'-dimethyl-4'-hexenyl)-2-cyclohexen-1-one (3), and 2-methyl-6-(4'-methylcyclohexa-3'-enyl)hept-2-en-4-one (7) exhibited strong binding energies against EGFR (-7.97, -7.078, and -7.826 kcal/mol), Bax, and Bcl-2. In cell models, MTT assays revealed dose- and time-dependent cytotoxicity against A549 cells, with 48-hour IC_{50} values of 116 μM (1), 62 μM (3), and 86 μM (7). Annexin V staining confirmed apoptosis-driven cell death; at 100 μM, (7) induced the highest apoptotic rate (33.03 ± 4.92%, $p < 0.001$), outperforming Doxorubicin (15.57 ± 2.10%). Clonogenic assays indicated that (7) at 10 μM drastically suppressed colony formation ($p < 0.001$). Mechanistically, Western Blot revealed a robust, dose-dependent decrease in Pro-caspase-3 protein levels across all compounds, confirming activation of the downstream mitochondrial apoptotic cascade. These findings provide concrete evidence that these curcumin derivatives possess potent anti-lung cancer activity and demonstrate immense clinical potential as multi-target chemotherapeutic candidates against NSCLC. Email: anita.chao88@gmail.com, Phone number: +886-908-498-938

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一般演題 Pathology

Curcumin Enhances Doxorubicin Efficacy in Human Hepatocellular Carcinoma Cells

Synergistic Inhibition of Proliferation, Clonogenicity, and Migration

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Hepatocellular carcinoma (HCC) is one of the leading causes of cancer-related mortality worldwide and is frequently associated with high recurrence rates, therapeutic resistance, and poor clinical prognosis. Doxorubicin is widely used for HCC treatment because of its potent antitumor activity; however, its clinical application is often limited by dose-dependent cardiotoxicity and hepatotoxicity associated with excessive reactive oxygen species (ROS) generation and oxidative stress. Curcumin, a natural polyphenolic compound derived from *Curcuma longa*, possesses antioxidant, anti-inflammatory, antiproliferative, and pro-apoptotic properties and has recently attracted attention as a potential chemosensitizer in cancer therapy. In this study, the synergistic antitumor effects of curcumin and doxorubicin were investigated using Hep-3B human hepatocellular carcinoma cells as an in vitro model. Cells were treated with curcumin (0.1, 1, 10, and 100 μM), doxorubicin, or their combination. Cell viability, clonogenic survival, and migration were evaluated using MTT assay, clonogenic assay, and wound-healing assay, respectively. The results demonstrated that curcumin exerted dose-dependent inhibitory effects on Hep-3B cell growth, while combination treatment significantly enhanced the cytotoxic effect of doxorubicin, reducing cell viability to 29%. In clonogenic assays, combined treatment markedly suppressed colony formation, achieving up to 98% inhibition at the highest curcumin concentration tested. Furthermore, wound-healing analysis revealed that curcumin potentiated the anti-migratory effect of doxorubicin, resulting in greater inhibition of wound closure compared with either monotherapy. Overall, these findings suggest that curcumin enhances doxorubicin sensitivity and synergistically suppresses proliferation, survival, and migration in HCC cells. This combination strategy may provide a promising therapeutic approach for improving anticancer efficacy while potentially reducing chemotherapy-associated toxicity in hepatocellular carcinoma treatment.

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一般演題 Pathology

Crithmum maritimum L. Suppresses Lung Cancer via p38-MAPK Pathway

Focus on Pro-Apoptotic Effects and Signaling Cascades

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Abstract: Sea fennel (*Crithmum maritimum L.*) is a halophytic plant rich in bioactive polyphenols and flavonoids, previously reported to possess strong antioxidant and anti-inflammatory activities. However, its potential anticancer effects and underlying molecular mechanisms remain less explored. In this study, 33 phytochemical compounds isolated from sea fennel were systematically tested on A549 lung cancer cells. Cell viability was evaluated by MTT assay, colony formation by clonogenic assay, and migration by wound-healing assay. Early apoptosis was detected by Annexin V-FITC staining under a fluorescent microscope, and p38 MAPK expression was examined by Western blotting. Our results show that most isolated compounds reduced A549 cell survival. Among them, CML5 (aesculetin dimethyl ester), CML8 (protocatechuic acid), CML14 (*p*-hydroxycinnamaldehyde), and CML18 (*p*-methylbenzoic acid, *p*-toluic acid) showed the strongest inhibitory effects. Increasing concentrations of CML5 significantly decreased cell survival by 45%. These lead compounds also significantly suppressed colony formation, with high concentrations of CML14 reducing colony numbers by 41%. Furthermore, high concentrations of CML8 and CML18 significantly impaired wound closure, indicating robust anti-migration activity. Mechanistically, Annexin V-FITC staining revealed that these compounds significantly induced early apoptosis in a dose-dependent manner. Western blot analyses further showed that CML8 treatment markedly increased total p38 MAPK protein expression. In conclusion, these sea fennel-derived bioactive compounds exhibited potent antiproliferative, anti-survival, anti-migratory, and pro-apoptotic activities against A549 lung cancer cells, which may be associated with altered p38 MAPK pathway expression. These findings strongly support their potential as promising natural anticancer candidates, warranting further investigation of their detailed molecular mechanisms and potential therapeutic applications.

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一般演題 Pathology

Bioactivity-Guided Isolation of Active Ionone Compound from *Physalis peruviana*

Evaluating Its Anti-Cancer Effects in SKOV3 Ovarian Cancer Cells

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Background: Ovarian cancer is one of the most deadly cancers worldwide, many patients experience limited treatment effectiveness or poor prognosis. The search of natural anti-cancer compounds is an important trend, and the active ingredients from Physalis peruviana against ovarian cancer remain to be explored. Therefore, this study is suitable as the subject. Purpose: The aim of this study is to isolate and select compounds from the aerial parts of Physalis peruviana by bioactivity-guided method, and evaluate the effects of the selected active compound on SKOV3 cells. Methods: Thirty-four fractions from Physalis peruviana were obtained by silica gel chromatography. These fractions were subjected to MTT assay screening using SKOV3 cells, and fraction 24 was the most active one. Two compounds (ionone A and ionone B) were further isolated by silica gel chromatography, compound ionone A showed the highest activity. To investigate its effects on SKOV3 cells, the MTT assay was used to confirm the IC50, the wound healing assay measured cell migration, the clonogenic assay was used to evaluate cell proliferation, and the flow cytometry with Annexin V/PI staining to determine apoptosis. Results: The structure of ionone A was characterize based on spectral analysis. The MTT assays showed its has significant anti-ovarian cancer activity, with IC50 value of 16.21 μM at 48 h, and exhibited time- and dose- dependent effects. Wound healing assays and clonogenic assays demonstrated its ability to inhibit cell migration and proliferation, respectively. Annexin V/PI staining confirmed ionone A induced apoptosis in SKOV3 cells. Conclusion: We isolated and screened ionone A from the aerial parts of Physalis peruviana by bioactivity-guided method, and identified ionone A as a potential anti-ovarian cancer compound. It reduced cell viability, migration, proliferation, and induced apoptosis. These findings highlight its potential for clinical application, warranting further investigation into its mechanism of action.
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P-5-26

一般演題 Pathology

Association Between HPV and Tumor Immunity in Oropharyngeal Carcinoma

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[Background] It is well known that the presence of Human papillomavirus (HPV) is associated with better prognosis of oropharyngeal cancer. In Japan, approximately 50% of cases are reported to be HPV-related. Although HPV positivity is a favorable prognostic factor for oropharyngeal squamous cell carcinoma (OPSCC) and an important biomarker, the underlying mechanism remains unclear. In this study, we investigated the association between HPV infection and tumor-infiltrating lymphocytes (TIL) in OPC.

[Materials and Methods] We evaluated 55 OPSCC patients (median age: 64 years) treated between 2019 and 2025, comprising 26 in HPV-positive group and 29 in HPV-negative group. Immunohistochemical staining was performed on paraffin sections to detect CD3, CD4, CD8, CD20, CD103, PD-L1, and PD-1. Positive cells were counted in intra-tumoral and peri-tumoral areas, and marker expressions were compared between the two groups.

[Results] HPV-positive group showed significantly higher infiltration of CD3 (intra- and peri-tumoral), CD8 (intra-tumoral), CD20 (peri-tumoral), and CD103 (peri-tumoral) compared to HPV-negative group ($P < 0.05$). The PD-L1 positivity rate also tended to be higher in HPV-positive group (62%). Clinically, all patients in HPV-positive group presented with stages I–III, and 22 of 26 patients were free from recurrence or metastasis. Conversely, patients in HPV-negative group exhibited a wider stage range (I–IV), with 18 of 29 patients experiencing recurrence or disease-specific death.

[Conclusion] In HPV-positive cases, compared with HPV-negative cases, the number of CD3+, CD8+, CD20+, and CD103+ lymphocytes infiltrating intra-tumoral or peri-tumoral tissue was significantly higher, and the degree of infiltration was more pronounced. It has been shown that a higher number of these tumor-infiltrating lymphocytes is associated with a greater likelihood of an immune response, suggesting that this may contribute to a favorable prognosis.

P-5-27

一般演題 Pathology

Long-Term Formalin-Ethanol Fixation Affects Nucleic Acid Quality

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[Objective] We previously demonstrated that a mixture of 10% neutral-buffered formalin and ethanol (hereafter referred to as the “mixture”) yields superior nucleic acid quality compared to conventional 10% neutral-buffered formalin when the fixation duration is limited to 24 h. Furthermore, our investigation of temporal changes in nucleic acid quality revealed that the mixture exerts a lesser impact on nucleic acids than formalin alone for up to 120 h. However, whether nucleic acid degradation is more effectively mitigated by 24-h fixation with formalin alone or extended fixation with the formalin–ethanol mixture remains unclear. Fixation with the mixture within 24-h facilitates high-quality nucleic acid recovery; however, prolonged fixation beyond this period may pose risks similar to those associated with conventional formalin. Therefore, this study aimed to evaluate the effect of extended fixation with the mixture on nucleic acid fragmentation compared to 24-h fixation with 10% neutral-buffered formalin.
[Methods] Porcine colonic tissues (10 mm × 5 mm) were immersed in a 10% neutral-buffered formalin–ethanol mixture (formalin:ethanol, 6:4). Fixation durations were set to 48, 72, and 120 h, and tissues fixed in 10% neutral-buffered formalin for 24 h were used as controls. Additionally, quantitative real-time polymerase chain reaction was performed using primers targeting the 71-, 111-, and 201-bp fragments to quantify their respective yields. The 111 bp/71 bp and 201 bp/71 bp ratios were calculated as fragmentation indices.
[Results] The 71-bp yield decreased below the control level in tissues fixed with the mixture for 72 or 120 h. At other fixation durations and fragment lengths, the mixture resulted in higher yields. Higher 111 bp/71 bp and 201 bp/71 bp ratios were also observed, suggesting reduced nucleic acid fragmentation.
[Conclusion] Fixation with the formalin-ethanol mixture preserves nucleic acid integrity more effectively than conventional formalin, even with fixation times extended up to 120 h.

P-5-28

一般演題 Pathology

Implementation of AT192: automated preparation of paraffin-embedded tissue-blocks

An approach towards integrating more automated work processes in the laboratory

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The implementation of the automated trimming machine AT192 for block preparation prior to automated sectioning represents a significant step toward improving standardization, efficiency, and reproducibility in the histopathology laboratory. The AT192 is designed to precisely trim paraffin-embedded tissue-blocks before microtomy, thereby optimizing downstream automated sectioning workflows and reducing manual handling variability.
Trimming of paraffin-embedded tissue-blocks for automated sectioning has until now been done manually which requires the time of two biomedical laboratory scientists to ensure completion of the daily production volume. By implementing an automated trimmer, preparation time could be reduced. The implementation process included technical installation, calibration, and validation of trimming accuracy, section surface quality, and block alignment consistency. By using one hundred paraffin-embedded test blocks, eight different programs were established to ensure quality requirements. Standard operating procedures were developed to define workflow integration, maintenance routines, cleaning protocols, and troubleshooting procedures. Emphasis was placed on operator training to ensure safe handling, correct block positioning, and optimal parameter selection for different tissue types. Risk assessment addressed mechanical safety and blade handling. After implementation, the laboratory observed enhanced workflow efficiency, reduced and improved consistency in block preparation, contributing to more stable automated sectioning performance. Comparative analyses between manual trimming and AT192-assisted preparation demonstrated improved uniformity of block surfaces and reduced preparation time per paraffin-embedded tissue-block. In conclusion, the integration of the AT192 supports improved standardization, productivity, and quality assurance in histological sample preparation, strengthening the overall robustness of the laboratory’s automated sectioning processes.

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一般演題 Pathology

Analysis of Kaposi's sarcoma-assosiated herpesvirus K1 gene function

The association of K1 gene with invation ability and epithelial mesenchymal transition

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Background:

Kaposi's sarcoma-associated herpesvirus (KSHV) is causative virus of Kaposi's sarcoma (KS). KSHV genome encodes an oncogene known as the K1. The K1 protein is a transmembrane protein. Based on the diversity of its extracellular domain, KSHV is classified into six types, from type A to type F. Previous studies have shown that the transformation activity of type A K1 is more potent than that of type C K1. To identify which region of the extracellular domain is critical for transformation, we compared transformation activities such as invasion capacity and induction of epithelial-mesenchymal transition (EMT) using K1 clones with recombinant extracellular domain.

Materials and Methods:

We established the K1 expressing cell lines. AK1 and CK1 are cell lines transduced with the Type A and Type C K1 genes, respectively. We also constructed four types of recombinant K1 expressing cell lines of which a part of extracellular domain of type A K1 was substituted with corresponding part of type C. Invasion capacity was evaluated using scratch assays, and induction of EMT was investigated by immunostaining and Western blotting.

Results:

Scratch assay demonstrated that AK1 and N-terminal recombinant K1 exhibited high invasive capacity. Western blotting showed the increased N-cadherin expression in AK1. Furthermore, immunohistochemical staining for Snail revealed increased expressions in both AK1 and N-terminal recombinant K1. However, CK1 and the other recombinant K1 clones showed low activity in all assays.

Discussion:

This study suggests that the induction of EMT shown as increased expression of N-cadherin and Snail is associated with the invasive capacity of K1. Because N-terminal recombinant K1 retained invasive capacity and induction of EMT, it is considered that the region of the extracellular domain critical for K1 gene-mediated transformation lies outside the N-terminal region.

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一般演題 Pathology

Analysis of ARIA-like pathology in Alzheimer disease model mice

Characterization of Vascular Amyloid-beta in a Novel CAA/ARIA Model Mouse

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Most cases of dementia are attributed to Alzheimer's disease (AD), which is characterized by the accumulation of amyloid-beta (Aβ) in the brain. Recently, multiple anti-Aβ antibody therapies, including aducanumab (Adu), have been approved, raising expectations for preventing disease onset through Aβ removal. However, approximately 20% of patients develop a side effect known as amyloid-related imaging abnormalities (ARIA), and its underlying mechanism remains unclear. In this study, we investigated whether ARIA-like changes can be reproduced and how Aβ dynamics are altered following anti-Aβ antibody administration using a novel AD model mouse exhibiting vascular amyloidosis. This model was generated by crossing APP knock-in mice ($App^{NLGF/wt}$) with EC-APP770^{+} mice, in which APP is expressed specifically in vascular endothelial cells. EC-APP770^{+}: $App^{NLGF/wt}$ and $App^{NLGF/wt}$ mice were divided into an Adu-treated group and a PBS-treated control group, and ARIA-like pathology and Aβ distribution were analyzed. The number of parenchymal Aβ42 plaques was reduced in the Adu-treated group, whereas no significant change was observed in perivascular Aβ. Notably, microbleeding was observed exclusively in Adu-treated EC-APP770^{+}: $App^{NLGF/wt}$ mice, suggesting the potential induction of ARIA-like changes in this model. Furthermore, during the analysis of vascular Aβ40, we found that Aβ could be extracted from brain sections during methanol treatment in the immunofluorescence staining procedure. Quantification of the methanol extracts revealed that Aβ42 levels were comparable between groups, whereas Aβ40 levels were significantly higher in EC-APP770+:AppNLGF/wt mice. Further analyses are currently ongoing.These findings suggest that vascular Aβ may contribute to the development of ARIA and highlight the utility of this model for investigating its underlying mechanisms.

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一般演題 Pathology

GALNT6 Expression and Localization in Luminal A Breast Cancer

Association with epithelial polarity and gland-forming architecture in clinical breast tissues

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Purpose: Breast cancer is the most commonly diagnosed malignancy in women worldwide. Polypeptide N-acetylgalactosaminyltransferase 6 (GALNT6), an initiating enzyme of mucin-type O-glycosylation, has been reported to promote breast cancer progression and malignant phenotypes. However, the relationship between GALNT6 and breast cancer subtypes remains unclear. This study aimed to investigate subtype-specific expression patterns and histopathological localization of GALNT6 in breast cancer tissues, focusing on luminal A breast cancer.

Methods: GALNT6 mRNA expression was evaluated by qPCR in clinical specimens of luminal A breast cancer (n = 13), triple-negative breast cancer (TNBC) (n = 12), and normal breast tissues (n = 9). Immunofluorescence analyses were performed to examine the relationship between histological architecture and the localization patterns of GALNT6, GM130, and MUC1 in luminal A breast cancer tissues.

Results: qPCR analyses demonstrated that GALNT6 expression was significantly elevated in luminal A breast cancer compared with TNBC and normal breast tissues. Immunofluorescence analyses revealed that, in gland-forming regions, GALNT6 was localized toward the apical/luminal compartment and adjacent to GM130-positive regions. In these regions, MUC1 was predominantly detected along the luminal surface and within the luminal space. In contrast, in non–gland-forming (solid) tumor regions, both GALNT6 and GM130 exhibited diffuse cytoplasmic localization patterns, whereas MUC1 expression was weak or absent.

Conclusion: GALNT6 demonstrated subtype-specific and structure-dependent localization patterns in breast cancer tissues. These findings suggest that GALNT6 may contribute to luminal epithelial polarity and gland-forming organization in luminal A breast cancer.

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一般演題 Pathology

Development of a Detection System for PTPRZ-MET Fusion in Glioma

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Glioma is one of the most common primary brain tumors. Because brain biopsy is required when it is difficult to distinguish glioma from other diseases such as multiple sclerosis (MS), the development of minimally invasive fluid biomarkers is needed. We previously demonstrated that soluble protein tyrosine phosphatase receptor-type zeta (sPTPRZ) is highly elevated in the cerebrospinal fluid (CSF) of glioma patients. We also established a detection system for sPTPRZ using an antibody recognizing the HNK-1 glycan specifically bound to sPTPRZ. However, approximately 20% of glioma samples were negative for sPTPRZ. Recent studies have identified PTPRZ-MET fusion genes in glioma. In our previous study, we found that the HNK-1 glycan-binding site on PTPRZ is located in exon 12, whereas all reported PTPRZ-MET fusion proteins lack this region. Therefore, we hypothesized that some glioma samples negative for sPTPRZ may be explained by the presence of PTPRZ-MET fusion genes. The aim of this study was to establish a method for detecting PTPRZ-MET fusion. HEK293T cells were transfected with an expression vector carrying an artificial PTPRZ-MET fusion gene. After collecting cell lysates and conditioned medium, PTPRZ-MET expression was examined using anti-PTPRZ and anti-MET antibodies. In addition, we established a qPCR-based detection system for identifying PTPRZ-MET fusion genes in glioma samples negative for sPTPRZ. Expression of PTPRZ-MET in cell lysates was confirmed by western blotting using an anti-MET antibody. However, cleavage products derived from the PTPRZ-MET chimeric protein were not detected in the conditioned medium. Currently, we are selecting glioma tissue samples showing low PTPRZ and high MET expression from patients with negative sPTPRZ levels in CSF and plan to detect PTPRZ-MET fusion genes by qPCR. In addition, we are constructing an N-terminally tagged PTPRZ-MET expression system to examine whether shed fragments derived from PTPRZ-MET can be detected in the conditioned medium.

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一般演題 Pathology

Rapid Fresh Pathology for Pulmonary Specimens

Whole-mount Gigapixel Imaging of Fresh Lung Surgical Tissue

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Purpose

Rapid evaluation of fresh pulmonary specimens remains challenging in routine pathology workflows. Conventional frozen section examination may introduce tissue artifacts and requires labor-intensive preparation, while formalin-fixed paraffin-embedded (FFPE) processing prolongs diagnostic turnaround time. This study investigated the feasibility of rapid fresh pathology (RFP) imaging for whole-mount visualization of fresh lung specimens.

Methods

Fresh pulmonary surgical specimens were processed using rapid whole-mount hematoxylin and eosin staining followed by nonlinear optical mesoscale imaging. Histology-like gigapixel virtual H&E images were generated without tissue sectioning or freezing. Imaging performance was evaluated for preservation of pulmonary architecture and large-area visualization capability.

Results

RFP enabled rapid generation of large-area histological images from fresh lung specimens within minutes. Pulmonary structures including alveolar architecture, stromal distribution, necrotic regions, and tumor-associated morphologic patterns were identifiable on whole-mount H&E-contrast images. The section-free workflow preserved tissue integrity while allowing visualization across centimeter-scale specimen areas. Rapid gigapixel imaging also demonstrated potential utility for fresh tissue mapping and rapid specimen assessment during pathology workflows.

Conclusion

RFP provides a rapid whole-mount imaging approach for fresh pulmonary specimens with preservation of large-scale tissue architecture. This workflow may support future applications in rapid pathology assessment and fresh tissue specimen management.

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一般演題 Pathology

KSHV Genotyping in Kaposi Sarcoma: Association with Clinical Subtypes

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Background : Kaposi sarcoma (KS) is a vascular intermediate malignant tumor associated with Kaposi's sarcoma-associated herpesvirus (KSHV). Although six KSHV genotypes have been identified, their clinical significance remains unclear. This study investigated the association between KSHV genotypes and clinical subtypes of KS.

Methods : Fifty-one patients diagnosed with KS at the University of the Ryukyus Hospital, Okinawa, Japan, between 2006 and 2025 were evaluated. Formalin-fixed paraffin-embedded tissue samples were analyzed. KSHV genotyping was performed by PCR amplification and sequence analysis of the K1 and K15 regions. Genotype distributions were compared among clinical subtypes, including classic and AIDS-related KS. Biological characteristics were analyzed by immunostaining.

Results : K1 genotype C was more prevalent than genotype A and predominated in classic and iatrogenic KS, whereas genotype A was more frequent in AIDS-related KS. Similarly, K15 genotype M predominated in classic and iatrogenic KS, whereas genotype P was more frequent in AIDS-related KS. Analysis of K1/K15 combinations showed that genotype A was associated with genotype P (A/P), while genotype C was associated with genotype M (C/M). These genotype associations differed from those reported in European and African populations, suggesting distinct geographic characteristics of KSHV in Okinawa. Furthermore, A/P tended to be associated with AIDS-related KS, whereas C/M was more frequently identified in classic KS. These findings suggest an association between KSHV genotype and KS subtype.

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一般演題 Pathology

11,13-Dehydrolanuginolide Attenuates the Progression of Hepatocellular Carcinoma *In Vitro*

Suppression of Long-Term Proliferative Capacity and Tumor Cell Migratory Potential

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Sesquiterpene lactones have garnered significant attention in cancer pharmacology due to their diverse therapeutic properties, structural distinctiveness, and potential to overcome drug resistance. In this study, we comprehensively investigated the anti-cancer potential and underlying molecular mechanisms of 11,13-dehydrolanuginolide, a specific sesquiterpene lactone, across multiple in vitro tumor cell dimensions. The MTT assay demonstrated that 11,13-dehydrolanuginolide significantly reduced cancer cell viability in a dose- and time-dependent manner, exhibiting potent cytotoxicity with low inhibitory concentrations. Long-term proliferative capacity was assessed using a clonogenic assay, which revealed a strong, concentration-dependent inhibition of both colony formation frequency and colony size. Furthermore, Wound-healing assays indicated that the compound effectively suppressed cancer cell migration, suggesting its promising potential to inhibit tumor invasion and metastasis. To elucidate the precise mode of cell death induced by this compound, Annexin V/PI double staining followed by flow cytometry was employed. The quantitative results showed a marked, significant increase in both early and late apoptotic cell populations, confirming that the treatment effectively triggers programmed cell death rather than non-specific necrosis. Western blot analysis further validated these phenotypic findings by delineating the involvement of the intrinsic apoptotic pathway. Treatment with 11,13-dehydrolanuginolide triggered a significant upregulation of the pro-apoptotic protein Bax and the proteolytic activation of cleaved Caspase-3, accompanied by a concomitant downregulation of the anti-apoptotic protein Bcl-2. In conclusion, our findings demonstrate that 11,13-dehydrolanuginolide exerts robust anti-cancer activity by effectively inhibiting cell proliferation and migration while triggering programmed cell death via mitochondrial-dependent apoptotic pathways. This natural compound represents a viable candidate for further preclinical development as a novel therapeutic agent against aggressive cancer malignancies.

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一般演題 Pathology

Protective Effects of Naringenin Against Hepatic Steatosis and Fibrosis

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Metabolic dysfunction-associated steatotic liver disease (MASLD) is a global health burden driven by long-term high-fat diet (HFD) consumption, leading to lipid accumulation, glucose intolerance, and progressive fibrosis. Naringenin (NAR), a natural flavonoid abundant in citrus fruits, shows promise in treating metabolic disorders, but its role in regulating hepatic fibrosis and glycogen storage remains to be elucidated. In the study, male C57BL/6J mice were randomly assigned to four groups (n=8): Control, HFD, HFD+50 mg/kg NAR, and HFD+100 mg/kg NAR. Mice were fed a HFD for 12 weeks with daily oral administration of NAR. Physiological parameters, including body weight and fasting blood glucose, were monitored weekly. On Day 84, oral glucose tolerance tests (OGTT) and biochemical analyses were performed. Liver tissues were harvested for histopathological assessment using Hematoxylin and Eosin (H&E), Periodic Acid-Schiff (PAS), and Masson's Trichrome staining to evaluate steatosis, glycogen content, and fibrosis. Results showed that NAR supplementation substantially attenuated HFD-induced weight gain and hyperlipidemia, without altering food intake. Functionally, NAR restored glucose tolerance and area under the curve (AUC) levels. Histologically, NAR markedly reduced steatosis area and reversed glycogen depletion. Furthermore, Masson's Trichrome staining confirmed that NAR significantly inhibited collagen accumulation and fibrosis. In conclusion, Naringenin exerts potent multi-targeted effects by enhancing glucose homeostasis, restoring glycogen storage, and suppressing fibrotic progression, positioning it as a promising nutraceutical candidate for managing MASLD and its associated fibro-metabolic complications.

Key words: naringenin, high-fat diet, metabolic dysfunction-associated steatotic liver disease, glucose tolerance, hepatic fibrosis, glycogen storage

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一般演題 Pathology

Elucidation of microenvironmental changes in precancerous lesions

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【Introduction】Pancreatic intraepithelial neoplasia (PanIN), a precursor lesion of invasive pancreatic ductal carcinoma (IDC), is classified into PanIN1 to 3 based on the histological grade.Recent studies have shown that PanIN is often accompanied by fibrosis and atrophic interstitium, but the interstitial changes during the progression of PanIN have not been fully elucidated.The purpose of this study was to clarify the pathological characteristics of PanIN at various stages of progression and to verify its mechanism of development.

【Material and method】The following study was conducted on FFPE specimens prepared from pancreatic cancer resection material (not treated before surgery) resected between 2016 and 2024, including normal and PanIN1-3 cases.①Comprehensive gene expression analysis: RNA was extracted from each of the 18 cases and analyzed using the nanoString and nCounter® Analysis System.②PCR quantitative analysis: RNA was extracted from 30 cases and PPARɤ was analyzed using the QuantStudioTM 6Pro real time PCR system. ③ Immunohistochemical analysis: Immunohistochemistry (CD31, CD36, α -SMA, IL-6) was performed on 300 cases to confirm changes in blood vessels and fibroblasts.

【Result】In the advanced stages of PanIN,①Among blood vessel-related genes, CCL28, which promotes angiogenesis, and CD36, which is expressed in vascular endothelial cells, were down-regulated.②PPARɤ, which induces CD36 expression, was upregulated. ③ In the area less than 50 μ m beneath the epithelium, the number of CD36+ blood vessels decreased, while the number of α SMA+, IL-6+ fibroblasts increased.

[Conclusion]

These findings suggest that the progression of PanIN may result in phenotypic changes in vascular endothelial cells and fibroblasts.

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一般演題 Pathology

Antcin Boosts Cisplatin Efficacy in Non-Small Cell Lung Cancer

Suppressing Cell Survival and Migration through Combined Therapy

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Non-small cell lung cancer (NSCLC) remains a leading cause of cancer-related mortality worldwide. Although cisplatin is widely used as a standard first-line chemotherapy, its long-term clinical efficacy is severely limited by the development of drug resistance and cumulative systemic toxicity. Therefore, identifying low-toxicity natural compounds that can enhance chemosensitivity is an important direction in cancer research. This study investigates the synergistic anticancer effects of Antcin, a purified bioactive compound from the Taiwanese endemic fungus (Antrodia cinnamomea), combined with cisplatin against NSCLC.Using the human A549 cell line as an in vitro model, the therapeutic impact of Antcin and cisplatin co-treatment was evaluated. Short-term cell viability and synergistic cytotoxicity were measured using the MTT assay, while long-term proliferative and colony-forming capacities were assessed via clonogenic assay. Cell migration was examined using a wound healing assay. Furthermore, apoptosis was detected through Annexin V staining, and the expression of apoptosis-related proteins and downstream signaling pathways was quantified using Western blot analysis.The expected results demonstrate that combining Antcin with cisplatin significantly reduces A549 cell viability in a dose- and time-dependent manner, confirming that Antcin enhances cisplatin chemosensitivity. In long-term assessments, the combination therapy group showed a substantial reduction in colony formation compared to single-agent treatments. Additionally, co-treatment markedly delayed wound closure, inhibiting cell migration. Mechanistically, Annexin V analysis confirmed that the combination therapy significantly induced apoptosis, corroborated by Western blot results showing altered expression of apoptosis-related proteins and key survival pathways.In conclusion, Antcin effectively enhances the anticancer efficacy of cisplatin in NSCLC cells by inducing apoptosis and suppressing migration, establishing a solid theoretical foundation for future clinical applications.

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一般演題 Pathology

Apigenin as a Therapeutic Agent Against Ovarian Cancer

An In Vitro Evaluation of Antitumor Mechanisms in the SKOV3 Cell Line

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Ovarian cancer remains a major cause of gynecological cancer-related mortality worldwide. Apigenin, a natural flavonoid compound, has demonstrated anticancer activity in several malignancies; however, its effects on ovarian cancer remain incompletely understood. This study investigated the antitumor activity of apigenin in the human ovarian cancer cell line SKOV3. Cell viability was assessed using an MTT assay, while long-term proliferative capacity was evaluated by colony formation assay. Cell migration was examined using a wound-healing assay. Cell cycle distribution and apoptosis were analyzed by flow cytometry and Annexin V/PI staining, respectively. Apigenin significantly inhibited SKOV3 cell viability in a dose- and time-dependent manner, with a 48-h IC50 value of 46.67 μM. Colony formation and wound-healing assays further demonstrated that apigenin suppressed cell proliferation and migration. In addition, apigenin induced cell cycle arrest and significantly promoted apoptosis in SKOV3 cells.

In conclusion, apigenin exerts antitumor effects against SKOV3 ovarian cancer cells by inhibiting proliferation and migration and by inducing cell cycle arrest and apoptosis. These findings support the potential application of apigenin as a therapeutic candidate for ovarian cancer and provide a basis for future mechanistic studies.
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一般演題 Pathology

FFPE-Compatible RT-PCR for Endometrial Stromal Sarcoma

Detection of *JAZF1::SUZ12* and *YWHAE::NUTM2A/B* Fusion Transcripts

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【Background】Endometrial stromal sarcoma (ESS) is a rare uterine mesenchymal neoplasm classified into Low-grade ESS and High-grade ESS. These tumors are characterized by recurrent fusion genes, including *JAZF1::SUZ12* in low-grade ESS and *YWHAE::NUTM2A/B* in high-grade ESS. Identification of these fusion transcripts aids diagnosis, particularly in challenging cases. However, molecular testing of formalin-fixed paraffin-embedded (FFPE) specimens is often hampered by RNA degradation and fragmentation, reducing the reliability of conventional assays. This study aimed to develop an FFPE-compatible real-time reverse transcription polymerase chain reaction (RT-PCR) assay using short amplicons for sensitive and specific detection of ESS-associated fusion transcripts.

【Methods】Primer and probe sets were designed for *JAZF1::SUZ12* (150 bp) and *YWHAE::NUTM2A/B* (101 bp). Specificity was evaluated using Primer-BLAST. Synthetic gene constructs containing each fusion sequence were used as positive controls, while five human cell lines confirmed negative by conventional RT-PCR served as negative controls. Amplification efficiency was assessed using FFPE-derived RNA. Analytical sensitivity was evaluated by serial dilution of synthetic fusion constructs.

【Results】No significant off-target amplification was identified in silico. Both assays produced clear amplification curves in positive controls, whereas no amplification was observed in any negative control cell lines, demonstrating high specificity. Efficient amplification was achieved using FFPE-derived RNA. Both fusion transcripts remained detectable at a 1% positive fraction, indicating high analytical sensitivity.

【Conclusions】We established an FFPE-compatible real-time RT-PCR assay for sensitive and specific detection of *JAZF1::SUZ12* and *YWHAE::NUTM2A/B* fusion transcripts. This assay may aid molecular diagnosis of ESS using FFPE specimens. Validation is ongoing.
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一般演題 Pathology

Trends in Asbestos Body Counting at a Japanese Hospital

A Retrospective Analysis of 305 Cases

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【Introduction】Asbestos body counting is a crucial laboratory analysis that provides objective medical evidence of asbestos exposure for the certification of asbestos-related lung cancer under Japan's Workers' Accident Compensation Insurance Act and the Asbestos-related Health Damage Relief System. Because asbestos bodies indicate asbestos exposure and support assessment of disease-exposure relationships, ensuring the accuracy and reliability of asbestos body counting is essential. We present our hospital-based experience and describe recent trends in submitted specimens and case characteristics.

【Materials and Methods】We retrospectively reviewed 305 cases submitted for asbestos body counting between January 2007 and April 2026. All analyses followed a standardized counting protocol. The cases were evaluated with respect to referral source, sex, asbestos body concentration, specimen type, lung sampling site, clinical diagnosis, and occupation.

【Results】Approximately half of the cases were submitted in relation to the Asbestos-related Health Damage Relief System, and approximately 90% involved male patients. Asbestos body concentrations met or exceeded the certification criteria in approximately 30% of cases. Over the study period, the use of bronchoalveolar lavage fluid (BALF) for asbestos body counting decreased, whereas the use of formalin-fixed paraffin-embedded lung tissue blocks increased. Specimens from the right lung were more common than those from the left lung, and upper-lobe specimens were more frequent than lower-lobe specimens. Approximately 80% of cases involved lung cancer, while approximately 10% involved asbestosis. Construction workers represented approximately 80% of cases.

【Discussion】The majority of submitted cases involved male workers in construction-related occupations, consistent with the importance of occupational asbestos exposure in the evaluation of asbestos-related lung cancer. Furthermore, we discuss the quality control program for asbestos body counting and ongoing training activities for future specialists in Japan.

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一般演題 Pathology

Could Cytokine Profiling Refine Immune Stratification in Colorectal Cancer Patients?

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In solid cancers, particularly colorectal cancer (CRC), the tumor microenvironment (TME) provides a protective milieu that can be shaped by the density and spatial distribution of the immune infiltrate (IIF), as well as by its functional state, driven by the cytokine secretion profile. Pro-inflammatory T helper type 1 (Th1) cells produce signaling proteins such as tumor necrosis factor (TNF) and C-X-C motif chemokine ligand 9 (CXCL9), which enhance the cytotoxic activity of $CD8^+$ T cells and contribute to a favorable prognosis in CRC. In contrast, high levels of interleukin 6 (IL-6) and interleukin 10 (IL-10), secreted by M2-polarized macrophages and regulatory T cells, contribute to sustained inflammation, stromal remodeling, and immune evasion, correlating with tumor progression.

This study aimed to investigate whether the combined analysis of lineage-defined IIF and both pro-inflammatory and immunosuppressive cytokines provides a more comprehensive assessment of tumor clinical behavior.

A panel of lineage markers (CD3, CD8, FOXP3 and CD163) was used to characterize the spatial organization of the IIF in FFPE CRC tissue samples immunostained using a multiplex chromogenic approach. Additionally, a panel including CXCL9, TNF, IL-6, and IL-10 was used to evaluate functional immune states. Signal quantification and spatial analysis were performed at both single-cell and tissue-compartment levels.

The combined spatial and functional analysis revealed that tumors with higher CXCL9 expression showed increased infiltration of $CD8^+$ T cells. In contrast, elevated levels of IL-6 and IL-10 were associated with increased densities of $CD163^+$ macrophages and $FOXP3^+$ T cells. TNF expression varied across samples and was not consistently associated with specific immune cell populations. These findings support that cytokine-based signatures may improve patient stratification based on tumor immune functional profiles, with the potential to refine prognostic assessment and support the development of more personalized therapeutic strategies in CRC.

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一般演題 Pathology

Improve the processing procedures for frozen sections of breast tissue

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Introduction:
Rapid frozen section(FS) is a method used for intraoperative pathological diagnosis. After receiving the surgical specimen, the pathologist makes a diagnosis within approximately 20 minutes and verbally notifies the surgeon by telephone. Intraoperative radiotherapy (IORT) is a new technology for the treatment of stage I breast cancer. The surgical procedure involves: (1) removing the breast tumor, and (2) directly subjecting the tumor cavity to high-dose radiation therapy. In the pathology department, pathological tissue specimens are as important as the patient.
Methods:
1. Assemble a TRM team. 2. Review the “IORT FS process” and identify areas for improvement, including: (1) The FS submission form did not specify the surgical type as IORT. (2) Unmarked lesion in breast tissue. (3) Medical Technician unable to perform IORT FS simultaneously while performing routine FS. 3. The “IORT FS Process” was implemented in January 2026. Fifteen IORT cases were collected between January and April 2026. Target value: breast surgeon IORT FS timeliness satisfaction score >3.5.
Results:
1. The "IORT FS process" was led by the breast surgeon and discussed and confirmed with the pathologist and radiation oncologist. This is TRM's "Leadership: Brief".2. FS submission form did not clearly indicate the surgical type as IORT, and the breast tissue was not marked with a lesion. Improvement measures include requiring breast surgeons to add "IORT" to FS submission forms, marking the 12 o'clock position of the tumor with a long line and the 3 o'clock position with a short line. This is TRM's "two Challenge Rule."3. When a MT encounters an IORT case while performing routine FS, they should seek assistance from other technicians to collaboratively complete the IORT. This is the TRM's "Call and Collaborate" rule.
4. The average "IORT FS Timeliness Satisfaction Score " in January and April 2026 was 3.93.

P-5-44

一般演題 Pathology

Chromatin Instability by Telomere Dysfunction Promotes Neutrophil Extracellular Trap Formation

Association of TRF2 Downregulation and DNA Damage Response with Neutrophil Extracellular Trap Formation

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Background: Neutrophil extracellular traps (NETs) are a unique form of neutrophil cell death involved in host defense, whereas excessive NET formation contributes to inflammatory diseases. NET formation is characterized by chromatin decondensation and PAD4-dependent histone citrullination (CitH3), although multiple upstream pathways have been suggested. Telomeric repeat-binding factor 2 (TRF2) contributes to telomere protection and chromatin stability, and its downregulation triggers a DNA damage response.
This study investigated whether TRF2-related chromatin instability is associated with NET formation.
Methods: HL-60 cells were cultured with 1.0% dimethyl sulfoxide (DMSO) for 4 days to induce neutrophil-like differentiation, followed by phorbol 12-myristate 13-acetate (PMA) stimulation to induce NET formation. Differentiation was assessed by side scatter analysis, Giemsa staining, and immunostaining for CD11b and lactoferrin (LF). NET formation was evaluated by CitH3 immunostaining. DAB intensity was quantified using QuPath software, and statistical analysis was performed in EZR with Bonferroni correction. TRF2 knockdown was performed using TRF2 siRNA, and knockdown efficiency was confirmed by Western blotting. Formalin-fixed paraffin-embedded appendicitis tissues were examined for TRF2, γ-H2AX, and CitH3 expression by immunohistochemistry.
Results: HL-60 cells exhibited segmented nuclei and increased SSC after 4 days of DMSO treatment. DAB intensities of CD11b and LF significantly increased, confirming neutrophil-like differentiation. Four-hour PMA stimulation significantly increased CitH3 immunoreactivity and induced NET-like structures characterized by extracellular chromatin release. TRF2 protein expression was reduced following siRNA transfection. In appendicitis tissues, reduced TRF2 expression and γ-H2AX positivity co-localized in a subset of CitH3-positive cells.
Conclusion: These findings suggest that chromatin instability and DNA damage responses induced by TRF2 downregulation may contribute to NET formation.

P-5-45

一般演題 Pathology

Effect of Mumefural on Neutrophil Extracellular Trap Formation

Characterization of NETs Responses to a Japanese Apricot-Derived Bioactive Compound

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Background: Neutrophil extracellular traps (NETs) are web-like structures released by neutrophils to capture and kill pathogens, playing a crucial role in host defense. Although NET formation is essential for infection control, its dysregulation has been implicated in autoimmune diseases, thrombosis, and cancer metastasis. Japanese apricots are known to exhibit antioxidant and anti-inflammatory properties; however, their direct effects on NET formation remain unclear. This study investigated the effects of Mumefural (MF), a compound generated during the heat processing of Japanese apricot, on NET formation.

Methods: To examine the effects of MF, we evaluated its cytotoxicity and apoptosis in neutrophil-like differentiated HL-60 cells. HL-60 cells differentiated by dimethyl sulfoxide (DMSO) treatment were cultured with various concentrations of MF for 24 h. Cell viability was assessed using a 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay. Morphological changes were evaluated by Giemsa staining, and apoptosis was assessed by Annexin V staining.

Results: MTT assays demonstrated concentration-dependent decreases in cell viability: 94.37% at 5 μM, 88.31% at 50 μM, and 80.05% at 100 μM compared to the control (100%), suggesting that MF affects cellular activity. Giemsa staining revealed morphological changes, including cell shrinkage and nuclear alterations, in MF-treated groups. In contrast, Annexin V-positivity showed no significant differences and no dose-dependent changes, with values of 39.85% for the control (0μM), 40.43% at 5μM, 38.60% at 50μM, and 39.38% at 100μM.

Conclusion: These findings suggest that MF may promote alternative cell death pathway, such as NETosis, rather than conventional apoptosis. We are currently conducting quantitative and morphological analyses of PMA-induced NET formation following MF pretreatment to further elucidate these effects.

P-6-1

一般演題 Cytology

HPV DNA Genotyping and E6/E7 mRNA for Cervical Precancer Diagnosis

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Objective This study aimed to analyze the risk factors for cervical precancerous lesions using a combined approach of HPV DNA genotyping and E6/E7 mRNA testing, and to develop a diagnostic predictive model. Methods A cross-sectional study was conducted among patients with suspected cervical cancer who were admitted to Liangping District People ’ s Hospital and Nanchuan District People's Hospital in Chongqing, China, from February 2023 to July 2025. All participants underwent histopathological examination. The patients with CIN2+ were assigned to the study group(n=86), and others were assigned to control group(n=156). Results A total of 242 female patients were included in this study, with a mean age of 42.6 ± 8.9years. Histopathologic findings showed that 27.3%(66/242) patients had inflammation, 37.2%(90/242) had CIN1, 19.0%(46/242) had CIN2, 11.6%(28/242) had CIN3, and 5.0%(12/242) had cervical cancer. The prevalence of HPV16 infection was significantly higher in study group than in the control group [41.9%(36/86) vs 12.2%(19/156), P<0.05]. The study group had a significantly higher E6/E7 mRNA positivity rate compared with the control group [74.4%(64/86) vs 25.0%(39/156), P<0.05]. Multivariable logistic regression analysis showed that HPV16 infection [aOR=3.28(95%CI,1.76-6.10), P=0.01] and E6/E7 mRNA positivity [aOR=5.74(95%CI,3.06-10.77), P=0.01] were risk factors for the development of cervical precancerous lesions. The combined predictive model demonstrated good diagnostic performance [AUC=0.78(95%CI,0.72-0.84)]. Conclusion Both HPV16 infection and E6/E7 mRNA positivity were identified as high-risk factors for the development of cervical precancerous lesions.

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P-6-2

一般演題 Cytology

Immunohistochemical analyses of hydroxylase-immunoreactive amacrine cells in the gerbil retina

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The development of catecholaminergic neurons in mammalian retina has been examined with antibody against tyrosine hydroxylase (TH). The gerbil has specific characteristics in retaining the central retinal artery. The Gerbil eyes open in postnatal day (P) 19 of age. We have examined shape localization and change in number of the TH-IR cells in the retina from P1 to adult gerbils using immunocytochemical method. We have found two kinds of TH-IR amacrine cells. The two types were clearly different in somata and stratifications of dendrites in the inner plexiform layer (IPL) from P7 to adult. Materials and methods: The gerbils were perfused intracardially with a fixative. After the removed eyeballs were frozen with a rapid jet of liquid carbon dioxide, they were cut with section of 18mm using a cryostat. The sections and the wholemounts were examined by ABC immunocytochemical staining method. Results: Two types of TH-IR cells were identified; type A and type B, the former which extended dendrites to the outer part of the IPL, but the latter sent dendrites to the middle stratum in the IPL. Type A somata were larger and more densely stained than those of type B. After P28, the range of type A soma diameters did not overlap those of the type B. Type B somata showed a significant growth between P7 and P14 days. After P14, little change was seen. Type B mean density decreased drastically between P7 and P28 days, while little change was seen in type A. Conclusions: These results suggest that two kinds of TH- IR cells have different developmental properties in the developing gerbil retina. Eye opening is an important period for the maturation of dopaminergic amacrine cells and for the maturation of the IPL.

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P-6-3

一般演題 Cytology

Deep Ocean Water in Cytology Processing

A Preliminary Study of Morphologic Preservation

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Background: Deep ocean water from Toyama Bay, Japan, is highly clean and mineral-rich, suggesting its possible utility in laboratory medicine. We conducted a preliminary study to evaluate whether deep ocean water could be applied to cytology specimen processing and whether it could help preserve cellular morphology and staining quality during specimen preparation.
Methods: Cytology specimens were processed using deep ocean water and compared with specimens prepared using NaCl, an isotonic solution, and Medi-Wash. Morphological assessment was performed using Papanicolaou staining. In addition, exploratory morphometric analysis was performed on 100 nuclei per condition for lymphocytes, histiocytes, and carcinoma cells, including measurements of nuclear area, maximum caliper, minimum caliper, and hematoxylin optical density (OD).
Results: In lymphocytes, the deep ocean water group showed a larger mean nuclear area than the comparison groups (24.81 vs. 22.69, 20.35, and 18.88). In histiocytes, the difference was more pronounced, with a mean nuclear area of 102.84 versus 53.98, 42.72, and 42.32, respectively, and a greater mean maximum caliper (15.03 vs. 9.68, 8.50, and 8.54 μm). In carcinoma cells, size-related parameters were broadly comparable among groups, whereas hematoxylin OD remained the lowest in the deep ocean water group (0.721 vs. 1.052, 0.828, and 0.832). However, microbial growth, including that of yeast-like fungi, was observed under certain conditions.
Conclusion: Deep ocean water may be a promising processing reagent for cytology specimens, particularly for morphological preservation in selected cell populations. Further optimization of sterility control, protocol standardization, reproducibility assessment, and validation using a larger number of specimens are necessary before practical application.
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P-6-4

一般演題 Cytology

Signet-Ring-Like Macrophages in Pleural Effusion

Cytologic Features and Diagnostic Pitfalls: A Case Report

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Purpose
Pleural effusion cytology is essential for distinguishing benign reactive processes from malignant pleural diseases. Highly vacuolated macrophages may mimic signet-ring carcinoma cells, particularly in elderly patients with suspected malignancy.
This study aims to characterize the cytologic features of signet-ring-like macrophages and identify key diagnostic pitfalls to avoid misinterpretation.
Methods
A 92-year-old male with type 2 diabetes mellitus with nephropathy, mixed hyperlipidemia, and essential hypertension presented with chest pain. Imaging confirmed pleural effusion, and diagnostic thoracentesis was performed. The specimen was centrifuged, and smears were prepared and stained with Wright–Giemsa. Cytologic evaluation was performed by experienced medical laboratory scientists and a pathologist.
Results
Cytologic examination revealed predominantly singly dispersed macrophages with numerous cytoplasmic vacuoles of varying sizes. These vacuoles displaced the nucleus peripherally, producing a signet-ring-like appearance. The nuclei were round to reniform with fine, uniform chromatin and no prominent nucleoli or nuclear atypia. The background showed proteinaceous material and scattered inflammatory cells. No tumor cell clusters, glandular formations, or necrosis were identified. These findings were consistent with highly vacuolated foamy reactive macrophages.
Conclusion
Signet-ring-like macrophages in pleural effusion represent reactive changes rather than malignancy. Careful evaluation of nuclear morphology, cellular arrangement, and background features is essential to avoid diagnostic errors. This case highlights the importance of cytomorphologic expertise and diagnostic experience, particularly in elderly patients with complex clinical conditions.
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P-6-5

一般演題 Cytology

Validation of Immunocytochemistry Controls in Liquid-Based Cytology

Effects of Fixatives and Storage Conditions

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【Background】Immunocytochemistry（ICC） is essential in cytological diagnosis, particularly when morphological evaluation alone is insufficient. However, the reliability of staining depends on appropriate control materials, which remain challenging to maintain in cytological practice due to the limited preservation of fresh specimens. In our hospital, control slides for smear specimens are prepared using a cell transfer technique. With the widespread adoption of liquid-based cytology (LBC), there is increasing interest in its application for ICC controls. Nevertheless, the effects of different LBC fixatives and storage conditions on antigen preservation and staining performance have not been systematically evaluated, and no consensus has been established. This study aimed to compare these factors to optimize LBC-based control materials.【Materials and Methods】 Control materials were prepared from residual cytology specimens. Samples were divided into four LBC fixatives (ThinPrep, BD, Cellprep, and Liqui-PREP) and stored under three conditions: 4°C, −20°C, and −80°C. After a defined storage period, slides were prepared, air-dried, and alcohol fixed. Staining quality was evaluated in terms of staining intensity, cellularity, and background staining, along with handling characteristics. 【 Results 】 Consistent and satisfactory immunoreactivity was observed across multiple markers, including nuclear (PAX8, WT1), cytoplasmic (synaptophysin), and membranous (claudin 4) proteins. In terms of handling, ThinPrep and Cellprep showed increased spreading during application, posing a risk of cross-contamination on the same slide. In contrast, Liqui-PREP and BD demonstrated superior localization and handling. 【Conclusion】 LBC-based control materials are feasible and effective for ICC, providing practical advantages over conventional cell transfer methods. Both fixative type and storage conditions significantly influence staining performance and handling. These findings support the routine implementation of LBC-based controls, with further studies warranted to establish long-term stability and standardization.

P-6-6

一般演題 Cytology

Atypical Cells in Septic Ascites

Diagnostic Pitfalls in Severe Sepsis with Septic Shock

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Purpose
To describe a case of severe sepsis with concurrent multiple primary malignancies presenting with atypical cytological findings in ascitic fluid, and to evaluate the diagnostic implications for clinical laboratory practice.
Methods
A 64-year-old male with severe sepsis and septic shock, malignant neoplasm of the left lung, hepatocellular carcinoma (HCC), and cachexia was evaluated. Ascitic fluid was collected and processed for cytological examination using standard preparation and staining techniques. Cellular morphology and leukocyte distribution were assessed by light microscopy.
Results
Cytological examination revealed numerous degenerated inflammatory cells, predominantly neutrophils. Marked nuclear alterations were identified, including karyolysis, pyknosis, and karyorrhexis. A subset of cells appeared as ghost cells with indistinct cytoplasmic outlines. Cytoplasmic vacuolization and structural disintegration were prominent throughout. The background exhibited abundant cellular debris and necrotic material, producing a characteristically "dirty" background. No definitive malignant cell clusters were identified.
Conclusion
In patients with severe sepsis and septic shock, profound degenerative cytological changes may develop in ascitic fluid, reflecting hypoxia-driven and inflammation-mediated cellular injury. These atypical morphological features can closely mimic or obscure malignant cells, posing significant diagnostic challenges. Careful cytological interpretation integrated with clinical and laboratory correlation is essential to prevent misdiagnosis and ensure appropriate patient management.

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P-6-7

一般演題 Cytology

Prolongation Factors Among General Applicants in Cytotechnologist Certification Examination

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Background: General applicants constitute the largest proportion of cytotechnologist certification candidates in Japan, yet consistently achieve the lowest pass rates among the three eligibility categories. Despite this disparity, no systematic nationwide study has investigated the factors associated with prolonged time to certification in this group.

Objective: To identify and quantify factors associated with prolonged certification time among general applicants, and to propose evidence-based support interventions.

Methods: A nationwide anonymous, multiple-response survey was administered to 169 cytotechnologists certified through the general application pathway. Participants reported difficulties during the first (written/cytological image) and second (microscopic identification/screening) examinations, and their preferred support environments. The proportion of respondents selecting each item (Need) and Spearman rank correlation coefficients (ρ) between item selection and years required for certification were calculated. The Prolongation Risk Score (PRS) was defined as Need × ρ^{+}, where ρ^{+} denotes the positive component of ρ (negative values set to zero).

Results: In the first examination, "lack of study time" demonstrated the highest PRS (Need=44.4%, ρ=0.179, PRS=7.93), followed by "uncertain study content or methods" (PRS=5.29) and "unclear textbook selection" (PRS=4.28). In the second examination, "limited access to specimens/cases" yielded the highest PRS (Need=62.7%, ρ=0.085, PRS=5.31). Notably, "uncertain proficiency level," despite the highest Need in both examinations, showed negligible or negative ρ, resulting in PRS=0. Among desired support environments, "availability of instructors" showed the highest PRS (Need=11.8%, ρ=0.143, PRS=1.69), whereas "on-demand lectures," despite the highest Need (20.1%), had a negative ρ (PRS=0).

Conclusions: Insufficient study time and limited access to cytological specimens are the primary factors associated with prolonged certification time. Publication of official past-examination answers, clarification of examination scope, and interactive, expert-guided instruction sessions are recommended as priority interventions to reduce certification time and strengthen the cytotechnologist workforce.

Conflict of Interest: All authors declare no conflicts of interest relevant to this study.
Ethics: Approved by the Institutional Review Board of Kio University (No. R6-08).
Category: 06 – Cytology

P-6-8

一般演題 Cytology

Imprint Cytology Supports Safer OSNA Practice

A laboratory quality safeguard for discordant sentinel node assessment

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One-step nucleic acid amplification (OSNA) is widely used for intraoperative sentinel lymph node assessment in breast cancer and integrates well into routine laboratory workflows. However, because OSNA relies on cytokeratin 19 (CK19) messenger RNA and consumes tissue during analysis, discordant results may be difficult to verify morphologically unless an appropriate pre-analytical safeguard is implemented. We aimed to demonstrate the practical value of imprint cytology as a quality support tool in OSNA-based testing.

We retrospectively analyzed a breast cancer case in which imprint cytology was performed on the bisected surface of sentinel lymph nodes prior to OSNA. Cytological findings were compared with permanent histology and CK19 immunohistochemistry in both the primary tumor and metastatic lymph nodes.

Two sentinel lymph nodes were negative by OSNA, whereas imprint cytology suggested metastatic carcinoma in one node. Subsequent permanent histology confirmed nodal metastasis. Further evaluation revealed markedly heterogeneous CK19 expression in the primary tumor, while most metastatic tumor cells in the lymph node were CK19-negative, with only a limited CK19-positive component. These findings indicated biological discordance associated with low or heterogeneous CK19 expression. Importantly, imprint cytology preserved traceable morphological evidence prior to tissue consumption and prompted careful pathological reassessment.

This case highlights the value of combining molecular testing with a simple morphological backup approach in routine laboratory practice. Pre-OSNA imprint cytology may enhance quality assurance, improve traceability, and facilitate effective communication of potential limitations of OSNA results within the pathology team. It may also serve as a practical educational tool for biomedical laboratory professionals involved in intraoperative diagnostics.

P-6-9

一般演題 Cytology

A Case of Ependymoma Detected in Pleural Effusion

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Introduction

Ependymoma is a rare tumor, accounting for 1% of primary brain tumors and 7% in children. Despite total surgical resection, recurrence rates remain high, with metastases typically confined to the central nervous system. We report a metastatic ependymoma identified by cytological examination of pleural effusion.

Case Report

A woman in her 20s with a history of a cerebral tumor diagnosed 15 years prior—initially presenting features of anaplastic ependymoma and glioblastoma—experienced two intracranial recurrences of anaplastic ependymoma. She presented with dyspnea and chest pain. Chest radiography revealed massive left-sided pleural effusion. Pleural fluid cytology and pleural tissue biopsy confirmed metastatic ependymoma.

Pleural Effusion Cytology Findings

Atypical cell clusters with hyperchromatic nuclei formed rosette-like structures. Cell block immunohistochemistry showed staining patterns identical to the primary tumor. Genetic testing detected a *ZFTA::RELA* fusion gene.

Pleural Biopsy Findings

Histological examination revealed proliferation of epithelioid cells with clear cytoplasm and round-to-oval nuclei within fibrous connective tissue, resembling the previous brain tumor. The immunohistochemical profile supported metastatic ependymoma. The Ki-67(MIB-1) index was high at 40-60%.

Conclusion

We report an ependymoma detected in pleural effusion, showing a longer clinical course than typically expected. When atypical cells of unknown origin are detected in body cavity fluids, molecular biological techniques are useful alongside morphological observation, medical history, and clinical findings.

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P-6-10

一般演題 Cytology

Astroblastoma initially suspected as ependymoma on intraoperative cytology

a case report with emphasis on differential cytological feature

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Introduction: Astroblastoma is a rare cerebral tumor predominantly affecting children and young women, and cytological descriptions remain limited. We report a case initially interpreted as ependymoma on intraoperative cytology but finally diagnosed as astroblastoma, focusing on differential cytological features.

Case summary: A teenage female presented with a headache. MRI revealed a cystic tumor in the right frontal lobe. Surgical tumor resection was performed.

Cytological Findings: Intraoperative imprint smears and direct smears from cyst fluid showed columnar tumor cells with round to oval nuclei and mild pleomorphism in a clear background. Tumor cells exhibited papillary and rosette-like perivascular structures arranged radially around vascular cores. The cytoplasm of individual tumor cells tapered toward and appeared directly attached to the vascular cores, and cell borders were relatively distinct. Based on the prominent rosette-like structures, ependymoma was initially considered.

Histopathological Findings: Histologically, tumor cells with round nuclei and eosinophilic cytoplasm predominantly formed papillary perivascular structures, with focal micropapillary and gland-like features. No perivascular anucleate zone was identified. Instead, astroblastic rosettes in which the cytoplasm directly contacted the vascular wall were observed. Immunohistochemically, the tumor cells were positive for GFAP, OLIG2, S100, EMA, and vimentin, supporting the diagnosis of astroblastoma. In addition, next-generation sequencing identified an *EWSR1*::*BEND2* fusion, further confirming the diagnosis.

Conclusion: Astroblastoma and ependymoma may both show perivascular and rosette-like structures on cytology. However, the absence of a perivascular anucleate zone, relatively distinct cell borders, and direct cytoplasmic attachment to vessels are useful clues favoring astroblastoma. Careful evaluation of the tumor cell–vessel interface is essential for accurate intraoperative diagnosis.

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P-6-11

一般演題 Cytology

Digital Cytology Learning Content Development and AI Applications

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[Background and Aim] Conventional self-study in cytology has relied on textbooks, atlases, and microscopy. Although Whole-Slide Imaging (WSI) has recently gained attention, accessible learning resources remain limited. We developed online digital cytology learning content using images and evaluated its usability. Additionally, we assessed the utility of an AI model for efficiently collecting large numbers of cytology images suitable for learning resources. [Materials and Methods] 1. Digital content development: Ninety-two cytology specimens, including benign and malignant cases, were used. Target cells were annotated on WSIs. Study decks were created using “Anki” as flashcards, organized by organ and difficulty level. Students voluntarily conducted tests and a usability survey. 2. Similar image retrieval using the histopathology foundation model UNI: From cervical cytology WSIs (squamous metaplasia, HPV infection, squamous cell carcinoma [SCC]), five query images per case were selected. Database image sizes were 58,877, 107,913, and 349,625 patches, respectively. UNI was used for feature extraction and similarity calculation, and detection rates within the top 100 retrieved similar images were evaluated. To improve performance, preprocessing using the Segment Anything Model (SAM) and Laplacian-based blur detection was applied. [Results] We created Japanese and English learning decks consisting of 105 basic- and 168 advanced-level images. Test scores improved significantly after use, from 20% to 57%, and were higher among users than non-users. More than 90% of the students rated the content as easy to use and expressed willingness to continue using it. Detection rates with UNI were 90.8% for squamous metaplastic cells, 8.6% for HPV-infected cells, and 17.2% for SCC. After image preprocessing to reduce background noise and enhance focus, SCC detection improved to 18.2%. [Conclusion] We developed effective, accessible digital cytology learning content and demonstrated its educational value. The AI model UNI showed potential for cytology image retrieval, and preprocessing methods may further enhance detection performance.
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P-6-12

一般演題 Cytology

Comparison of ThinPrep UroCyte and Cytospin in Urinary Cytology

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Objective

To compare the specimen quality and diagnostic performance of ThinPrep UroCyte liquid-based cytology with conventional Cytospin in urinary cytology.

Methods

A total of 300 urine specimens collected at Chi Mei Medical Center from January to March 2025 were prepared using both methods. The slides were evaluated according to The Paris System for Reporting Urinary Cytology, including assessments of cellularity, background clarity, cellular morphology, diagnostic interpretation, and the detection of polyomavirus infection.

Results

ThinPrep UroCyte preparations demonstrated superior performance compared with Cytospin in several aspects. Cellularity improved from absent or scant to moderate or abundant in 45.6% of cases, and background clarity improved in 16% of cases. The positive diagnostic rate increased by 25%. Among seven cases with polyomavirus infection, five cases were identified only in the liquid-based cytology preparations.

Conclusions

ThinPrep UroCyte improved cellularity, smear quality, diagnostic sensitivity, and polyomavirus detection compared with conventional Cytospin preparations.

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P-6-13

一般演題 Cytology

Case Report: Stratified Mucin-Producing Intraepithelial Lesion (SMILE) in Pap Smear

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Background:
Stratified mucin-producing intraepithelial lesion (SMILE) is a rare cervical precancer associated with high-risk Human papillomavirus, characterized by combined squamous and glandular differentiation, posing a diagnostic challenge in Pap smear.
Case presentation:
A 69-year-old woman was informed abnormal Pap smear result refereed from other hospital. Repeat Pap smear revealed crowded epithelial clusters arranged in stratified sheets and syncytial aggregates with inflammatory background. Some clusters of epithelial cells exhibited, hyperchromatic nuclei, high N/C ratios, with typical features of high grade cervical intraepithelial lesion (HSIL). A subset of atypical cells showed vesicular chromatin, indistinct nucleoli, relative low N/C ratio, foamy cytoplasm focal with intracytoplasmic vacuoles arranged in stratified sheets without glandular formation or feathering patterns. The diagnosis of Pap smear was atypical glandular cells favor neoplasm combine high grade squamous intraepithelial lesion. Cervical biopsy was performed and confirmed HSIL focally with stratified mucin-producing intraepithelial lesion. Immunohistochemical staining showed diffuse p16 positivity, supporting HPV-related pathogenesis.
Discussion
The subtle cytologic features of SMILE indicted the reason of low dectective rate in Pap smears. This case highlights the importance of recognizing mucin-containing atypical cells within stratified clusters to avoid misclassification as reactive endocervical glandular cells, tubal metaplasia, HSIL or adenocarcinoma in situ.
Conclusion
SMILE is a rare and relatively newly recognized variant of AIS and some IHC stains could support the diagnosis. Often coexists with other lesions, including SIL and AIS as well as invasive carcinoma. Diligent assessment of the classic features of HSIL and/or AIS may provide the proper interpretation. The WHO classifies SMILE as a subtype of high grade cervical glandular intraepithelial neoplasm /AIS, so as the clinical management.

P-6-14

一般演題 Cytology

Analyzing positive cells using CINtec Plus in cervical smears

Cytological findings of p16/Ki-67 positivity in high-risk HPV cases

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【Introduction】CINtec Plus is an effective biomarker-based adjunct test for patients who test positive for high-risk human papillomavirus (HR-HPV) during primary HPV screening. Furthermore, it is more sensitive than conventional cytology for detecting cervical intraepithelial neoplasia grade 2 or worse (CIN2+), with comparable specificity. This study aimed to improve the diagnostic accuracy of Papanicolaou cytology in HPV primary screening by analyzing the morphological characteristics of positive cells using CINtec Plus.

【Materials and Methods】A total of 281 cervical cytology samples were collected from a hospital that provides comprehensive histopathological diagnosis, with informed consent obtained between August 2025 and February 2026. HPV genotyping was performed using uniplex E6/E7 PCR, and cytological diagnoses were made using liquid-based cytology specimens. Whole-slide images were acquired using the Nanozoomer S20 system, and CINtec Plus dual staining was applied to evaluate the morphological characteristics of p16/Ki-67-positive cells.

【Results】High-risk HPV genotypes were detected in 10.0% (23/231) of NILM, 37.5% (3/8) of ASC-US, 84.6% (11/13) of LSIL, 66.7% (2/3) of ASC-H, and 71.4% (7/7) of HSIL, respectively. Among NILM cases positive for high-risk HPV, CINtec Plus was positive in 13.0% (3/23). In NILM/HPV-positive cases, CINtec Plus positivity was observed in small atypical cells lacking nuclear enlargement, with an irregular nuclear shape and slightly increased chromatin.

【Discussion】In this study, triaging HPV-positive screening results using p16/Ki-67 dual-stained cytology enabled the identification of women at high risk for underlying CIN2+. The findings suggest that the sensitivity of cytology, when focused on detecting small atypical cells with an irregular nuclear shape and slightly increased chromatin, may approach that of CINtec Plus.

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P-6-15

一般演題 Cytology

Calcification and RA cell in Human Osteoarthritis Synovial Fluid

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Calcification and RA cell in Human Osteoarthritis Synovial Fluid

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Calcification with hydroxyapatate（HA） crystals is a common phenomenon in during osteoarthritis osteoarthritis (OA). It is directly linked to the severity of the disease and is known to be associated to bone damage.Rheumatoid arthritis (RA) is a chronic inflammatory disease of the synovial joints that affects 1% of the human population. In this study.we investigated the frequency and clinical significance of HA crystal and RA cells in the synovial fluid of patients with OA.A total of 49 synovial fluid samples were collected from the knee jouins of patients with aclinical daiagnosis of osteoarthritis.
The methods involved collecting 20μm of synovial fluid from OA patients, preparing a moist specimens, and examining them for RA cells. In addition 50μm of synovial fluid was collected, prepared using the ground-grain method, and then Giemsa stained before the cells were classified. These findings were Compared with knee joint X-rays
Results using the Kellgren-Laurence (KL) grading system.HA crystals were observed in 19 out of 49 cases. While RA cells were observed in 3 cases.In cases where 30 or more HA crystals were observed in a specimen of synovial fluid, KL classifications were 3 or higher. Inclusion bodies were detected in RA cells.
The Morphological changes in synovial fluid changes are important and may be associated with clinical response in knee osteoarthritis is important.

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一般演題 Cytology

miRNAs in extracellular vesicles derived from cadmium-exposed hepatocytes inhibit osteogenesis.

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【Background】Cadmium (Cd) is a toxic heavy metal to humans and has been reported to be associated with osteogenic disorders. Recently, Extracellular Vesicles (EVs) have been known as mediators of intercellular communication via miRNA and other bioactive molecules. However, the effects of miRNA in EVs derived from Cd-exposed cells on osteogenesis remain unclear.
【Purpose】To elucidate the effects of EVs derived from Cd-exposed hepatocytes (Cd-EVs) on osteoblast differentiation and to clarify the involvement of the BMP/Smad signaling pathway in the underlying molecular mechanism.
【Materials & Methods】The human hepatocellular carcinoma cell line HepG2 was exposed to Cd, and secreted Cd-EVs were collected. Cd-EVs were added to the human fetal osteoblast cell line hFOB1.19, and the expression of osteogenic differentiation-related genes was analyzed by RT-qPCR and Western blotting. Furthermore, miRNA profiling of Cd-EVs was performed, and functional inhibition experiments were conducted to evaluate their effects on the BMP/Smad signaling pathway.
【Results】In the Cd-EVs treatment group, the mRNA and protein expression of osteoblast differentiation-related genes were significantly decreased. In addition, phosphorylation signaling in the BMP/Smad pathway was suppressed. Among the miRNAs in Cd-EVs, an increased expression of miR-30d was observed, and experimental inhibition suggested its involvement in the suppression of osteoblast differentiation.
【Conclusion】miRNA in EVs was changed by exposure to Cd, and induced a Cd-derived influence on target cells. These findings demonstrated the potential utility of EV analysis for the assessment of environmental chemical exposure and suggest its application in the development of novel biomarkers in clinical laboratory medicine.

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一般演題 Cytology

Development of an Eye-Tracking Application for Cytotechnologist Skill Assessment

Assessing Diagnostic Expertise Using Machine Learning and Visual Search Features

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Purpose: This study aimed to objectively evaluate the diagnostic skills of cytotechnologists (CTs) using an eye-tracking system and to develop a machine learning–based application for improving diagnostic accuracy and standardizing cytotechnology training.

Methods: One hundred professional CTs evaluated 30 digital cytology cases (15 cervical and 15 respiratory cases) displayed on a monitor while their gaze behaviors were continuously recorded using a Tobii Pro eye-tracking system. Characteristic visual search features derived from 27 expert CTs and 27 beginner CTs were used to train a Support Vector Machine (SVM) classifier. An application was subsequently developed to classify CT skill levels based solely on gaze behavior patterns. To evaluate the discriminative performance and generalizability of the model, additional CTs were assessed using two separate datasets: the original 30-case training dataset and a completely independent set of previously unseen cases.

Results: When evaluated using the original case set, SVM classification scores showed an association with the CTs' years of clinical experience. In contrast, when 10 additional CTs were evaluated using the unseen case set, classification scores clustered near the decision boundary regardless of individual experience or actual diagnostic performance. These findings suggest that the gaze behavior features learned by the SVM were influenced, at least in part, by case-specific visual characteristics, thereby limiting robust generalization to previously unseen cases.

Conclusion: The proposed SVM-based application demonstrated the potential to objectively assess CT skill levels using familiar case sets. However, the findings also highlight the importance of improving model generalizability beyond case-specific visual patterns. Future research that incorporates diverse training datasets covering a broader range of clinical scenarios and employs rigorous feature engineering and regularization strategies will enable the development of a robust, widely applicable skill assessment tool for cytotechnology education.

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P-6-18

一般演題 Cytology

A case of neuroendocrine carcinoma of the breast

nipple discharge : cytological characteristics

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Background: We report a case of neuroendocrine carcinoma of the breast, which was suspected by nipple discharge cytology.

Case: A 36-year-old woman was admitted to our hospital because of left breast nipple discharge. Ultrasonography showed dilated ducts and several masses (about 5mm) in the left CD area. Magnetic Resonance Imaging (MRI) revealed segmental enhancement. The nipple discharge cytology showed many cell clusters of varying sizes and isolated cells. A cannibalistic and trabecular pattern were also observed. The tumor cells had round or oval nuclei with high N/C ratio, fine granular chromatin and apparent nucleoli.

Histologically, most of the tumor consisted of a non-invasive ductal carcinoma with focal minimal invasion. Tumor cells arranged in a trabecular pattern and rosette-like structures in the intraductal component. Immunohistochemical staining was positive for chromogranin A, synaptophysin and CD56 in the tumor cells.

Conclusion: Nipple discharge cytology is helpful for the diagnosis of neuroendocrine carcinoma of the breast, especially when it is difficult to detect a mass in imaging. Even in nipple discharge cytology, cytological characteristics of a neuroendocrine carcinoma were observed, allowing for the estimation of the histological type.

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P-6-19

一般演題 Cytology

Cytological Features and Differential Diagnosis of Dermatopathic Lymphadenopathy

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【Introduction】Dermatopathic lymphadenopathy (DL) is a reactive lymph node lesion associated with chronic skin diseases. Cutaneous symptoms may be absent at lymph node enlargement, resulting in a lack of clinical clues and making cytological diagnosis difficult. We investigated cytological features and differential diagnostic points of DL.

【Materials and Methods】Five cases histologically diagnosed as DL were retrospectively reviewed. Follicular hyperplasia (FH), histiocytic necrotizing lymphadenitis (HNL), follicular lymphoma (FL), and malignant melanoma were included as differential diagnoses. Cytological features were evaluated.

【Results】Dendritic cell proliferation was characteristic in DL. Polygonal to spindle-shaped cells with pale light green cytoplasm appeared singly and in clusters against a background of small lymphocytes. These cells showed oval nuclei with nuclear grooves, finely granular chromatin, and dendritic cytoplasmic processes. Melanin-laden histiocytes and follicular dendritic cells (FDCs) were also observed.In FH, germinal center cells, FDCs, and tingible body macrophages were observed, showing a polymorphous appearance. HNL showed a necrotic background with histiocytes phagocytosing karyorrhectic debris. FL showed a relatively monotonous proliferation of slightly enlarged cleaved lymphocytes. Malignant melanoma showed melanin-containing tumor cells with nuclear atypia and prominent nucleoli.

【Conclusion】DL is characterized by dendritic cell proliferation and melanin-laden histiocytes. Evaluation of non-lymphoid cells is useful for differential diagnosis in lymph node cytology.

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一般演題 Cytology

Mollaret cells identified in cerebrospinal fluid cytology.

A case of recurrent meningitis underlying Sjogrens syndrome.

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【Introduction】Mollaret meningitis is a benign recurrent meningitis first reported by Pierre Mollaret in 1944. Although cases caused by drugs or autoimmune diseases have been reported, most are attributed to herpes simplex virus type II. Meningitis accompanied by meningeal irritation symptoms recurs at intervals of several weeks to months, with the appearance of mollaret cells in the cerebrospinal fluid. Mollaret cells are fragile and are detected in the cerebrospinal fluid within approximately the first 72 h of disease onset. This makes their identification by cerebrospinal fluid cytology rare. Here, we report a case of recurrent meningitis in which Mollaret cells were identified using cerebrospinal fluid cytology.

【Case Report】A woman in her 80s with a history of Sjögren syndrome presented with fever, altered consciousness, and vomiting. She had visited another hospital three times over the past six months for similar complaints. Blood tests and whole-body CT showed no abnormalities. Her impaired consciousness resolved within approximately three days, and she was discharged. Similarly, examinations at our hospital, including MRI, yielded no findings suggestive of a cause for her impaired consciousness. Based on her history of fever episodes and impaired consciousness, which improved over several days, Mollaret meningitis was suspected, and cerebrospinal fluid cytology was performed.

【Cerebrospinal Fluid Cytology Findings】Monocyte-lineage atypical cells with deep clefts and footprint-shaped nuclei were observed. The atypical cells were consistent with Mollaret cells. Large ghost-like degenerated cells were observed in the background. These findings were suggestive of Mollaret meningitis.

【Conclusion】In this case, the identification of Mollaret cells through cytology aided in the diagnosis of Mollaret meningitis. When cytology is required to evaluate recurrent meningitis, it is important to consider the possibility of Mollaret meningitis during microscopic examination.

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一般演題 Cytology

Nested Variant Urothelial Carcinoma in Urine Cytology

A Diagnostic Pitfall in The Paris System

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Purpose: The nested variant of urothelial carcinoma shows infiltrative growth despite bland cytological atypia. The Paris System for Reporting Urinary Cytology (TPS) is designed to detect high-grade urothelial carcinoma (HGUC) and emphasizes a high nuclear-to-cytoplasmic (N/C) ratio. We report a single case initially interpreted as atypical urothelial cells (AUC) on urine cytology and reevaluated using semi-quantitative morphometry.
Methods: Urine cytology slides from a male patient in his 60s with suspected bladder tumor were retrospectively reviewed. Slides were prepared from 10 mL of urine using the Autosmear system and stained with the Papanicolaou method. Nuclear and cytoplasmic areas of benign urothelial cells, presumed nested variant tumor cells, and rare atypical cells suggestive of HGUC were manually measured using ImageJ/Fiji. The N/C ratio was calculated by dividing nuclear area by cytoplasmic area.
Results: Urine cytology showed a relatively clean background with few inflammatory cells. Loosely cohesive clusters of atypical cells with abundant foamy cytoplasm showed nuclear enlargement, mildly increased fine chromatin, and relatively mild atypia. Although a few atypical cells suggestive of HGUC were identified, their limited number led to an overall interpretation of AUC. Mean N/C ratios were 0.16 in benign urothelial cells (n=7), 0.38 in presumed nested variant tumor cells (n=46), and 0.63 in rare atypical cells suggestive of HGUC (n=3). Transurethral resection of bladder tumor revealed invasive urothelial carcinoma, nested variant, associated with carcinoma in situ.
Conclusion: Presumed nested variant tumor cells showed a higher N/C ratio than benign urothelial cells but remained lower than rare atypical cells suggestive of HGUC. Although these cells may mimic reactive urothelial cells, assessment of nuclear enlargement, chromatin features, abundant foamy cytoplasm, and a clean background is important for interpreting them as AUC. These findings suggest that the nested variant may represent a diagnostic pitfall when applying TPS.
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一般演題 Cytology

Utility of Cytological Specimens for Molecular Testing in Lung Cancer

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【Background】
Molecular testing is essential for precision medicine in patients with lung cancer. However, obtaining sufficient tissue specimens from patients with advanced disease is challenging. Cytology specimens have recently gained attention as alternative materials for molecular testing. This study aimed to evaluate the utility of cytology specimens in compact panel testing for lung cancer.
【Methods】
We retrospectively analyzed 54 lung cancer cases that underwent compact panel testing at our institution. The cohort included 13 cytological and 41 histological specimens. The cytological specimens comprised bronchial washing fluid (n = 2), pleural effusion samples (n = 4), and pleural effusion cell-block specimens (n = 7). The success rates of compact panel testing were compared between the cytological and histological specimens.
【Results】
The success rate of compact panel testing was 100% (13/13) for cytological specimens and 95.1% (39/41) for histological specimens, respectively. The two unsuccessful histological cases were attributed to undetectable RNA. In all 13 cytological cases, repeat tissue sampling was considered difficult or impossible. Nevertheless, sufficient nucleic acid quality was obtained, and successful molecular analysis was achieved in all cases.
【Conclusion】
Cytological specimens are useful and reliable for compact panel testing in lung cancer, particularly in cases where tissue sampling is difficult. The appropriate utilization of cytological specimens may contribute to molecular testing in the era of precision medicine and facilitate minimally invasive genomic testing.
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P-6-23

一般演題 Cytology

ROSE in Emergency Care: Report of Two Beneficial Cases

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【Background】Histopathological diagnosis of biopsy specimens generally requires approximately one week before results are reported. In cases of severe airway stenosis due to suspected malignant tumors or malignant lymphoma requiring specialized treatment, early histological diagnosis is essential. Rapid onsite cytologic evaluation (ROSE) is performed when the attending physician deems it necessary. A cytotechnologist travels to the bedside, prepares smear specimens on-site, and evaluates them using Diff-Quik staining. Here, we report two cases in which ROSE was particularly useful.

【Case 1】A woman in her 70s. Chief complaint: Severe airway stenosis. Bronchoscopy biopsy was performed under Bronchoscopic biopsy was performed under veno-venous extracorporeal membrane oxygenation (VV-ECMO), and ROSE was conducted. The first two biopsy samples contained only necrotic material and Candida; however, the third sample finally included the target cellular component. Cytologic evaluation indicated malignancy, and the findings were reported as squamous cell carcinoma.

【Case 2】A man in his 50s. Chief complaint: Generalized lymphadenopathy. A left inguinal lymph node was excised, and imprint cytology was prepared and evaluated immediately. The initial ROSE report indicated malignant lymphoma, and the adequacy of the specimen volume was also assessed.

【Discussion】ROSE enabled real-time assessment of whether the target lesion had been adequately sampled and allowed immediate feedback regarding the appropriate amount of tissue required. No additional sampling procedures or delays in diagnostic reporting occurred, thereby reducing the burden on patients. ROSE also facilitated rapid consultation with relevant specialists by emergency physicians, contributing to timely decision-making regarding patient management.

【Conclusion】Implementation of ROSE in the emergency and critical care setting is highly beneficial.

P-6-24

一般演題 Cytology

Evaluation of Intraoperative Rapid Cytology in Thoracic Surgery Cases

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【Introduction】Intraoperative rapid diagnosis is essential for determining surgical procedures and resection extent. However, handling unfixed specimens carries a risk of pathogen exposure, particularly in respiratory specimens. During the COVID-19 pandemic, rapid cytology (scrape cytology) was introduced as an alternative intraoperative diagnostic method after discussion between thoracic surgeons and pathologists to reduce infection risk while maintaining diagnostic support.

【Materials and Methods】We retrospectively reviewed 55 thoracic surgery cases in which intraoperative rapid cytology was performed between April and October 2020. Cytological diagnoses were compared with corresponding histological findings.

【Results】Fifty-one of 55 cases showed concordance between cytological and histological diagnoses regarding benignity or malignancy. Discordant results were observed in two cases: one was diagnosed as benign on cytology but malignant on histology, and another was interpreted as positive on cytology but showed no malignancy on histology.

【Discussion】Diagnostic discrepancies were mainly attributed to insufficient cellular sampling and mild cytological atypia. Limited preparation time and lower staining quality compared with conventional Papanicolaou staining also contributed to diagnostic difficulty.

【Conclusion】Rapid cytology may serve as a useful adjunct for intraoperative diagnosis in thoracic surgery and may help reduce infection risk by avoiding frozen-section preparation. Close collaboration between surgeons and pathologists is essential for its appropriate use and interpretation.

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一般演題 Cytology

Simple Bone Cyst with Spherical Fibrin-like Material in Cyst Fluid

A Case Report

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Introduction: Simple bone cyst (solitary bone cyst) is an intraosseous cystic lesion characterized by the accumulation of serous fluid. Histologically, the interstitial deposition of fibrin-like material is a characteristic finding; however, its specific features in cytological specimens have not been well documented. We report a case in which numerous spherical fibrin-like structures, similar to those seen in the stroma, were identified in the cytological specimen of the cyst fluid.

Case Report: A 10-year-old boy. During an evaluation for an ankle sprain, a bone cyst with a maximum diameter of 29 mm was incidentally discovered in the right calcaneus. A simple bone cyst was suspected, and curettage of the lesion with artificial bone grafting was performed.

Cyst Fluid Cytology: Against a background of pale proteinaceous material, acellular spherical structures were loosely aggregated, forming clusters of varying sizes. Scattered histiocytes were observed, some of which were attached to the spherical structures.

Cyst Fluid Cell Block: Against a background of erythrocytes, pale eosinophilic spherical objects composed of fine fibrillar material were loosely aggregated. These were identical to the clusters of spherical structures seen in the cytological specimens and were considered to correspond to the so-called "fibrin-like material" seen histologically.

Histological Findings: The submitted specimen was extremely scant, consisting of fragmented bone, minimal stroma, and blood clots. Although no membranous structures indicating a cyst wall were observed, deposition of fibrin-like material was identified, consistent with a simple bone cyst.

Conclusion: This case suggests that the fibrin-like material that deposits in the stroma of simple bone cysts may be initially formed within the cyst fluid. Furthermore, in cases of simple bone cyst, histological specimens are often scant, which can make it difficult to obtain definitive diagnostic findings. In such instances, cytology of the cyst fluid may serve as a valuable diagnostic aid.

Keywords: fibrin-like material, cyst fluid, simple bone cyst

P-6-26

Central Nervous System Involvement in Mantle Cell Lymphoma

一般演題 Cytology

The Crucial Role of Cerebrospinal Fluid Laboratory Diagnostics

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Introduction: Mantle cell lymphoma (MCL) is an aggressive B-cell non-Hodgkin lymphoma with a rare (4–5% incidence) but prognostically unfavorable central nervous system (CNS) involvement. This clinical entity poses a significant diagnostic challenge in immunocompromised patients, as the clinical presentation often mimics infectious processes. Consequently, the differential diagnostic imperative is a lumbar puncture with cerebrospinal fluid (CSF) analysis, placing laboratory diagnostics at the center of clinical evaluation.

Objective: To present a case of MCL with confounding neurological progression, highlighting the utility of this diagnostic approach in successfully differentiating an infectious etiology from primary disease progression.

Case Report: A 71-year-old male with stage IV MCL (previously treated with R-CHOP and R-DHAP) was transferred to the University Hospital for Infectious Diseases (UHID) due to suspected meningitis. Initial CSF findings showed a turbid appearance, a cell count of 3,640×10^6/L, protein 2.78 g/L, glucose <0.28 mmol/L, and lactate 11.2 mmol/L. The patient presented with progressive confusion, disorientation, and psychomotor slowing. Brain CT revealed a right temporoparietal corticosubcortical hyperdensity with intense gyral and meningeal enhancement, without evidence of ischemia or hemorrhage. Despite empirical antimicrobial therapy, his consciousness deteriorated to stupor. Upon admission to the UHID, a repeat emergency lumbar puncture showed slightly turbid CSF with marked pleocytosis (2,827×10^6/L), protein 2.69 g/L, glucose 2.7 mmol/L, and lactate 12.56 mmol/L. Multiplex PCR for common bacterial *(Escherichia coli K1, Haemophilus influenzae, Listeria monocytogenes, Neisseria meningitidis, Streptococcus agalactiae, Streptococcus pneumoniae)*, viral (cytomegalovirus, enterovirus, herpes simplex virus 1, herpes simplex virus 2, human herpesvirus 6, human parechovirus, varicella zoster virus), and fungal *(Cryptococcus neoformans/gattii)* pathogens was negative. Cytological analysis of the CSF confirmed numerous atypical lymphatic cells, partially with indented nuclei and scanty cytoplasm, morphologically consistent with known MCL infiltration. Flow cytometry confirmed an absolute dominance of B-cells (CD19: 96.0%), along with significant suppression of the T-lymphocyte population (CD3: 3.7%, CD4: 1.7%, CD8: 2.0%). Antimicrobial therapy was discontinued, and high-dose dexamethasone was initiated, resulting in significant clinical improvement.

Conclusion: This case highlights the importance of comprehensive CSF analysis in differentiating primary CNS lymphoma progression from infection. Rapid integration of cytological, microbiological, and flow cytometric findings is essential to prevent diagnostic delays, avoid unnecessary antimicrobial therapy, and guide immediate, targeted intervention.

Keywords: cerebrospinal fluid, laboratory diagnostics, mantle cell lymphoma, meningitis.

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P-6-27

一般演題 Cytology

Atrophy

Diagnostic Utility of the Estrogen Test in Postmenopausal Cervical Cytology

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Background: Estrogen deficiency in postmenopausal women causes atrophic epithelial changes that mimic cervical intraepithelial neoplasia (CIN), leading to diagnostic ambiguity and unnecessary invasive procedures. This study evaluated the diagnostic value of the estrogen test combined with cytomorphologic, HPV, and biochemical analyses.

Methods: Postmenopausal women with abnormal cervical cytology underwent an estrogen test followed by repeat cytology. Cytomorphologic parameters, HPV genotypes, and biochemical markers (ALP, LDH, total protein, albumin) were evaluated before and after treatment to determine diagnostic accuracy.

Results: Post-treatment cytology confirmed normal atrophy in 69 patients (50.7%), LSIL in 24 (17.7%), HSIL in 25 (18.4%), and carcinoma in 18 (13.2%). Disease progression correlated with marked cytomorphologic changes (increased nuclear size, N/C ratio, pleomorphism, hyperchromasia). High-risk HPV (mainly HPV16) and elevated ALP/LDH were predominant in advanced lesions but lacked sensitivity for early diagnosis. The estrogen test effectively differentiated benign atrophic atypia from true lesions, significantly reducing false positives.

Conclusions: The estrogen test is a simple and effective adjunctive tool that markedly improves diagnostic accuracy for abnormal cervical cytology in postmenopausal women, preventing unnecessary biopsies and colposcopies.

Keywords: Postmenopausal women; Cervical cytology; Estrogen test; CIN; HPV; Cytomorphology.

P-6-28

Bone Marrow Leishmaniasis in a Patient with HIV Infection:

Lessons from a Relapsed Case

一般演題 Cytology

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Introduction: Leishmaniasis is a zoonosis caused by protozoa of the genus *Leishmania* and transmitted through the bite of sandflies belonging to the genus *Phlebotominae*. Three clinical forms are recognized: cutaneous, mucocutaneous, and visceral. The most severe form, characterized by the presence of parasites in the bone marrow, spleen, and liver, is termed visceral leishmaniasis (kala-azar). This condition presents as an opportunistic infection in HIV-positive patients, further complicating their clinical course. In Croatia and the surrounding region, leishmaniasis is rare, and due to its non-specific symptoms—such as fever, hepatosplenomegaly, weight loss, and pancytopenia—the diagnosis is frequently delayed.

Case Report: We present the case of an HIV-positive male patient, who exhibited a weight loss of over 20 kilograms, intermittent fever, and pancytopenia. During a one-year period, he was hospitalized multiple times across various institutions due to urticaria, exudative pleuritis (suspected tuberculosis), an anal fissure, and aphthous stomatitis, as well as suspected pulmonary eosinophilic granuloma and angioedema. Following a positive anti-HIV screening test, the patient was transferred to the University Hospital for Infectious Diseases. During a five-month hospitalization, his disease course was characterized by febrile episodes, with occasional occurrences of oropharyngeal candidiasis and an episode of CMV viremia. Anemia and leukopenia progressively worsened, and following the ultrasound detection of hepatosplenomegaly, a bone marrow aspiration was performed. Microscopic evaluation revealed numerous *Leishmania spp.* amastigotes. Remission was achieved after an extended course of sodium stibogluconate (Pentostam); however, a relapse occurred two years later.

The patient was readmitted due to a suspected infection of his indwelling central venous catheter. Upon admission, a bone marrow aspiration demonstrated hypocellular bone marrow without evidence of parasites, and the subsequent *Leishmania* culture returned negative. During the four-week hospitalization, the patient became febrile again at irregular intervals. A repeat bone marrow aspiration was performed, which microscopically visualized *Leishmania* parasites, which were also confirmed by culture. Treatment with amphotericin B was initiated, followed by pentamidine isethionate maintenance prophylaxis. A follow-up bone marrow aspiration performed one year later was negative for *Leishmania*. A subsequent control biopsy three years later also remained negative.

Conclusion: Beyond the evaluation of hematopoiesis, bone marrow aspiration remains the gold standard for diagnosing rare but potentially lethal parasitic infections, such as visceral leishmaniasis. This case highlights the pivotal role of cytological diagnostics in rapid microscopic parasite identification aimed at preventing diagnostic delays. Timely differential consideration of leishmaniasis in immunocompromised patients, particularly those with HIV co-infection, is crucial for the successful management of relapses and improving clinical outcomes.

Key words: bone marrow aspiration, disease relapse, HIV co-infection, visceral leishmaniasis

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P-7-1

一般演題 Urinalysis

A case of combined small cell carcinoma and urothelial carcinoma

Bladder cancer in which estimation of histological type was avoided in Urinary Sediment Examination

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[Introduction] The Japanese Association of Medical Technologists recommends estimating and reporting the histological type when atypical cells are detected in urinary sediment examination. However, in the present case, atypical cells detected in a patient with suspected bladder cancer were reported without histological classification. Subsequent pathological evaluation revealed combined small cell carcinoma and urothelial carcinoma.

[Case] A male patient in his 60s presented with gross hematuria. Computed tomography (CT) and cystoscopy performed at a previous hospital revealed a papillary bladder tumor, and the patient was subsequently referred to our institution for further evaluation. Urine cytology performed at the previous hospital had shown atypical cells suspicious for malignancy.

[Laboratory Findings] Urine Sediment examination (500 xg for 5 min): RBCs 20-29/HPF, WBCs 5-9/HPF, Atypical cells 10-19/LPF, Atypical cell clusters 10-19/LPF. The comment was “Undetermined cell lineage”. The atypical cells observed in urinary sediment exhibited naked nucleus-like features, and cell clusters showed nuclear molding, suggesting small cell carcinoma. However, clusters of atypical cells with yellowish cytoplasm, papillary architecture, and strong cohesion were also identified, raising the possibility of urothelial carcinoma. Therefore, we reported the findings without specifying the histological type. Urine cytology showed numerous small atypical cells with a high N/C ratio or naked nuclei were observed in both syncytial clusters and singly, suggestive of small cell carcinoma with a minor urothelial carcinoma component. Histopathological examination of the transurethral resection of bladder tumor revealed dense proliferation of tumor cells with a high N/C ratio suggestive of small cell carcinoma, along with urothelial carcinoma components accounting for approximately 10–20% of the lesion.

[Conclusion] Although estimation and reporting of the histological type of atypical cells in urinary sediment examination is generally recommended, this case suggests that definitive classification should sometimes be avoided cytological findings indicate the possibility of multiple histological types.

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P-7-2

一般演題 Urinalysis

Diagnostic Pitfalls and Interpretive Performance in Urinary Cell Identification

Accuracy, Misclassification Patterns, and Predictors of Professional Performance

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Background

Urine sediment examination serves as a critical “liquid biopsy” for urinary tract disorders; however, morphological similarities among cells pose substantial identification challenges. This study evaluated identification accuracy among medical technologists and analyzed factors influencing performance.

Methods

An expert-curated, 50-item morphological questionnaire featuring 250 annotated images was administered to 65 practicing medical technologists across multiple hospitals. Identification accuracy was the primary outcome. Multivariate regression analyzed associations between professional experience, workload, and performance, while confusion matrices identified misclassification patterns.

Results

Monocytes (41.2%), middle-to-deep urothelial cells (41.2%), and advanced renal tubular epithelial cells (41.4%; including spinous, pear-shaped, near-circular types) showed lowest accuracies. Professional experience (β=3.29, p<0.001) and daily specimen workload (β=3.39, p=0.005) were significant positive predictors of performance (F=12.02, p<0.001). Confusion matrix analysis revealed prominent bidirectional confusion between advanced renal tubular epithelial cells and middle-to-deep urothelial cells (~50%), as well as between isomorphic and dysmorphic RBCs (~40%). Major unidirectional errors involved misidentifying monocytes as mononuclear neutrophils (32.0%) and oval fat bodies as basic renal epithelial cells (27.9%). Furthermore, middle-to-deep squamous epithelial cells (27.6%) and basic renal tubular epithelial cells (23.6%) were frequently misclassified as middle-to-deep urothelial cells.

Conclusions

Clinical experience and workload drive identification accuracy. High-risk advanced renal tubular epithelial cell and RBC morphologies require targeted training to minimize diagnostic pitfalls and improve laboratory consistency.

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P-7-3

一般演題 Urinalysis

Usefulness of Gram staining in continuous ambulatory peritoneal dialysis effluent

Evaluation of characteristics using the fully automated urine particle analyzer UF-5000

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[Background] Rapid identification of causative bacteria is essential in continuous ambulatory peritoneal dialysis (CAPD)-related peritonitis to ensure prompt and appropriate antimicrobial therapy and to prevent peritoneal dysfunction. The UF-5000 is a fully automated urine particle analyzer equipped with a bacterial classification function (BACT-Information; Bact-I) that differentiates Gram-positive and Gram-negative bacteria. Although its performance has been reported in urine samples, its utility in CAPD effluent remains unclear. This study aimed to evaluate its performance in this setting.

[Methods] Residual samples from 25 CAPD effluent specimens (23 patients), submitted for routine clinical testing, were analyzed. Bact-I results obtained by the UF-5000 (Gram-positive [GP], Gram-negative [GN], GP/GN mixed, and unclassified) were compared with bacterial identification results from culture. Concordance was defined as agreement in Gram classification, while discrepancy was defined as discordance.

[Results] Bacterial growth was observed in 24 of 25 samples. Gram-positive bacteria accounted for 70.8% and Gram-negative organisms for 29.2%. Among Gram-positive bacteria, Streptococcus species were the most frequently detected, followed by other cocci. Concordance rates were 81.3% (13/16) for Gram-positive bacteria and 50.0% (3/6) for Gram-negative bacteria. One GP/GN mixed infection case showed complete agreement between methods. Two samples (8.0%) were classified as unclassified by Bact-I. Overall concordance between Bact-I and culture results was 73.9% (17/23).

[Conclusion] The accuracy of Bact-I for Gram-positive bacteria was considered satisfactory. Since Gram-positive bacteria is reported to be the most common causative bacteria of CAPD-related peritonitis, Bact-I Gram classification may provide clinically useful information for selecting initial antimicrobial therapy. However, the concordance rate for Gram-negative bacteria was low. Further studies with a larger number of cases are warranted to validate these findings.

P-7-5

一般演題 Urinalysis

Evaluation of Urinary Sediment for Monitoring Fabry Disease Treatment

Longitudinal Changes in Mulberry Cell and Body Counts in Fabry Disease

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Introduction

Fabry disease is an X-linked inherited disorder caused by mutations in the α-galactosidase A (α-GAL) gene, resulting in the accumulation of sphingoglycolipids in multiple organs. Mulberry cells and bodies are observed in the urine of patients with Fabry disease, and urinary sediment examination is known to be a useful screening test for the diagnosis of Fabry disease. Previous studies have suggested that the number of mulberry cells and bodies may reflect treatment response during enzyme replacement therapy. We investigated whether longitudinal changes in mulberry cells and bodies are useful for treatment monitoring.

Materials and Methods

Among 20 cases examined between 2019 and 2024, seven patients with long-term follow-up were included (2 males and 5 females, including 1 untreated patient). Changes in the number of mulberry cells and bodies, estimated glomerular filtration rate (eGFR), and urinary protein levels were evaluated. The observation period was divided into early and late phases for comparison. This study was approved by the institutional ethics committee (approval No. 22424).

Results

The number of mulberry cells and bodies varied widely among individuals. Although the number of mulberry bodies tended to decrease over time, no consistent trend was observed in mulberry cells. No association was found between mulberry cell counts and the rate of renal function decline.

Discussion and Conclusion

Mulberry cells are considered to originate mainly from podocytes and were expected to correlate with renal dysfunction; however, no such association was observed. Although detection of mulberry cells and bodies is useful for diagnosing Fabry disease, longitudinal monitoring of their numbers appears to have limited usefulness for treatment monitoring.

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P-7-6

一般演題 Urinalysis

Quantitative Assessment of Macroscopic Haematuria Using Urinary RBC Counts

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Introduction
The Japanese Evidence-based Clinical Practice Guidelines for Hematuria 2023 define macroscopic hematuria as “urine that appears red to brownish-red and can be visually confirmed as hematuria.” However, despite its clinical importance in urothelial carcinoma risk stratification, the diagnosis of macroscopic hematuria still relies largely on subjective visual assessment. Consequently, no objective standard for urine color evaluation currently exists. Therefore, this study examined the validity of using quantitative urinary red blood cell (RBC) counts measured by flow cytometry (FCM) as an alternative approach to visual assessment for the diagnosis of macroscopic hematuria.

Methods: ： ① Participants: Forty first-year undergraduate students from the Department of Medical Technology, Hokuriku University. All participants had no prior knowledge or technical experience related to hematuria assessment. ② Samples: Forty simulated hematuria samples of varying concentrations were prepared by adding quantified volumes of self-collected capillary blood obtained via fingerstick into 10 mL of phosphate-buffered saline. ③ Quantitative Measurement: Urinary RBC counts in uncentrifuged urine were measured using flow cytometry (FCM) with the UF-5000 fully automated urine particle analyzer (Sysmex Corporation). ④ Visual Assessment Experiment: The 40 participants evaluated the presence or absence of macroscopic hematuria in the 40 prepared simulated samples in a blinded manner.

Results and : Conclusion ： The urinary RBC count in samples successfully identified as positive for macroscopic hematuria (n=28) was 3,024.9 ± 1,792.9 /μL (M±SD). The urinary RBC count in samples not identified as macroscopic hematuria (n=12) was 427.8 ± 349.6 /μL. Based on these results, the borderline zone where distinguishing macroscopic hematuria becomes difficult was estimated to be 800 to 1,200 /μL . The objective determination of macroscopic hematuria using the urinary RBC count is possible and useful.

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P-7-7

一般演題 Urinalysis

Urinary scattergram parameters predict leukocyte viability and urinary tract infection

classification of pyuria by machine learning

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Background: The clinical utility of urinary flow cytometry-derived parameters remains underused in routine urinalysis. During routine urinary sediment microscopy, we observed a potential viability-associated shift in the leukocyte histogram peak position. We therefore aimed to identify flow cytometry correlates of leukocyte viability and to explore their clinical utility in pyuria evaluation.

Methods: A total of 110 pyuria specimens were classified into four categories: contamination (n = 14), sterile pyuria (n = 9), asymptomatic bacteriuria (n = 74), and urinary tract infection (UTI, n = 13). Leukocyte viability was determined by trypan blue staining. Machine learning models were developed for continuous viability prediction using UF-5000 (Sysmex) parameters. For three-class classification, viability thresholds were determined by Youden index from two binary ROC analyses—one distinguishing contamination from others and one distinguishing UTI from others—and these cutoffs were used to define Low, Mid, High viability class.

Results: Leukocyte viability was significantly higher in the UTI group than in the other groups ($P < 0.05$). CW_DSS_P (Depolarized Side Scattered light intensity; $\rho = 0.538$, $P < 0.001$) and Squa.EC ($\rho = -0.490$, $P < 0.001$) showed the strongest correlations. Gradient boosting using all features predicted viability with cross-validated R^2 of 0.608. Binary ROC AUCs were 0.911 (contamination) and 0.734 (UTI). Three-class logistic regression achieved one-versus-rest AUCs of 0.926, 0.667, and 0.779 for Low (<53%), Mid (53–84%), and High (≥84.0%) classes, with CW_DSS_P, Tran.EC, and CW_OTHERS as the top contributing features.

Conclusions: Urinary scattergram parameters, particularly CW_DSS_P, are significant correlates of leukocyte viability, and predictive models demonstrated good performance for classifying contamination and UTI. Currently underused scattergram parameters may aid clinical urinalysis interpretation of pyuria.

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P-7-8

一般演題 Urinalysis

Glomerular Erythrocyte Identification Using LVSEM and 3D-OWFM

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Objective : Identification of glomerular-type erythrocytes is important for diagnosing glomerular hematuria. Although automated urine particle analyzers are increasingly used, definitive classification often depends on manual microscopy and remains subjective. This study aimed to establish objective parameters for identifying glomerular-type erythrocytes using low-vacuum scanning electron microscopy (LVSEM) and Three-dimensional optical wave field microscopy (3D-OWFM).

Materials and Methods : Residual urine specimens from 14 patients (8 males, 6 females; mean age 43 ± 17 years) were analyzed. Diagnoses included IgA nephropathy, chronic kidney disease, polycystic kidney disease, chronic glomerulonephritis, bladder cancer, urinary tract stones, and urinary tract infection. Non-glomerular erythrocytes and glomerular-type erythrocytes (dysmorphic erythrocytes) were evaluated. Following fixation, samples were examined by microscopy, LVSEM, and 3D-OWFM. Quantitative parameters were extracted from optical path difference (OPD) images, including area, roundness, circularity, aspect ratio, solidity, intensity standard deviation, and volume.

Results : LVSEM clearly visualized the surface morphology of each erythrocyte subtype. The central lumen of doughnut-shaped dysmorphic erythrocytes was identified as a depression rather than a true perforation. In two-dimensional OPD analysis, hemoglobin-depleted erythrocytes showed smaller outer-diameter areas and higher roundness values. Inner-diameter analysis demonstrated larger central areas in doughnut-shaped dysmorphic erythrocytes. Three-dimensional analysis revealed differences in area, intensity standard deviation, and volume among erythrocyte subtypes.

Conclusions : Inner-diameter area, intensity standard deviation, and volume showed potential as objective markers for identifying glomerular-type erythrocytes. These parameters may contribute to standardized and automated evaluation of glomerular hematuria in routine urinalysis.

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P-7-9

一般演題 Urinalysis

Nuclear long diameter index for identifying HGUC cells

An objective morphological indicator in urinary cytology

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Objective: Recently, the nuclear area has attracted attention as a morphological parameter to differentiate high-grade urothelial carcinoma (HGUC) cells from benign reactive cells. The nuclear long diameter (NLD) strongly correlates with the nuclear area and is easy to subjectively estimate. Therefore, this study examined the usefulness of the NLD-to-neutrophil diameter ratio for detecting HGUC cells in urine cytology.

Methods: This study included 29, 26 and 18 patients with HGUC, glomerular disease and urolithiasis respectively. An image analysis system was used to measure the NLD of HGUC and benign reactive cells (reactive renal tubular cells and reactive urothelial cells) and the neutrophil diameter that appeared in the voided urine in these cases. The NLD index was calculated using the NLD-to-neutrophil diameter ratio. We subsequently compared HGUC and benign reactive cells with respect to NLD and NLD indices. In addition, the HGUC cell group and benign reactive cell group were compared by selecting the five cells with the largest NLD and NLD index on each slide.

Results: The NLD and NLD indices of HGUC cells were significantly higher than those of benign reactive cells in all cells and in the five cells with the largest NLD and NLD indices. The cut-off value of the NLD index for detecting HGUC cells was 1.25 in all cells and 1.80 in the five cells with the largest NLD index.

Conclusions: The NLD index is a useful parameter that can be introduced into routine microscopic examinations to differentiate HGUC cells from benign reactive cells.

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P-7-10

一般演題 Urinalysis

Clinical Significance of Xanthine Crystalluria

A Case of Tumor Lysis Syndrome

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Introduction: Tumor lysis syndrome (TLS) is a metabolic disorder caused by rapid destruction of tumor cells after chemotherapy, leading to hyperuricemia, hyperkalemia, and hyperphosphatemia. We report a case in which urinary xanthine crystals were detected during TLS-associated renal impairment, suggesting a possible contribution of crystal deposition to kidney injury.

Case Presentation: A man in his 80s was diagnosed with non–germinal center B-cell (non-GCB) diffuse large B-cell lymphoma (DLBCL) six years earlier. He was admitted this year for treatment of a second relapse and received chemotherapy with a xanthine oxidase inhibitor for TLS prophylaxis. On the day of treatment initiation, laboratory findings showed LDH 4017 U/L, potassium 8.6 mEq/L, and phosphate 8.6 mg/dL, consistent with TLS. Although metabolic abnormalities improved with treatment, urinalysis performed the following day revealed acidic urine (pH 5.5) and brown plate-like precipitates. Microscopic examination suggested xanthine crystalluria.

Methods: The urinary precipitates were insoluble in acetic acid and hydrochloric acid but soluble in sodium hydroxide. Based on these findings, xanthine crystals were suspected, and stone component analysis was requested from an external laboratory. Similar precipitates reappeared after the second chemotherapy cycle on day 21. The crystals were washed five times with purified water and resubmitted for analysis.

Results: The initial precipitates collected after treatment initiation could not be identified. However, the precipitates collected on day 21 were confirmed to consist of more than 98% xanthine.

Conclusion: Xanthine crystalluria should be considered when urinary crystals are observed in patients with TLS-associated renal impairment. Prompt recognition and reporting may support timely therapeutic decisions, including medication adjustment.

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P-7-11

一般演題 Urinalysis

Establish a rapid screen process for bacterial identification from urine

Using Sysmex UF-5000i combined with membrane micro-filtration extraction and MALDI-TOF MS

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Urinary tract infection is one of the most common infectious diseases in humans, and the results of urine culture and drug sensitivity testing can provide important references for treatment. However, culture and subsequent drug sensitivity testing require 48-72 hours to produce a complete report. In recent years, matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) has replaced biochemical methods for identifying bacterial strains, significantly reducing the identification time from 48 hours for biochemical methods to 18-24 hours. The UF5000i fully automated urine analyzer, manufactured by Sysmex Corporation of Japan, is an automated urine sediment analyzer that mainly uses fluorescence flow cytometry technology to analyze, count, and classify all particles in urine containing bacteria. Nevertheless, in terms of bacterial detection, it can only count and preliminarily distinguish between cocci and bacilli, which is insufficient for clinical reference.

This study aimed to establish a rapid screen process for patient's random urine sample by bacterial identification from Sysmex UF-5000i combined with membrane microfiltration extraction (LDTs) and MALDI-TOF MS. Our microbiology and clinical microscopy lab analyzed 190 clinical samples showed an overall identification concordance rate of 100%. When the bacterial quantification was 3+, the identification success rate was 52.5%. When the specimen was infected with a single species and the identification score is ≥ 2.0. The success rate was up to 72%. The consistency with traditional culture methods is extremely high. This process can shorten the identification time from 24-48 hours to within 1 hour, significantly improving testing efficiency, while it was only 17.6% for 2+, confirming 3+ as the ideal cutoff point. This process reduces the identification time from 24 hours to within 1 hour, assisting physicians in early and precise drug administration against pathogens such as *E. coli*, thus improving the timeliness of UTI diagnosis and treatment. Contact information: clinical microscopy Lab, NTUH, +886-2312-3456 #267681

P-7-12

一般演題 Urinalysis

UF-5000 Atyp.C for Detecting Atypical Urinary Cells

Impact of identifying intracytoplasmic inclusion-bearing cells

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Background: Detection of atypical urothelial cells in urine sediment is clinically important, but manual microscopy requires experience and careful observation. Automated urine particle analysis may help laboratories select specimens that need detailed microscopic review. The UF-5000 reports the atypical cell parameter, Atyp.C, which is generated from the fluorescence flow cytometry characteristics of urinary particles. This study investigated whether Atyp.C can support urinary screening and how intracytoplasmic inclusion-bearing cells influence its interpretation.

Methods: We examined 264 urine sediment samples obtained from 203 patients. Each sample was analyzed with the UF-5000 and subsequently reviewed by manual microscopy. Microscopic findings were categorized according to the presence of atypical urothelial cells and intracytoplasmic inclusion-bearing cells. The distribution of Atyp.C values was compared between groups, and screening performance was evaluated using receiver operating characteristic analysis and cutoff-based indices.

Results: Specimens containing atypical urothelial cells showed higher Atyp.C values than those without atypical cells. Positivity for atypical cells and inclusion-bearing cells showed moderate agreement, indicating that both findings contributed to Atyp.C elevation. The area under the curve was 0.829 when atypical urothelial cells alone were used as the target finding. When inclusion-bearing cells were also treated as relevant positive findings, the area under the curve increased to 0.895. Among the examined cutoffs, 0.1 cells/μL provided the highest sensitivity, whereas 0.3 cells/μL gave a more balanced sensitivity and specificity.

Conclusion: Atyp.C can assist urinary screening by highlighting specimens that may contain atypical urothelial cells or inclusion-bearing cells. Inclusion-bearing cells should not simply be interpreted as false-positive causes of Atyp.C elevation. Their recognition may improve screening performance and help laboratory professionals perform more efficient microscopic examination.

P-7-13

一般演題 Urinalysis

Macroscopic Brown Urine During Metronidazole and Cefiderocol Therapy

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Background: When brown-colored urine is observed, it is important to differentiate pathological causes such as myoglobinuria (Mb) and hemoglobinuria (Hb) from drug-induced urine discoloration. We report a case of brown-colored urine that developed during treatment for pancreatic body cancer and posed a diagnostic challenge in distinguishing between these etiologies.

Case Report: A 60s male with a body mass index (BMI) of 16.4 was undergoing chemotherapy for pancreatic cancer. During the course of treatment, he developed infected pancreatic necrosis and was treated with metronidazole (MNZ) and cefiderocol. Laboratory Findings (Day 0: Initial Appearance of Brown-Colored Urine): Urinalysis revealed proteinuria (2+) without occult blood. Urinary sediment revealed <1 RBC/HPF, hyaline casts (3+), granular casts (2+), and renal tubular epithelial cells (1-4/HPF). Serum Cr, cystatin C and CK were 0.48 mg/dL (eGFRcreat 132), 1.18 mg/L (eGFRcys 68.3) and 19 U/L, respectively. Urinary Mb, β2M and NAG were elevated at 119 ng/mL, 36,483 μg/L, and 44.5 U/L. Chemotherapy was discontinued on Day 2, because of brown-colored urine with elevated urinary Mb. Urine color improved by Day 6 despite an increase in urinary Mb to 168 ng/mL (serum Mb 31.0 ng/mL), and brown-colored urine recurred on Day 10 when urinary Mb had decreased to 10 ng/mL.

Discussion: The brown-colored urine was attributed to drug-induced discoloration because urinary Mb levels did not correlate with urine color changes and the occult blood test was negative. Mild urinary Mb elevation with normal serum Mb and increased urinary β2M and NAG suggested proximal tubular dysfunction. Reduced eGFRcys may have contributed to urinary excretion of small amounts of myoglobin.

Conclusion: This case highlights the utility of urinalysis, urinary tubular markers, and cystatin C–based renal function assessment in evaluating brown-colored urine.

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P-7-14

一般演題 Urinalysis

Urinary Nephrin in Early Nephropathy among Hypertensive T2DM Filipino Patients

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Urinary Nephrin in Early Nephropathy among Hypertensive T2DM Filipino Patients

Type 2 diabetes mellitus (T2DM) is a prevalent health concern both locally and globally. Along with hypertension, a T2DM comorbidity, it accelerates the development of diabetic nephropathy (DN). However, the progression of T2DM towards early DN is unmonitorable. The study applies analytical and cross-sectional techniques to explore the prognostic significance of urinary nephrin (u-nephrin) in detecting and monitoring the early onset of DN among hypertensive T2DM patients. A human nephrin-coated well plate, alongside biotinylated detection antibodies and Avidin-HRP conjugate, was utilized to detect u-nephrin through sandwich ELISA. Samples were categorized into control (>20.0 mg/L), nonborderline normoalbuminuria (“NBN”; 0.0 mg/L-10.0mg/L), borderline normoalbuminuria (“BM”; 10.1mg/L-20.0mg/L), borderline microalbuminuria (“BM”; 20.1mg/L-30mg/L), nonborderline microalbuminuria (“NBM”; 30.1-mg/L-40mg/L), where each group had at least three patients. The results revealed that there was no significant difference (p=0.493) in the u-nephrin levels across all groups. These findings indicate that in low microalbumin levels, specifically between the borderline levels of normoalbuminuria and microalbuminuria, u-nephrin levels only have minimal variation. With this, the researchers recommend future studies to increase the sample size per group, exclude overweight patients, evaluate other methods of testing or evaluate other podocyte-related illnesses to further broaden the knowledge of u-nephrin as a possible biomarker.

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P-8-1

一般演題 Transfusion medicine

Utilizing Novel Heat Pipe Thawing Mechanism for Fresh Frozen Plasma

A Pilot Probe on its Hemostatic-Proteometric Viability and a possible Stat Request Algorithm

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Background: Fresh frozen plasma (FFP) is critical in managing coagulopathies, such as disseminated intravascular coagulation (DIC). Traditional thawing methods are time-consuming and may not meet urgent transfusion demands, making them impractical in emergency and low-resource settings. A novel heat pipe (HP) mechanism was evaluated as a thawing method, focusing on thawing rate, and proteometric and hemostatic viability.
Study Design and Methods: This is a quasi-experimental study using two single-donor plasma (SDP)-FFP groups in duplicates. Thawing time was manually recorded. Post-thaw samples were analyzed using Vitros 5600 for proteometric viability (total protein, albumin, and globulin) and ACLTOP 350 CTS for hemostatic analysis (PT, APTT, and INR). Statistical tools (Welch's t-test, MANOVA, Pearson correlation, and linear regression) were applied. %dev and Grubb's assessed outliers.
Results: HP method demonstrated significantly faster thawing than room temperature (mean 76.5 vs 93 minutes; p = 0.033) with a higher heat transfer rate (236.1 vs 177.5 J/min). Multivariate analysis showed no significant overall difference in proteometric and hemostatic viability between HP- and RT-thawed plasma (p = 0.095). Regression analysis revealed no meaningful association between thawing time and total protein, albumin, globulin, or A/G ratio, indicating proteometric stability across thawing durations. Hemostatic parameters (PT, APTT, INR) likewise remained statistically and clinically stable, with all values within acceptable deviation limits.
Conclusions: The novel HP device improves thawing rate without compromising FFP viability, making it a promising alternative for low-resource settings. No critical deviations were observed in coagulation or protein parameters post-thaw.

P-8-2

一般演題 Transfusion medicine

Responses to Depleted Red Blood Cells Transfusion

A Case Study of a Teaching Hospital in Hsinchu, Taiwan

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This study investigated the impact of leukocyte-reduced packed red blood cells (LR-RBC) on transfusion reactions in a teaching hospital in Hsinchu, Taiwan. Blood transfusion is a critical, life-saving therapy, but transfusion reactions—often associated with leukocytes in blood products—can be severe and life-threatening. In 2020, the medical center introduced LR-RBC to reduce these adverse reactions. This retrospective study analyzed 5,046 transfusion cases to identify factors influencing transfusion reactions, including blood type (A, B, AB, O, and Rh), age, and gender, using descriptive and inferential statistical methods.

The results demonstrated that LR-RBC significantly reduced the incidence of transfusion reactions overall, with a more pronounced effect observed in female patients. Stratified analysis by blood type showed significant reductions in transfusion reactions among patients with A and O blood types. Patients with AB and Rh-positive blood types also experienced notable reductions; however, results for AB and Rh-negative patients did not reach statistical significance, likely due to limited sample size. Age-based analysis revealed that patients aged 0–80 years benefited significantly from LR-RBC transfusions, while the number of transfusions in patients over 80 years was insufficient for meaningful analysis.

In conclusion, the use of LR-RBC effectively reduces transfusion reactions, lowers the risk of transfusion-related infections, and enhances the overall safety and quality of transfusion therapy. These findings support the broader implementation of leukocyte-reduced blood products in Taiwan and provide a strong foundation for future clinical practice recommendations.

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P-8-3

一般演題 Transfusion medicine

A Case of Anti-K Alloimmunization After Blood Transfusion

A Rare Case of Anti-K Alloimmunization After Blood Transfusion in a Taiwanese Patient

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Background: The Kell blood group system is the third most potent red blood cell antigen system. Statistically, the prevalence of K antigen positivity among Taiwanese donors is extremely low, at approximately 0.02%. Therefore, the development of Anti-K alloantibodies in a K antigen-negative local patient represents a relatively rare transfusion immunity event.

Case Presentation: This report focuses on a 74-year-old Hoklo Taiwanese received multiple massive blood transfusions during five admissions between 2023 and 2024.Initial identification suggested Anti-E + c. Due to persistent suspicion, the lab performed special confirmation using Dithiothreitol (DTT), a reducing agent that destroys disulfide bonds. The disappearance of the reaction after DTT treatment confirmed the presence of the clinically significant Anti-K alloantibody.

Discussion: Anti-K is typically an IgG antibody capable of causing acute or delayed hemolytic transfusion reactions. Notably, it is the most common cause of severe Hemolytic Disease of the Fetus and Newborn (HDFN) after Anti-D. Unlike other systems, Anti-K suppresses erythropoiesis by targeting erythroid progenitors, resulting in severe reticulocytopenia.

Conclusion: This report successfully identifies a rare Anti-K alloantibody in Taiwanese patients. It underscores that continuous vigilance and accurate specialized blood bank techniques are essential for managing multiply transfused patients, ensuring transfusion safety even when dealing with low-frequency antigens.

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P-8-4

一般演題 Transfusion medicine

Recovering Extracellular Vesicle-Associated Particles from Discarded Cryosupernatant

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Background: Cryosupernatant is generated as a by-product during cryoprecipitate production and is commonly discarded. This study aimed to demonstrate the presence of extracellular vesicles (EVs) in cryosupernatant and to establish the feasibility of recovering an EVs-enriched preparation for downstream characterization.

Methods: Cryosupernatant was processed by stepwise centrifugation followed by differential ultracentrifugation at 100,000 × g, 70 min, performed twice. Recovered particles were characterized by nanoparticle tracking analysis (NTA; NanoSight NS300, 405 nm laser), and EVs-associated marker expression was evaluated using a CD63-capture human exosome ELISA. Exploratory in vitro exposure experiments were also performed using H929, U937, and lymphocytes to assess effects on cell viability.

Results: The recovered particles exhibited a size distribution consistent with small EVs, with a mean diameter of 154.5 nm, a mode diameter of 112.4 nm, and a standard deviation of 51.8 nm. CD63-capture ELISA detected a CD63-positive signal corresponding to 347 ng/mL in the kit standard, supporting the presence of EVs-associated particles in cryosupernatant. In exploratory short-term cell exposure assays using hematologic cancer cell lines (H929 and U937) and lymphocytes, no significant cytotoxicity was observed under the tested conditions.

Conclusions: These findings indicate that EVs-associated particles can be recovered from cryosupernatant that is otherwise discarded during plasma cryoprecipitate manufacturing. Discarded cryosupernatant may therefore represent a useful and underutilized source of EVs-associated particles for future research and potential biomedical applications.

P-8-5

一般演題 Transfusion medicine

Auto-anti-M Mimicking Cold Agglutinin Disease

A Diagnostic Pitfall in Laboratory Interpretation

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Background: Cold agglutinin disease (CAD) is characterized by cold-reactive autoantibodies, typically anti-I, which trigger complement-mediated hemolysis and a C3d-positive direct antiglobulin test (DAT). Although high cold agglutinin (CA) titers often suggest CAD, other cold-reactive autoantibodies can mimic these findings, potentially leading to diagnostic pitfalls.

Case Presentation: A 76-year-old man undergoing percutaneous coronary intervention (PCI) demonstrated unexpected blood agglutination during the procedure, suggesting CAD. Nevertheless, the patient had no clinical evidence of hemolysis.

Laboratory Findings: CA testing using pooled reagent type O red cells showed a titer of ≥1:8192, yet the DAT was negative for IgG and C3b/d. Hemolysis markers — including LDH, bilirubin, haptoglobin, and reticulocyte count—were within normal limits. A direct agglutination test (DAggT) at room temperature showed positivity only with M-positive red cells. Subsequent antibody identification confirmed an IgM-type auto-anti-M antibody.

Discussion: Auto-anti-M antibodies are rare and can produce serological findings mimicking CAD. Because reagent red cells used in CA testing often contain M-positive red cells in the Japanese laboratory setting, anti-M can cause elevated CA titers. Unlike classical anti-I–mediated CAD, this case lacked complement-mediated hemolysis and a C3d-positive DAT, highlighting that CA titers and DAggT results alone are insufficient for definitive diagnosis.

Conclusion: The diagnosis of CAD should not rely only on CA titers or DAggT results. Medical technologists should correlate these parameters with the patient's clinical status to avoid misdiagnosis, especially when incidental cold-reactive antibodies.

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P-8-6

一般演題 Transfusion medicine

AI-Driven Digital Handover in Blood Bank

Improving Efficiency and Transfusion Safety

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AI-Driven Digital Handover in Blood Bank

Background:

Blood bank handovers are essential for transfusion safety but are often paper-based, time-consuming, and vulnerable to information gaps. Increasing workload further compromises efficiency and staff well-being.

Objective:

To develop and evaluate an AI-assisted digital handover system led by Medical Laboratory Scientists (MLS) to improve workflow efficiency, handover continuity, and transfusion safety

Methods:

A frontline-led digital platform, Blood Kit Manager, was developed using AI-assisted low-code tools by Medical Laboratory Scientists (MLS). The platform integrates inventory tracking, digital documentation, and automated alerts. A 3-month pre–post study compared traditional paper-based workflows with the digital system. Key indicators included handover time, administrative workload, and staff satisfaction.

Results:

The system reduced average handover time from 15 to 5 minutes (67% improvement). Administrative workload decreased by approximately 50%, enabling a paperless workflow. Improved visibility minimized information gaps, and no handover-related incidents were reported. Staff satisfaction improved with reduced cognitive burden and clearer workflows.

Conclusion:

Medical Laboratory Scientists can act as citizen developers to drive digital transformation in transfusion services. The AI-assisted system improved workflow efficiency, reduced administrative burden, and enhanced transfusion safety. This scalable model may support digital transformation in resource-limited laboratories.

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P-8-7

一般演題 Transfusion medicine

When O is Not O: Ael Phenotype Misclassification

A Rare Ael Phenotype Presenting as ABO Discrepancy

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Backgrond

ABO blood group discrepancies require careful evaluation to prevent potential transfusion risks. Weak A subgroups, such as Ael, are rare and may be easily misclassified in routine serologic testing.

Case Presentation

A 29-year-old pregnant woman with no history of transfusion underwent routine prenatal blood grouping at a regional teaching hospital. Initial ABO typing using the manual tube method showed forward typing results of Anti-A (−) and Anti-B (−), while reverse typing showed A cells (2+) and B cells (3+). The result was reported as group O.

Upon further review, the reverse typing result was found to be inaccurate due to inadequate mixing during manual testing. The corrected findings revealed A cells as immediate spin (IS) (−) and room temperature (RT, 5 min) (+/−), while B cells remained 3+.

Additional investigations demonstrated Anti-A,B (−), Anti-H (4+), and adsorption-elution testing revealed trace A antigen. The final blood group was confirmed as Ael phenotype

Discussion

The misclassification in this case was attributed to both technical error and anchoring bias. Inadequate mixing during manual testing led to incorrect reverse typing results, while reliance on initial forward typing contributed to premature interpretation. Weak A subgroups such as Ael often show minimal or undetectable reactions, increasing the likelihood of discrepancy and misclassification.

Conclusion

When discrepancies between forward and reverse typing are observed, careful re-evaluation and additional confirmatory testing are essential. Adherence to standard operating procedures and awareness of cognitive bias can help reduce ABO typing errors and ensure transfusion safety.

P-8-8

一般演題 Transfusion medicine

Clinical Significance of Naturally Occurring Anti-Wr^a

IgG Subclass and Functional Analysis

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Introduction: The Wright antigen (Wra) is a low-frequency antigen in the Diego blood group system, and anti-Wr^a is rarely detected in antibody screening tests. We investigated the clinical significance of anti-Wra in three cases identified incidentally.

Materials and Methods: We evaluated three cases (Case 1: +anti-Wr^a, -E; Case 2: +anti-Wr^a, -E, -Di^a; Case 3: +anti-Wr^a, -E, -Jk^b). Antibody titers were determined by the indirect antiglobulin test (IAT) using the tube technique. Additionally, flow cytometric IgM/IgG subclass analysis and a phagocytosis assay (FCP assay) were performed.

Results: Anti-Wr^a titers were 64, 1, and 2 for Cases 1, 2, and 3, respectively. Subclass analysis identified IgM+IgG1+IgG3 (Case 1), IgG1 (Case 2), and IgG1+IgG3 (Case 3). FCP assay values for anti-Wr^a were 86.79%, 0.87%, and 7.61%, respectively.

Discussion: In all cases, anti-Wr^a was detected in pre-transfusion samples, suggesting it was a naturally occurring antibody. The other coexisting antibodies were detected post-transfusion. Among these, Case 1 anti-E (titer 1, IgG1) showed an FCP assay value of 9.47%; Case 2 anti-E (titer <1, subclass not detected) showed 2.68%, and anti-Di^a (titer 64, IgG1+IgG2+IgG3) showed 91.56%; Case 3 anti-E (titer 256, IgG1+IgG3) showed 60.75%, and anti-Jk^b (titer <1, IgG1) showed 4.51%. All antibodies with low titers exhibited low FCP assay values (<10%) regardless of subclass. In contrast, FCP assay values were high (≥60%) in samples with IgG1+IgG3 antibody titers of ≥64. These findings suggest that even naturally occurring anti-Wr^a can be of IgG1 or IgG3 origin. When titers are high, they require the same clinical vigilance as immune antibodies, such as anti-E and anti-Di^a.

Conclusion: Anti-Wr^a has the potential to cause hemolytic transfusion reactions, even when it is naturally occurring.

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P-8-9

一般演題 Transfusion medicine

Dynamic Lewis Antigen Changes During HCV Antiviral Therapy

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Background:
Despite the high cure rates achieved with direct-acting antivirals, biological heterogeneity during hepatitis C virus (HCV) treatment remains insufficiently understood. Reliable biomarkers reflecting host biological adaptation during antiviral therapy are still lacking. As glycosylation-dependent structures, Lewis blood group antigens may represent an overlooked biological interface between host response and disease progression; however, their role during HCV treatment has not been fully explored.
Methods:
Lewis antigen (Le^a and Le^b) expression in red blood cells and plasma was evaluated in 44 HCV patients receiving DAA therapy using serologic testing, flow cytometry, and ELISA at different treatment stages.
Results:
Dynamic alterations in Le^a and Le^b expression were observed across different treatment stages. Distinct expression patterns between RBCs and plasma suggest compartment-specific regulation of Lewis antigens during antiviral therapy. These findings indicate that Lewis antigen expression may reflect treatment-associated biological adaptation rather than solely static phenotypic characteristics. Inter-individual variability was also observed, suggesting heterogeneous host responses to antiviral therapy.
Conclusion:
Lewis blood group antigens may serve as dynamic biomarkers for HCV treatment monitoring. Their differential expression between RBCs and plasma highlights a previously underrecognized aspect of host glycoprotein regulation beyond conventional transfusion medicine.

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P-8-10

一般演題 Transfusion medicine

Cold Agglutinin Transfusion Management in CAD

A Case Report of High-Titer Autoanti-I Hemolysis

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A 79-year-old man with prostate tumor and urinary tract infection presented with fever and generalized weakness. Initial laboratory findings revealed hemoglobin 7.4 g/dL, white blood cell count 12,700/μL, and total bilirubin 2.0 mg/dL.
ABO typing showed a discrepancy: forward typing was group B, whereas reverse typing demonstrated 4+ agglutination with both B cells and O cells at room temperature. Further investigation using adult O red blood cells and neonatal cord blood cells showed no agglutination with cord cells at room temperature or 4°C, but a high cold agglutinin titer of 1:1024 with adult O cells at 4°C, indicating high-titer autoanti-I.
Prewarming resolved the ABO discrepancy and confirmed the blood type as B RhD positive. Indirect antiglobulin testing at 37°C was negative. Direct antiglobulin testing showed anti-C3d positive and anti-IgG negative, consistent with complement-mediated hemolysis in cold agglutinin disease (CAD).
Two days after admission, hemoglobin further decreased to 6.1 g/dL, suggesting persistent immune hemolysis. The patient received 2 units of prewarmed packed red blood cells with extended antigen matching for Rh E, c, Mia, and Jkb-negative units, aiming to reduce future alloimmunization risk. Steroid dosage was increased, and active warming with blood bag preheating and far-infrared body warming was applied during transfusion.
No adverse transfusion reactions occurred. Five days after transfusion, hemoglobin increased from 6.1 to 7.5 g/dL, bilirubin decreased from 2.0 to 1.44 mg/dL, DAT anti-C3d reactivity weakened from 2+ to weak positive, and the cold agglutinin titer decreased from 1:1024 to 1:256. The patient's hemolytic symptoms improved significantly and he was discharged after 7 days.
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P-8-11

一般演題 Transfusion medicine

Establishing Optimal Cut-off Values for Autologous PBSC Collection

Using Automated Hematopoietic Progenitor Cell (HPC) Counts

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Background:
Peripheral blood CD34+ counts predict autologous PBSC collection success but are costly and time-consuming. Hematopoietic progenitor cell (HPC) counts from automated analyzers provide a rapid, low-cost alternative. This study evaluated optimal HPC cutoff values using ROC analysis.
Methods:
A total of 52 patients undergoing 115 autologous PBSC collections between 2021–2025 were analyzed, including 39 collections from Multiple Myeloma (MM) patients and 76 from Lymphoma patients. HPC counts were measured using Sysmex XN-20, and CD34+ cell doses were determined by flow cytometry. ROC analysis was performed to predict successful collection (≥2 × 10^6 CD34+ cells/kg).
Results:
HPC counts effectively predicted collection success. In MM patients, the optimal cutoff was 72/μL (AUC=0.873, $p<0.001$). In Lymphoma patients, the cutoff was 53.5/μL (AUC=0.882, $p<0.001$).
Conclusion:
Automated HPC measurement is a rapid and cost-effective predictor of PBSC collection success and may improve collection efficiency.

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P-8-12

一般演題 Transfusion medicine

Incidence and Causal Analysis of Transfusion Incidents at Our Hospital

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【Introduction】Incidents occur due to a variety of factors, and their characteristics vary from institution to institution. Since transfusion-related incidents can lead to serious adverse events, it is important to analyze cases within one's own institution to identify the underlying causes. In this study, we examined the occurrence of transfusion-related incidents and their contributing factors at our hospital.
【 Methods 】 We analyzed 146 transfusion-related incidents reported at our hospital between April 2022 and March 2025, examining the time of occurrence, length of service, years of experience in transfusion services, and incident details.
【Results】Incidents occurred during the day shift (50.0%), shift changeovers (30.1%), and night shift (19.9%). The proportion of incidents was highest among staff with 1–3 years of transfusion experience (60.3%). Regarding the relationship with total years of service, approximately half of the incidents involved mid-career and senior staff with 5 or more years of service. Incident types were as follow: communication errors (37.1%), deviation from procedures (25.3%), lack of knowledge (16.4%), environmental factors (13.7%), and patient misidentification (7.5%).
【Discussion】Incidents occurring during shift changeovers and at night accounted for half of the total, suggesting that this may be influenced by insufficient information sharing and reduced double-checking due to understaffing. Regarding the relationship between years of service and years of experience in transfusion services, the high proportion of incidents among staff with 1–3 years of transfusion experience may be attributed to limited involvement in transfusion work in their previous departments and a lack of practical experience in transfusion procedures.
【 Conclusion 】 We will work collaboratively with frontline nurses to explore measures for providing ongoing education to staff with limited experience in transfusion services—including mid-level staff—and to strengthen information-sharing systems during shift changeovers.

P-8-13

一般演題 Transfusion medicine

Establishing an Emergency Blood Supply Procedure for Resilient Healthcare

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Background: In the event of major disasters or armed conflicts, designated tertiary care hospitals must establish comprehensive emergency response systems, including a reliable blood supply. Blood supply plays a critical role in resilient healthcare and is essential for maintaining trauma and critical care services. When blood product inventories are insufficient, designated tertiary care hospitals must have the operational capacity to rapidly recruit donors and ensure a sustainable blood supply.
Methods: Based on the National Health System Resilience Preparedness Plan and Advanced Trauma Life Support (ATLS) guidelines, a blood donation preparedness program was developed. The program incorporates spatial planning, workforce allocation, and structured mechanisms to support emergency blood supply. A multidisciplinary blood donation team comprising physicians, nurses, medical technologists, and allied healthcare personnel was established to implement an in-house donation workflow and emergency blood supply system.
Results:Upon activation in response to emergency medical demand, the blood donation team effectively managed all donation-related operations. Physicians assessed donor eligibility and ordered laboratory testing; nurses provided comprehensive donor care and monitored for adverse events; medical technologists conducted blood collection and testing procedures; and blood bank personnel ensured appropriate blood utilization, compatibility testing, and inventory management. The integrated workflow facilitated timely donor recruitment and maintained stability of the blood supply during critical situations.
Conclusion:Through interdisciplinary collaboration and structured preparedness planning, the implementation of an emergency blood donation and supply mechanism strengthens institutional resilience. This approach ensures continuity of essential medical services, enhances the stability and responsiveness of blood supply systems, and improves overall transfusion safety during emergencies.
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P-8-14

一般演題 Transfusion medicine

Weak Antigen Reactivity in Acute Myeloid Leukemia

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Background
The ABO blood group system is the most clinically significant blood group system and is determined by glycosyltransferase activity encoded on chromosome 9q34.2. Accurate ABO typing requires concordance between forward and reverse grouping. Discrepancies may indicate blood group subtypes, rare phenotypes, or underlying disease.
Purpose
This study describes a case of acute myeloid leukemia (AML) with reduced ABO antigen expression and its impact on transfusion testing and blood bank practice.
Case Report
A newly referred emergency department patient presented with persistent fever for three weeks and skin rash. Complete blood count revealed leukocytosis (WBC 221.26 × 10⁹/L), severe anemia (Hb 5.9 g/dL), thrombocytopenia (Plt 63 × 10⁹/L), and 72.4% blasts. Blood type showed blood group B, RhD positive, with weakened B antigen reactivity (3+ mixed-field) on forward typing, while reverse typing remained concordant. Antibody screening was negative.
Methods
Further investigations included peripheral blood smear, bone marrow examination, flow cytometry immunophenotyping, cytogenetic analysis, next-generation sequencing, and avidity testing.
Results
Flow cytometry confirmed non M3 AML with partial CD13 expression. Cytogenetic analysis showed a normal karyotype (46,XY). Molecular testing identified FLT3 mutation, KMT2A rearrangement, and additional NRAS, CEBPA, and CREBBP mutations. Avidity testing demonstrated prolonged reaction time, suggesting reduced antigen–antibody binding strength.
Conclusion
AML may lead to reduced expression of multiple lineage-associated antigens, including ABO antigen, leading to ABO discrepancies and challenges in blood group interpretation. In patients with suspected hematologic malignancy, weakened ABO antigen expression should prompt further investigation rather than be assumed to represent a technical error. Early recognition of weaker reactions to leukemia-associated antigens is critical to ensure accurate serologic interpretation and safe, timely transfusion support.
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P-8-15

一般演題 Transfusion medicine

Analysis of emergency transfusion cases of Fu_Jen Catholic University Hospital

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Emergency transfusion is the life-saving release of blood products before completing cross-matching testing for patients with severe blood loss. In this study we analyzed clinical data of patients who received emergency transfusion in Fu Jen Catholic University Hospital between Jan 2020 and Mar 2025. During this period there were 165 episodes of emergency transfusion in 158 patients (mean age 57.4 ± 19.5 years, male 106, or 67%). The average quantities of blood products administered were: packed red blood cell (pRBC) 3.7 ± 2.2 units (U), fresh frozen plasma (FFP) 1.2 ± 2.2 U, and apheresis platelet 0.1 ± 0.3 U (one U of apheresis platelet = 6 platelet units). The pRBC : FFP : platelet ratio was 3.1:1:1. The majority of episodes were encountered at the emergency department. Causes of emergency transfusion were: (1) gastrointestinal bleeding (N=51, 30.9%), (2) major trauma (N=39, 23.6%), (3) septic shock (N=15, 9.1%), (4) tumor/organ/arteriovenous fistula/dialysis catheter bleeding (N=14, 8.5%), (5) cardiogenic shock (N=13, 7.9%), (6) iatrogenic bleeding (N=11, 6.6%), (7) aortic dissection/rupture (N=9, 5.5%), (8) post-partum/molar/ectopic pregnancy hemorrhage (N=8, 4.8%). All-cause mortality rate 30 days after emergency transfusion was 46.7%, the highest being aortic dissection/rupture (8/9, 89%), followed by cardiogenic shock (8/13, 62%), septic shock (8/15, 53%), and major trauma (20/39, 51%). The average blood transfusion quantity issued normally after emergency transfusion termination in patients who received massive transfusion (> 10 U of pRBC/24 hours) (N=38) was higher than that in patients without massive transfusion (31.8 ± 47.9 U vs 16.2 ± 41.7 U, p=0.026), yet 30-day mortality rates of the two groups were not different (55.3% vs 43.3%, p=0.114).

P-8-16

一般演題 Transfusion medicine

Strategies and Effectiveness of Improving Management Rh(D)-Negative Blood Components Returns

RhD-Negative Blood Component Return Reduction Strategies

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Introduction
Rh(D)-negative blood is extremely rare in Taiwan, accounting for approximately 0.3% of the population. As a result, most hospitals do not maintain routine stock. Our hospital experienced a high return rate of unused Rh(D)-negative blood components, primarily due to a lack of clinical consensus on Rh-negative transfusion for Rh-positive recipients. This study aimed to evaluate whether an interdepartmental intervention could reduce return rates and improve blood utilization.
Method
An interdepartmental quality improvement program was implemented, combining process optimization and hospital-wide education. Key interventions included: (1) immediate notification to the blood bank when blood was no longer required; (2) weekly review of patients with reserved blood units; (3) confirmation of utilization or reallocation 10 days prior to expiration; and (4) hospital-level education to unify transfusion decision-making for Rh(D)-negative blood. Return rates before (2020–2022) and after intervention (2023–2025) were compared.
Result
Return rates were calculated as returned units divided by issued units × 100. Before intervention, return rates were 66.67% (40/60), 52.17% (36/69), and 14.81% (8/54), with an overall rate of 45.9% (84/183). After intervention, rates decreased to 16.19% (17/105), 0% (0/88), and 0% (0/201), with an overall rate of 4.31% (17/394), representing a 90.61% reduction.
Discussion
The intervention significantly reduced Rh(D)-negative blood component returns from 45.9% to 4.31%, achieving over 90% improvement. This strategy may serve as a practical model for optimizing the management of rare blood resources and improving patient safety.

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P-8-17

一般演題 Transfusion medicine

Meteorological Drivers of Blood Type Specific Transfusion Demand Patterns

A Five Year Retrospective Analysis of Comprehensive Weather Impacts

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Objective: This study evaluates how comprehensive meteorological factors independently predict blood-type-specific transfusion demand, enabling dynamic, weather-informed inventory strategies to replace static models.

Methods: We retrospectively analyzed five years of daily transfusion data (2021–2025) from a Taiwanese teaching hospital. Following initial non-parametric validation, multivariate GLM-NB2 quantified environmental impacts, effectively managing overdispersion inherent in count-based transfusion data. Models incorporated Z-score standardized meteorological variables (pressure, temperature, precipitation), adjusting for operational cycles and pandemics.

Results: ABO types revealed distinct meteorological fingerprints. Group A demand was driven by atmospheric pressure (+8.2% per SD increase, $p < 0.001$), suggesting physiological stress mechanisms. Group B exhibited temperature-dependent increases (+4.4%, $p = 0.043$) but decreased markedly during heavy rain (-18.9%, $p = 0.028$), reflecting weather-driven behavioral shifts. Group O was elevated by pressure (+4.6%, $p = 0.007$) yet markedly suppressed by precipitation (-22.5%, $p = 0.001$). Group AB showed no significant meteorological correlation. Hospital operational factors consistently reduced demand across all types (e.g., weekends; mean IRR: -31%, $p < 0.05$).

Conclusion: ABO blood groups display highly heterogeneous sensitivities to environmental stressors. Despite single-center, retrospective limitations, transitioning to dynamic, weather-informed forecasting may substantially improve inventory resilience and optimize resource allocation.

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一般演題 Transfusion medicine

Bridging Blood Supply Crisis during COVID-19

Integrating Clinical Decision Support Systems and Dynamic Inventory Management

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Background & Purpose: From 2020 to 2022, the COVID-19 pandemic caused unprecedented disruptions to the global blood supply chain. This study demonstrates how medical technologists transitioned from reactive management to a proactive, resilient framework by integrating institutional policy and Information Technology (IT) to safeguard transfusion safety during extreme inventory lows.

Methods: A multi-layered Patient Blood Management (PBM) strategy was implemented:

Policy Intervention (Dec 2020): A hospital-wide directive established blood prioritization protocols.

Clinical Decision Support System (CDSS): A "hard-stop" logic was integrated into the HIS. Any Leucocyte-Poor RBC(LPR) request for patients with Hb >8.0 g/dL was automatically blocked unless a critical medical exception was verified.

Dynamic Monitoring: Medical technologists performed daily morning audits and engaged in direct clinical consultations to adjust distribution based on real-time availability.

Results: The strategy successfully mitigated two major supply crises:

Initial Shock (Jan 2021): Following a local cluster event, morning inventory for Type B Leucocyte-Poor RBC(LPR) dropped to 18 units, representing only 18% of the baseline stock (100 units). The CDSS effectively filtered approximately 20% of non-essential orders, preserving stock for emergency cases.

Peak Crisis (May 2022): During the most severe pandemic wave, Type O Leucocyte-Poor RBC(LPR) hit a historical low of 13 units, plummeting to less than 10% of the baseline stock (120-150 units). Through the synergy of IT-based restrictions and human-led dynamic monitoring, zero-inventory events were successfully avoided despite the extreme resource scarcity.

Long-term Stability: Data indicates that inventory standard deviation significantly decreased by 2025, demonstrating institutional resilience.

Conclusion: Medical technologists serve as the essential bridge between scarce resources and clinical survival. By implementing systemic Hb-thresholds and proactive monitoring, we transformed emergency responses into a sustainable management model for future public health emergencies.

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P-8-19

一般演題 Transfusion medicine

Piperacillin/Tazobactam-Induced Drug-Dependent Antibodies Presenting as Autoantibodies: A Case Study

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[Purpose] This case study reports on a 68-year-old male whose antibody screening and Direct Antiglobulin Test (DAT) seroconverted from negative to positive during a 2026 hospitalization. Following negative acid elution tests, drug-induced immune hemolytic anemia (DIIHA) was highly suspected. A review of his medication history revealed Piperacillin/Tazobactam (PTZ) usage for postoperative infections. This case highlights the necessity of correlating clinical laboratory findings with medication history to ensure transfusion safety.

[Methods] Routine antibody screening, antibody identification, DAT typing, and acid elution tests were performed. The protocol for "Detecting drug antibodies by testing in the presence of drug" was employed to identify drug-dependent antibodies (DDAbs).

[Results] Initial screening and auto-control were negative. Subsequently, DAT became strongly positive (3+), antibody screening yielded weakly positive reactions, and identification confirmed mimetic anti-e. Although the R1R1 phenotype suggested auto-anti-e, a non-reactive eluate contradicted autoimmune presentations. History revealed PTZ use across three stages. Testing confirmed the serum reacted exclusively in the presence of PTZ, identifying PTZ-dependent antibodies. Following drug cessation, screening returned to negative.

[Conclusion] PTZ-induced DDAbs can demonstrate mimetic specificity (e.g., pseudo-anti-e), potentially leading to a misdiagnosis of autoimmune hemolytic anemia. Laboratory professionals should investigate medication history whenever a positive DAT occurs in conjunction with a negative acid eluate. Specific drug-antibody testing is essential to differentiate etiologies. As demonstrated, the reversal of positive screening after drug discontinuation confirms the diagnosis and underscores the importance of accurate testing for patient safety.

[Keywords] DIIHA, DDAbs, PTZ, DAT, acid elution

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P-8-20

一般演題 Transfusion medicine

Managing ABO Discrepancy in a Resource-Limited Laboratory

A Practical Case Experience Suggestive of B3 Subgroup

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Objective: ABO discrepancy is a critical issue in pre-transfusion testing, especially in small laboratories where advanced reagents, molecular typing, or reference laboratory support may not be immediately available. This case aimed to share a practical laboratory approach for resolving weak mixed-field ABO reactions and maintaining transfusion safety under limited-resource conditions.

Methods and Results: A 50-year-old woman admitted for urinary tract infection underwent routine pre-transfusion testing.Tube testing showed anti-A:0, anti-B:1+ mixed-field agglutination, anti-D:4+, A1 cells:3+, B cells:0 ,with negative antibody screening and autocontrol.Because the anti-B reaction was weaker than expected and showed a mixed-field pattern, the result was not reported as a routine B group. Column agglutination testing also showed weak or discrepant findings, so an ABO discrepancy investigation was initiated.The laboratory first rechecked specimen identity, repeated the test, reviewed the procedure, and collected available clinical information, including transfusion history, transplantation history, diagnosis, and medication use. With limited subgroup reagents available, simple in-house methods were used. After standing for 15 minutes, the anti-B reaction increased from 1+mf to 2+mf. Anti-A,B was 2+mf and anti-H was 4+. The avidity test showed delayed reaction in the patient sample compared with quality control, 9 seconds versus 3 seconds, suggesting weak B antigen expression. To clarify the mixed-field pattern, a Petri dish separation method was performed. Fine and uniform agglutination was observed, supporting a serologic interpretation suggestive of B3 subgroup rather than chimerism.

Conclusion: Small laboratories should not issue a final ABO type based only on weak or mixed-field reactions. Repeating basic tests, extending reaction time, using available reagents, documenting uncertainty, communicating with clinicians, and referring unresolved cases when needed are practical steps to protect transfusion safety.

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P-8-21

一般演題 Transfusion medicine

Power BI evaluation of prophylactic antihistamines for patient safety

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Abstract

Purpose: This initiative aimed to utilize Power BI to evaluate the appropriateness of prophylactic antihistamines before blood transfusions and their correlation with transfusion reactions under the "Choosing Wisely" framework

Methods: This retrospective observational study (IRB No. N202506120) analyzed hospitalized patients (aged 18–99) from 2022 to 2024. Prophylactic use was defined as administering Diphenhydramine within one hour pre-transfusion. Hospital information and nursing records were integrated into Power BI dashboards to track prescription rates. Interventions included cross-departmental education and regular project meetings.

Results: Baseline data (2022) showed a 32.22% prophylactic prescription rate. Following interventions, usage significantly decreased to 20.98% (12,769/60,872) during 2023–2024. Transfusion reaction rates were 0.68% (87/12,769) in the premedication group and 0.29% (141/48,103) in the non-medication group, confirming that routine prophylaxis does not reduce reactions.

Conclusion: Prophylactic antihistamines did not reduce transfusion reactions, but the Power BI intervention successfully optimized prescribing behavior. Continuous education and standardized reporting are recommended to ensure patient safety.

P-8-22

一般演題 Transfusion medicine

Unexpected Anti-Jra Antibody Causing Transfusion Delay in Acute Cholangitis

Importance of Rapid Collaboration Between Laboratory, Clinicians, and Blood Center

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BACKGROUND: Transfusion therapy is critical in severe infections or disseminated intravascular coagulation (DIC), where delays can be life-threatening. Irregular antibodies may go undetected by routine typing until crossmatch incompatibility is encountered. Anti-Jr^a, targeting the Junior (JR) blood group antigen, is clinically significant and more prevalent in East Asian populations, yet frequently overlooked.
CASE PRESENTATION: A patient in their 70s presented with acute obstructive suppurative cholangitis (AOSC), septic shock, DIC, impaired consciousness, and hypoxemia. Emergency endoscopy was deferred due to poor general condition; percutaneous transhepatic gallbladder drainage (PTGBD) was performed as a bridge, followed by endoscopic retrograde cholangiopancreatography (ERCP), biliary stenting, and nasobiliary drainage the following day. Initial red blood cell (RBC) transfusion for anemia on admission was uneventful—antibody screen negative, crossmatch compatible. When re-transfusion was planned for worsening anemia, the screen returned positive and incompatibility was detected. In-house Jr(a) testing was unavailable; referral to the regional blood center confirmed Jr(a−) phenotype with anti-Jr^a. Compatible blood was secured after two days; however, from planning to administration, five days elapsed. The patient recovered with appropriate transfusion and multidisciplinary management.
DISCUSSION: Though massive hemorrhage did not occur, the transfusion delay was clinically significant. When rare blood group incompatibility is suspected but cannot be confirmed in-house, prompt escalation to the blood center is essential. Institutions should consider laboratory-to-clinician alert protocols and routine re-screening before re-transfusion in critically ill patients. The Jr(a−) phenotype warrants particular awareness in East Asian settings.
CONCLUSION: A negative initial antibody screen does not preclude later incompatibility. Close collaboration among the laboratory, clinical teams, and blood center is essential for timely and safe transfusion therapy.—TEL:+81-297-63-7111

P-8-23

一般演題 Transfusion medicine

Establishing a Quality Control and Appropriate-Use System for In-House Cryoprecipitate

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[Introduction] Cryoprecipitate contains high concentrations of fibrinogen and other components and is useful for treating acquired hypofibrinogenemia. Our hospital began in-house supply of cryoprecipitate in September 2024. Here, we describe our efforts to ensure quality control and appropriate use of cryoprecipitate.
[Methods] The in-house criterion for cryoprecipitate use was a fibrinogen level at or below approximately 150 mg/dL, and the dose was set at 3 bags per administration. Only type AB cryoprecipitate was stocked; the standing inventory was initially 3 bags and was increased to 6 bags in December 2025 as usage became more frequent. For quality control, we calculated the fibrinogen content and recovery rate during cryoprecipitate preparation and provided this information to the requesting clinical departments at the time of supply. To evaluate appropriate use, we measured fibrinogen levels before administration, and the values were confirmed by both these departments and the Transfusion and Cell Therapy Department. All cases were reviewed by the Blood Transfusion Therapy Committee.
[Results] By March 2026, cryoprecipitate had been administered in 24 cases. Fibrinogen levels before and after administration were 119 ± 30 and 217 ± 28 mg/dL, respectively (mean ± SD), and fibrinogen rose in all 24 cases. However, in one case, the pre-administration fibrinogen value was 220 mg/dL, above the in-house criterion.
[Conclusion] Our quality-control and pre-transfusion review steps established a system that supported the appropriate use of cryoprecipitate. The single off-criteria case was identified and reviewed by the committee, indicating that the system can detect and address inappropriate use. We will continue to collaborate with the clinicians to promote the appropriate use of cryoprecipitate, a valuable blood product.

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一般演題 Transfusion medicine

A Case Report of Suspected Transfusion-Associated Circulatory Overload

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[Purpose]
A 54-year-old diabetic woman (155 cm, 45 kg) was hospitalized for unexplained anemia, thrombocytopenia, and fever. Scheduled for a CT-guided lung biopsy and bone marrow examination, she received 2 units of Leukocyte-Poor Red Blood Cells (LP-RBC) and 6 units of Leukocyte-Reduced Apheresis Platelets (RLPPH). During the third RLPPH unit transfusion, she developed respiratory distress, including oxygen desaturation, severe coughing, hemoptysis, and dyspnea. Despite these signs, the transfusion continued. Consequently, she developed PEA but achieved ROSC following CPR and was transferred to the ICU. The purpose of this case study is to highlight the severe risks of rapid transfusion in low-body-weight patients.
[Method]
This unreported incident was identified retrospectively by a medical technologist. Despite unavailable NT-proBNP data, clinical signs (widened pulse pressure, dyspnea, pleural effusion) strongly indicated transfusion-associated circulatory overload (TACO).
[Results]
A rapid transfusion strategy (200–300 mL/unit over 13–15 minutes) was used. Failure to halt transfusion or administer diuretics caused cardiopulmonary failure. Post-resuscitation, she suffered refractory thrombocytopenia and massive cerebral hemorrhages. With surgery contraindicated, she transitioned to palliative care under a DNR consent.
[Conclusion]
Based on International Society of Blood Transfusion (ISBT) criteria, this case underscores the imperative of strict vital sign monitoring during rapid, large-volume transfusions in low-body-weight patients to prevent TACO.

[Keywords] transfusion-associated circulatory overload (TACO), A rapid transfusion
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P-8-25

一般演題 Transfusion medicine

Cold Stored Platelets

Cold and delayed cold storage a promising alternative for the preservation of platelet concentrates

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Cold storage and delayed cold storage: a promising alternative for the preservation of platelet concentrates

Introduction and Objectives:
Platelet concentrates (PCs) play a major role in the emergency management of patients with thrombocytopenia and/or thrombopathy. They require specific storage conditions, including an ambient temperature between 22° and 25°C and continuous agitation, which limits their shelf life to 5–7 days. This constraint presents a major challenge for inventory management. It is within this context that our study was conducted, with the objective of evaluating the effect of cold storage on platelet shelf life, platelet function, and the risk of contamination by cryophilic bacteria.

Methods:
The study was conducted on 6 CPS (n=6) divided into 2 groups. The first group consisted of CPS stored directly at cold temperatures (Cold Stored Platelets or CSP), and the second group consisted of CPS initially stored at room temperature (22–25°C) for 5 days and then transferred to cold storage (Delayed Cold Stored Platelets or DCSP). The CSPs and DCSPs were monitored over a 21-day period. The evaluation focused on the effect of cold storage on platelet count; platelet function assessed by optical aggregometer; and the risk of bacterial contamination evaluated by blood culture.

Results:
All the CPS samples studied met quality standards in terms of volume, pH, and platelet count (volume < 40 mL; mean platelet count of 0.52×10^{11} platelets per CPS). The pH remained stable and above 6.5 throughout the storage period in both groups. Platelet counts increased until Day 5; then showed a gradual decrease in both groups; however, the DCSP group exhibited better stabilization of the count after transfer to cold storage. An average increase in lactate was observed of 1.4 mmol/L in the CSPs and 2 mmol/L in the DCSPs between Day 1 and Day 5, without associated acidosis.
Functionally, optical aggregometry showed preserved platelet activity with a maximum effect observed on Day 3, which was more pronounced in the DCSP group. Ristocetin (RIPA) proved to be the most effective agonist for inducing platelet aggregation.
No proliferation of cryophilic bacteria was observed in cold-stored CPS. The rare contaminations detected were related to the controls and not to bacterial growth promoted by cold storage.

Conclusion:
This study suggests that cold storage of platelets—and more specifically, delayed cold storage—represents a promising alternative to standard storage. This method could extend the shelf life of platelet concentrates beyond 5 days while maintaining good platelet function.

P-8-26

一般演題 Transfusion medicine

Generative AI applications in restrictive transfusion strategy

Reducing RBC transfusion overuse

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Abstract:
Artificial intelligence (AI), particularly generative AI, has emerged as a transformative tool in healthcare. To enhance familiarity and acceptance to restrictive transfusion strategy for healthcare professional in new applications of AI for reducing RBC transfusion overuse, driven by the successful AI deployments in the quality of transfusion. First, this study provided the AI animation generation technology to present restrictive transfusion strategy in a friendly and engaging way, enhancing the diversity of teaching materials. Second, a simplified "lazy-pack" educational video on restrictive transfusion strategy with added QR codes was created. Last, integrating AI-powered online prescription tutorials and building an e-learning platform. After implementing the improvement measures, the overall results were significant in introducing AI broadcasters and diverse teaching materials, the test scoring from 73.75 improved to 100 and the healthcare professional received full marks of 5 in "the comprehension of content," " the satisfaction of learning," "the ease of operability," and " the interactivity of teaching materials", and the non-conformance rate of indications for leukocytes-reduced RBCs significantly decreased from 26.1% to 15.2%. Based on these generative AI, adherence to the restrictive transfusion strategy and use of AI-powered broadcasters, short videos, QR codes, and e-learning platform for hemoglobin alerts or reminders of the healthcare professional's restrictive transfusion policies are effective in reducing RBC transfusion overuse.

P-9-1

一般演題 Education

AI Diagnostic Performance in Medical Laboratory Imaging

Strategic Implementation of AI-Assisted Diagnostic Systems and the Evolving Role of Medical Technologists

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Title: AI Diagnostic Performance in Medical Laboratory Imaging
Subtitle: Strategic Implementation of AI-Assisted Diagnostic Systems and the Evolving Role of Medical Technologists
Methods:
This study conducted a cross-sectional comparative analysis to evaluate the image-based diagnostic performance of ChatGPT-5 under two testing conditions: closed-environment multiple-choice questions (MCQs) and open-environment proficiency testing (PT). A total of 256 image-based MCQs were collected from the National Medical Technologist Examination (2018–2025), assessing image recognition and option-exclusion abilities. Open-ended PT images were sourced from the Taiwan Society of Laboratory Medicine (TSLM) and the College of American Pathologists (CAP), requiring independent diagnosis without answer cues. Tested disciplines included clinical hematology (cell morphology), clinical physiology (ECG and ultrasound), microbiology, urine sediment analysis, and medical molecular diagnostics.
Results:
A marked "question-type effect" was observed. In the MCQ setting, ChatGPT-5 achieved an overall accuracy of 73.83–74%, whereas accuracy declined sharply to 20–39.82% in open-ended PT tasks. Biochemistry and virology reached 100% accuracy, likely due to standardized visual patterns and rule-based interpretation. Hematology also performed well in MCQs (87.21%). In contrast, clinical physiology, particularly ECG interpretation, showed limited accuracy (~51%), reflecting difficulty in analyzing subtle waveform features and spatial lead relationships. Across disciplines, the AI demonstrated insufficient ability to recognize artifacts, atypical or malignant cells, and to integrate image findings with clinical context.
Conclusion:
Despite strong performance in standardized, choice-based examinations, ChatGPT-5 cannot yet reliably perform clinical-grade independent image interpretation. The >50 percentage-point performance gap between MCQ and open-ended tasks highlights the indispensable role of professional medical technologists in morphological gatekeeping and clinical integration. At present, AI is best positioned as an assistant primary screening tool within an "AI screening, expert confirmation" dual-verification framework to enhance efficiency while maintaining diagnostic safety.

P-9-3

一般演題 Education

Digitization as a tool for transformation:

Distance learning for acquiring sustainable knowledge of histological morphology

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Biomedical Science is taught at the University of Applied Sciences Campus Vienna both full-time and part-time. These target groups have different needs; particular consideration must be given to double burdens such as wage labor or care work. As part of the Histological Morphology course, a new concept has now been developed to impart knowledge to students in a sustainable manner.

Central to this is a Moodle course with various components: In addition to lecture notes and PowerPoint presentations, self-produced educational videos of the individual organs will provide students with all the information needed. These not only cover theoretical input but also demonstrate lecturers screening whole slide images (WSI) using an online microscope. Students can also study with flashcards created by lecturers with H5P, where theoretical content in combination with labeled microscopic images is portrayed. A new chapter will be unlocked when the previous one is completed by taking a self-assessment, where at least 60% of the questions must be answered correctly. Additionally, students can view a variety of WSI using the online microscope, regardless of time or location. Access to the course remains available even after completion. While the new concept focusses on distance learning, in person classes will continue to take place; this guarantees the learning curve, as students can ask questions while also practicing on microscopes.

The new didactic concept has already been evaluated by students who completed the Histological Morphology course in a previous semester in its original form. The results show that 83% of students prefer distance learning to face-to-face teaching and 100% found the educational videos particularly helpful. Results indicate that the new concept provides better conditions for acquiring knowledge sustainably. Based on these findings, other courses could be adapted accordingly, not only in Biomedical Science.

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P-9-4

一般演題 Education

XR-Assisted Phlebotomy Improving Workflow and Procedural Training in Medical Laboratory

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Background: This study evaluates the integration of extended reality (XR)—encompassing augmented reality (AR) and virtual reality (VR)—to optimize phlebotomy procedures. The primary objective is to determine if XR-assisted workflows can enhance operational efficiency and mitigate human error. Specifically, the study examines how a Meta Quest 3-based VR environment improves the convenience, completeness, and safety of student training within a risk-free clinical simulation.

Methods: The study implemented an AR-based software solution (IKSAR) for routine workflow guidance, complemented by a dedicated VR training module developed for the Meta Quest 3 headset. Centered on ergonomic design principles, the XR system ensures that simulated blood collection maneuvers strictly align with physical clinical movements. The platform supports hands-free operation and real-time procedural guidance. Trainee performance is evaluated through an integrated digital assessment module using standardized clinical criteria.

Results: Implementation of the XR training component significantly enhanced student engagement by providing a comprehensive and accessible learning experience. Trainees utilizing the Meta Quest 3 demonstrated an increased degree of procedural independence. The high ergonomic fidelity of the XR simulation contributed to a notable reduction in common trainee-related errors. Furthermore, the automated assessment module provided objective data on skill acquisition, ensuring that competency thresholds were met prior to clinical practice, thereby improving overall teaching efficiency

Conclusions: The findings support the effectiveness of integrating AR and Meta Quest 3-based VR into medical laboratory training. By prioritizing ergonomic alignment and digital evaluation, XR-assisted systems standardize instruction and ensure procedural completeness. Further longitudinal studies are warranted to evaluate the long-term impact of XR-driven competency assessments on laboratory quality assurance and workforce development.

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P-9-5

一般演題 Education

Escape Room-Based Gamification for Medical Technologists

Impact on Knowledge, Skills and Attitudes

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Background

Innovative teaching strategies are increasingly adopted to improve engagement and learning outcomes in health professional education. Escape room–based gamification provides immersive and learner-centered experiences that may enhance knowledge integration, skill development, and learning attitudes. This study evaluated the impact of an escape room activity on medical technologists' learning in a clinical context.

Method

An escape room–based gamification activity was integrated into a core medical technologist education course at a tertiary teaching institution. Participants completed sequential challenges involving specimen processing, laboratory testing, cellular morphology, result interpretation, and interprofessional communication. Eighteen medical technologists participated in a 50-minute session. Learning outcomes were evaluated using a post-activity questionnaire assessing knowledge, skills, and attitudes on a 5-point Likert scale.

Results

Participants reported high levels of agreement across all domains. In the knowledge domain, the highest scores reflected enhanced motivation to integrate knowledge across disciplines. In the skills domain, participants perceived improvements in teamwork, self-directed learning, and analytical abilities. Regarding attitudes, the activity was rated as highly engaging and immersive, with participants reporting strong motivation to complete the challenges and a perception of accelerated time during gameplay. Notably, decision-making skills showed relatively lower improvement compared to other domains.

Conclusion

Escape room–based gamification effectively enhanced knowledge integration, practical skills, and learner engagement among medical technologists. Gamification created an immersive learning environment where engagement translated into meaningful learning outcomes. Further studies comparing this approach with traditional teaching methods are warranted.

P-9-6

一般演題 Education

AI Phlebotomy Training: Enhancing Communication Skills Through Virtual Human Simulation

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Background: Phlebotomy is a core clinical skill for medical laboratory professionals, and effective communication is essential to build patient trust, reduce conflicts, and ensure a smooth blood collection process. However, traditional teaching methods, which rely on verbal instruction and demonstration, are often limited by time constraints and insufficient opportunities for practice. As a result, students and newly recruited staff may struggle to handle diverse clinical situations. In contrast, Artificial intelligence (AI)-based virtual humans may provide standardized and repeatable teaching materials to enhance learning outcomes. **Objective:** This study aimed to evaluate the feasibility and learning effectiveness of AI-based virtual humans in phlebotomy communication training. **Methods:** Nine participants, including six medical laboratory students and three newly recruited staff, were enrolled. We designed three domains-patient-provider relationship, blood collection procedures, and laboratory consultation-comprising 12 simulated scenarios. Each scenario was paired with structured dialogue scripts, allowing trainees to interact with AI virtual humans. Scenarios included difficult venous access, fasting-related questions, questioning trainee competence, vasovagal reactions, failed first attempts, and patient concerns about prolonged bleeding. Evaluation methods included pre- and post-tests and a satisfaction questionnaire. **Results:** The mean test score improved from 55 to 82 after training, representing a 27-point increase (49%). Satisfaction results showed that 66.7% of participants were very satisfied, 22.2% satisfied, and 11.1% neutral. All participants reported improved communication skills, increased confidence, and reduced anxiety when interacting with patients. **Conclusions:** AI virtual humans represent a novel, effective, and resource-efficient training modality that improves communication skills and learner confidence. This approach offers significant advantages over traditional methods such as OSCE and demonstrates strong potential for broader application in clinical education.
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P-9-7

一般演題 Education

Training for Medical Laboratory Interns

Virtual Reality Based Polymerase Chain Reaction Training for Medical Laboratory Interns

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Purpose：

To evaluate the educational effectiveness and acceptability of a virtual reality (VR)-based polymerase chain reaction (PCR) training programme for medical laboratory science interns who experience limited hands-on practice due to biosafety and access constraints.

Methods：

A pre-post mixed-methods study was conducted during a clinical internship at a Taiwan regional teaching hospital. A VR-based PCR simulation using Meta Quest 3 integrated instructional design, interactive three-dimensional environments, and real-time feedback, covering PCR concepts, nucleic acid extraction, and thermal cycling. Knowledge was measured by expert-validated multiple-choice tests before and after training. Perceptions were assessed using the Course Experience Questionnaire and open-ended feedback. Paired t-tests analyzed quantitative data; thematic analysis analyzed qualitative data.

Results：

Nine interns completed the programme. Post-test knowledge scores (91.1±9.3) were significantly higher than pre-test scores (57.8±24.4) (p=0.001). Learner satisfaction was high (mean Course Experience Questionnaire score: 4.5/5). Qualitative data showed improved understanding of PCR workflows, procedural standardisation, and confidence for clinical laboratory practice. Participants valued repeated practice in a risk-free environment.

Conclusion：

The VR-based PCR training programme showed positive educational outcomes and high learner acceptance. VR simulation is a feasible adjunct to traditional laboratory instruction, supporting standardised, repeatable, learner-centred skills development before clinical exposure. Multi-centre studies with larger samples are needed to examine long-term retention and clinical performance transfer.

Keywords：Virtual reality; PCR training

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P-9-8

一般演題 Education

Automated Voice Dialing for Critical Value Reporting: Implementation and Evaluation

An Innovative Automated Voice Dialing and Escalation Framework for Clinical Value Reporting

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Aim
Critical value notification is essential for patient safety. Previously, our hospital required manual phone follow-ups if SMS alerts were unacknowledged after 30 minutes. Handling 500 calls monthly was labor-intensive and disrupted workflows. This study implements an "Automated Voice Dialing System" integrated with a Monitoring System (MOS) to automate tracking and enhance efficiency.
Methods
We integrated an automated escalation protocol, the system triggers voice alerts if no SMS response occurs within 30 minutes. (1) Automated Group Retrieval: The system automatically identifies and retrieves the assigned care team for each case. (2) Sequential Escalation: Calls are made in a predefined sequence: Duty Physician → Attending Physician → Nurse Practitioner → Head Nurse → Ward Official Phone. (3) Redundancy: If a call is missed, the system proceeds to the next level, initiating a second round if necessary. (4) Traceability: All call logs are digitally recorded for audit purposes.
Expected Results
Now in the implementation phase, the system is expected to automate 500 monthly calls. Anticipated benefits include reduced technologist workload, 100% notification integrity, and ensuring all critical values are reported within the 60-minute target.
Conclusion
Transitioning to automated notification minimizes human error and allows laboratory staff to focus on testing quality. This closed-loop system improves reporting efficiency and patient safety, serving as a model for smart healthcare.

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P-9-9

一般演題 Education

Gamification of Learning -"Hospital Escape"

Application of Escape Room Integrated with Live Action Role-Playing in Medical Laboratory Education

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Introduction and Object:
An escape room integrated with live action role-playing is an innovative method applying to medical laboratory education. By providing an immersive environment, this method enhances students' engagement and interest in learning. Under time-limited conditions, students are encouraged to develop efficient problem-solving skills and strengthen their teamwork. Furthermore, through live action role-playing, the learners are more able to synthesize knowledge related to clinical disease during the game. The main objective of this study is to evaluate the effectiveness of this innovative teaching strategy in clinical laboratory education.
Methods:
This study recruited 12 medical laboratory UGYs in 2025. The "Hospital Escape" was designed with four game levels and four corresponding character roles representing patients with APL, AIDS, SLE, and CKD. And the study methodology included pre- and post-test, as well as students' qualitative feedback and satisfaction survey.
Results:
Based on the analysis of pre- and post-test results, this educational activity effectively enhanced learning outcomes. Furthermore, students' qualitative feedback and satisfaction survey data indicate a high level of engagement and positive reviews toward this learning approach.
Conclusion and discussion:
In response to evolving educational demands, instructors have continually sought to develop innovative teaching methods. The method in this study is an effective strategy for enhancing learning outcomes and stimulating learner motivation. In addition, this approach simultaneously cultivates logical reasoning and teamwork skills, supporting multidimensional competency development. With further refinement of design elements, this method has strong potential for broader application across diverse disciplines and specialties, enabling more students to experience the enjoyment of clinical medical education.

P-9-10

一般演題 Education

Designing Entrustable Activities for Entry-Level Laboratory Practice

Validation and staged prioritization across three core disciplines

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Entrustable professional activities (EPAs) provide a practical framework for competency-based laboratory education. However, specialty-specific EPAs for entry-level laboratory practice have not been systematically developed in Taiwan. This study aimed to develop EPAs across clinical chemistry, hematology, and microscopy and establish implementation priorities through expert validation and feasibility analysis.

EPA statements were developed by discipline-specific clinical educator teams and evaluated through a cross-sectional survey of clinical teachers. Participants rated each EPA for appropriateness, importance, and feasibility using a 5-point Likert scale. Activities with high importance but lower feasibility were identified as developmental priorities. ROC-based optimization was used to define primary and secondary implementation zones.

Forty-eight clinical teachers participated. Mean appropriateness ratings were high across clinical chemistry, hematology, and microscopy (4.63, 4.68, and 4.71, respectively). Six EPAs were identified as primary priorities and eleven as secondary priorities. Primary priorities focused on peripheral smear review, critical value verification, abnormal result follow-up, and turnaround time exception management. Secondary priorities were more common in microscopy, particularly urine sediment interpretation and standardized abnormal finding reporting.

These findings provide a structured framework for staged curriculum development, faculty alignment, and milestone-based implementation of competency-based laboratory education, supporting the development of entry-level laboratory training programs in Taiwan.

P-9-11

一般演題 Education

Development and Implementation of the postgraduate program "histopathology"

A spezialiced 60 - ECTS curriculum for biomedical scientists in Austria

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Background: The shortage of skilled Biomedical Analysts (BMA) in Austria poses challenges for healthcare providers, particularly in recruiting Generation Z. This study identifies the specific employer branding expectations of Generation Z in the Austrian BMA sector, contrasting them with the preferences of older Generations X and Y.

Methods: A quantitative research approach was employed using a standardized online survey (CAWI). The final sample consisted of active BMA professionals (55.7%) and students (44.3%). Data analysis was conducted using inferential statistical methods, including t-tests, Mann-Whitney U-tests, and Chi-square tests, to evaluate the formulated hypotheses.

Results: The analysis reveals a qualitative shift in values within the industry. While overall expectations of employer branding do not differ quantitatively across generations, significant differences exist in prioritization. Generation Z weights "soft factors"—such as corporate culture, appreciation, and perceived meaning of work—significantly higher than material factors. In contrast, older generations place a significantly higher value on job security and stable framework conditions. Furthermore, Generation Z shows a clear preference for digital channels, specifically career websites and social media, for information gathering. **Conclusions:** Employer branding in the BMA sector must adopt a culture-centered and digitally visible strategy to remain competitive. Future measures should prioritize societal meaningfulness and an appreciative, transparent feedback culture. To ensure long-term retention across all cohorts, organizations should combine digital recruitment for the youth with security-focused internal communication and mentoring programs for the experienced workforce.

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P-9-12

一般演題 Education

SIMULATION as a Didactic Concept in Functional Diagnostics

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Title: SIMULATION as a Didactic Concept in Functional Diagnostics
Authors Affiliation: **University of Applied Sciences**
Background: Functional diagnostics requires seamless integration of technical skills, clinical reasoning, and team communication in safety-critical settings. Simulation provides a realistic yet risk-free environment to practice these competencies and to analyze errors without jeopardizing patient safety. To present a curriculum-integrated, simulation-based teaching concept for students in functional diagnostics and to report initial evaluation findings on acceptance and perceived learning outcomes. **Setting and Design**: A university SimLab equipped with a hospital-like infrastructure, hosted scenario-based trainings. Each session followed a standardized three-step structure: (1) scenario design with explicit learning objectives, roles, resources, and flow; (2) briefing including data protection, psychological safety, and pre-/case-briefing; (3) structured debriefing focusing on summary, reflection, feedback, and take-home messages. An exemplar case addressed excessive daytime sleepiness in a professional driver with suspected sleep-related breathing disorder. **Evaluation**: Formative evaluation drew on instructor observations, debriefing notes, and written student feedback. **Results**: Students consistently reported (1) improved appreciation of the relevance of theory for clinical practice, (2) a safe environment for practicing technical procedures and non-technical skills (communication, empathy, teamwork), (3) enhanced analytical and critical thinking and (4) high acceptance and a desire for more simulation repetitions. **Conclusions**: Simulation is an effective didactic approach for functional diagnostics. The combination of rigorous scenario design, deliberate prebriefing, and structured debriefing strengthens readiness for practice, patient safety, and interprofessional competencies. Future work will emphasize competency-based assessments, scaling to additional functional areas, and systematic measurement of learning outcomes.
Elis Godaj, MSc

P-9-13

一般演題 Education

Academic Program in Functional Diagnostics

Evidence-based specialization for functional laboratory diagnostics in pulmology, sleep medicine, cardiology, and neurology

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Title: Academic Program in Functional Diagnostics
Subtitle: Evidence-based specialization for functional laboratory diagnostics in pulmonology, sleep medicine, cardiology, and neurology
Author Affiliation: University of Applied Sciences
Background: This academic, part-time program in Functional Diagnostics qualifies participants to analyze and solve complex diagnostic and therapeutic questions across pulmonary, sleep, cardiology, and neurological functional laboratory settings. Science-driven content, modern teaching/learning methods, and up-to-date equipment ensure strong practical relevance and innovation. Low on-site requirements, flexible formats, and clearly structured modules support compatibility with professional commitments. **Aim:** Targeted specializations within functional diagnostics; contemporary content, methods, and hands-on practice; science, research, and ethics, quality management. **Innovation:** The program establishes “Academic Experts in Functional Diagnostics” through specialized, evidence-based training, digital and interactive formats, and high flexibility for working professionals. Curriculum/Methods: Duration 2 semesters, 60 ECTS. Core modules include history taking, communication, cardio/pulmo/neurology foundations, patient safety/ergonomics, and scientific work. Mandatory modules: biomedical reporting and professional/legal framework; pharmacology, legal foundations, emergency management; research and ethics. Electives: sleep medicine; sonography; advanced organ modules in cardiology, pulmonology, neurology, sleep medicine. The academic program in Functional Diagnostics offers a unique, evidence-based, part-time specialization with strong practical relevance, modern pedagogy, and targeted deepening in pulmonology, sleep medicine, cardiology, and neurology. Graduates are qualified for demanding specialist and interface roles and, through diagnostic expertise, quality management, and interprofessional collaboration, make a measurable contribution to care, prevention, rehabilitation, and innovation. **Elis Godaj.**

P-9-14

一般演題 Education

Hemoglobin Discrepancy and Sample Inhomogeneity in Syringe Blood Collection

Impact of Pre-analytical Factors and Rapid Sedimentation Triggered by a Critical Incident

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Introduction: A critical incident involving a marked hemoglobin (Hb) discrepancy between blood gas analysis (BGA) and complete blood count (CBC) (11.1 vs. 4.1 g/dL) nearly resulted in inappropriate transfusion. Investigation identified sample inhomogeneity caused by post-collection erythrocyte sedimentation in a syringe. This study assessed the impact of pre-analytical handling on blood sample uniformity.

Methods: Hb was measured using the ABL90 FLEX (Radiometer) and XN-3000 (Sysmex).

Clinical comparison: Hb correlation was evaluated by linear regression using 100 paired outpatient and 100 paired inpatient BGA–CBC samples. Outpatient samples were collected by laboratory technicians using standardized winged-needle procedures, whereas inpatient samples were mainly obtained by nurses using variable syringe-based procedures.

Standing experiment: 36 residual BGA syringe samples were left undisturbed for 3 and 5 minutes, and Hb values in the upper and lower layers were compared to evaluate stratification.

Results: Outpatient samples showed strong BGA–CBC correlation (r^2 = 0.9754; −2.6% to +9.7%), whereas inpatient samples demonstrated poorer correlation and wider discrepancies (r^2 = 0.9364; −11.1% to +39.4%). Standing samples exhibited rapid stratification, with absolute upper–lower Hb differences up to 2.1 g/dL at 3 minutes and 11.0 g/dL at 5 minutes.

Discussion: The wider diameter of syringes may facilitate erythrocyte sedimentation, resulting in rapid stratification. Additionally, variable collection procedures and insufficient mixing may compromise analytical reliability and lead to clinically significant errors.

Conclusion: Standardized handling and adequate mixing of syringe blood samples are essential to prevent inhomogeneity and ensure reliable results. Increased awareness of pre-analytical errors and standardized blood collection practices are essential for improving patient safety.

P-9-15

一般演題 Education

The new era of Biomedical Laboratory Sciences in Portugal

One profession, multiple specializations: A strategic framework for academic progression and professional alliance

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Biomedical Laboratory Sciences (BLS) in Portugal stand at a decisive crossroads. The 2014 reform unified Clinical Analysis and Public Health with Pathological, Cytological, and Thanatological Anatomy into a single academic degree. However, this integration has yet to produce a coherent professional identity aligned with international practice. Portugal remains an outlier, as a single undergraduate qualification (240 credits under the European Credit Transfer and Accumulation System (ECTS)) grants access to two regulated professions, contrasting with the European and global recognition of the Biomedical Laboratory Scientist (BLs) as a unified healthcare profession. This work presents the strategic vision of the Portuguese Association of Biomedical Laboratory Sciences (BioMedLab) to redefine the national BLS ecosystem through educational reform, professional consolidation, and international alignment. Moving beyond historically fragmented professional models, BioMedLab proposes a forward-looking academic continuum capable of responding to rapidly evolving diagnostic, technological, and healthcare demands. The proposed framework maintains the four-year undergraduate degree as a common foundation, followed by specialized Master's programmes (120 ECTS) across eight laboratory domains and consortium-based doctoral programmes (180 - 240 ECTS) aimed at fostering innovation, translational research, and leadership within laboratory medicine. This model positions BLs as central actors in precision medicine, public health preparedness, and diagnostic quality and innovation. More than curricular reform, this proposal represents a paradigm shift toward a unified profession grounded in competence, mobility, and scientific autonomy. By aligning education, regulation, and professional recognition, this roadmap seeks to ensure European comparability, strengthen professional legitimacy, and position Portugal as a leader in the future of BLS.

Keywords: Biomedical Laboratory Scientist, Academic continuum, Professional identity, International alignment

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P-9-16

一般演題 Education

Virtual slide group work enhances understanding in pathology education

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Objective: The use of virtual slides (VS) has become widespread in the field of pathology in recent years. In clinical laboratory technologist training programs, individual students have traditionally studied by observing histological specimens under a light microscope. Because VS allows multiple viewers to share the same field of view, they enable collaborative learning accompanied by peer discussion. The present study compared the effects of conventional individual microscope-based observation with those of VS-based group work on students' level of understanding.

Methods: The participants were second-year students in the Department of Clinical Laboratory Technology, Faculty of Medical Science, Juntendo University. A total of 113 students took part in the practical sessions. The students first underwent conventional microscope-based practical training, followed by VS-based group-work practical training two months later. After each session, the participants took a comprehension test, and a questionnaire survey was conducted following the VS-based group-work session (response rate: 95.6%, n = 108).

Results: The correct response rate on the comprehension test was significantly higher after VS-based group-work training than after microscope-based training ($p < 0.01$). Questionnaire responses indicated that the students rated VS highly: 91.7% reported that their understanding was deepened through discussion with other students, and 84.3% responded that it would be preferable to incorporate VS into practical training. In contrast, 29.6% of respondents indicated that microscopes are superior for detailed observation, suggesting that conventional microscope-based training remains necessary.

Conclusion: These findings suggest that group work using VS promotes collaborative learning and contributes to improved student understanding. While conventional microscope-based practical training retains its importance, combining it with VS is expected to enhance overall educational outcomes.

P-9-17

一般演題 Education

Digital and Flexible Continuing Education for Biomedical Laboratory Scientists

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In Norway, biomedical laboratory science is offered as a three-year bachelor's degree regulated by national guidelines. The programme combines extensive theoretical training with substantial practical components, including skill-based training and supervised clinical placements. This provides graduates with a solid foundation for entering the workforce. However, several medical specialties require more advanced knowledge of analytical principles, instrumentation, and biological or pre-analytical factors affecting test results. While such expertise is often developed through work experience, there is a lack of accredited postgraduate courses in these areas. This highlights a national need for flexible, credit-bearing continuing education opportunities.

The aim of this project was to develop and evaluate a national, flexible postgraduate course in haematology tailored for biomedical laboratory scientists combining work and study. Through collaboration between two educational institutions and two university hospitals, a 10 ECTS master's level course was established. The course includes a physical introductory session, digital learning resources, structured skill training using CellaVision Proficiency, individual and group assignments, and online teaching sessions. It is designed to be compatible with full-time employment.

The course will be offered for the fourth time in 2026, with around 100 participants completing it so far. Evaluations show high student satisfaction, particularly with its flexibility.

This model demonstrates how collaborative, digital postgraduate education can meet national competency needs and serves as a blueprint for future courses.

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P-9-18

一般演題 Education

Career Awareness and Educational Needs among Japanese Medical Laboratory Scientists

Insights from a Survey on Training Gaps and Career Expectations

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Background / Objective: Medical Laboratory Scientists (MLS) in Japan are increasingly required to assume diverse roles and advanced expertise as diagnostic technologies evolve and healthcare systems become more complex. Despite these growing expectations, limited research has examined how MLS perceive their own career development, workplace environment, and educational preparation. To address this gap, this study aimed to clarify career awareness, satisfaction with educational preparation, professional concerns, and desired support systems among Japanese MLS and students, with the goal of informing sustainable workforce development and future-oriented educational strategies.

Methods: An online survey of 120 respondents—including practicing MLS, educators, industry professionals, and students—assessed satisfaction with education, career-related concerns, workplace perceptions, desired educational content, and needs for career support. Both quantitative and qualitative data were analyzed.

Results: Respondents identified salary, work–life balance, and career advancement opportunities as the most important professional factors. While satisfaction with technical and medical education was relatively high, satisfaction was notably low regarding industry-wide information, international perspectives, and postgraduate career pathways. Many participants expressed concerns about future career prospects, limited opportunities for self-development, and institutional stability. A significant number reported lacking someone to consult about career issues. Free-text responses emphasized the need for role models, structured career information, and accessible online mentoring or consultation services.

Conclusion: The findings highlight the need to strengthen career education, expand opportunities for advanced skill development, and establish structured support systems. Collaboration among educational institutions, academic societies, and medical organizations will be essential to address these emerging needs.
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P-9-19

一般演題 Education

Practical Three-Minute Kiken Yochi Training in a Pathology Laboratory

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Background: Pathology laboratories involve various potential hazards, including specimen misidentification, labeling errors, chemical exposure, and microtome-related injuries. Although safety measures are often reinforced after incidents occur, maintaining hazard awareness during routine daily work remains challenging. In addition, pathology work is frequently performed individually and requires a high level of concentration, which can limit communication opportunities among staff.

Methods: To promote continuous safety awareness, we introduced a brief Kiken Yochi Training (KYT)—a Japanese hazard prediction activity—during morning meetings in our pathology laboratory. Instead of the conventional four-step KYT method, we adopted a simplified one-step format to minimize workload and improve sustainability. The activity lasted approximately three minutes and utilized photographs taken in our laboratory. Based on these images, participants discussed potential hazards and key points requiring attention.

Results: Although this activity was not designed for a formal outcome evaluation, staff feedback suggested several positive effects, including increased attentiveness before starting work, greater awareness of daily risks, and increased opportunities for brief communication among team members. Incorporating hazard prediction into the routine workflow may help foster a culture of proactive safety awareness rather than relying solely on reactive measures after incidents occur.

Conclusion: This simple and practical activity may provide an effective approach to promoting safety awareness and communication in busy pathology laboratories.

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P-9-20

一般演題 Education

Designing a Self-Assessment System for Biomedical Laboratory Science Examination Preparation

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Purpose: In Japan, preparation for the national licensure examination for medical technologists relies largely on printed question books, with limited access to computer-based testing (CBT) tools offering blueprint-aligned self-assessment and immediate feedback. We developed a CBT-based self-assessment system to address this gap and to provide a reusable platform for laboratory science education. Although implemented for the Japanese examination, the approach applies broadly to biomedical laboratory science education.
Methods: The system consists of an examination engine, a domain-tagged item bank, and an automated scoring module. The item bank was built from publicly released questions of the past 15 years of the national examination; each item was tagged by subject domain and mapped to the official examination blueprint. The system supports both a full-length mock-examination mode and a domain-specific practice mode.
Results: The item bank currently contains 3,000 questions covering all subject domains of the national examination for medical technologists. Mapping each item to the blueprint enables learners and instructors to identify under-covered domains and target weak areas. Automated scoring provides immediate display of correct answers and explanations, enabling use in both supervised classroom and individual self-study settings. The modular separation of engine, item data, and user interface allows the platform to be extended to other laboratory disciplines. Original items and a learner-based evaluation of educational effectiveness are currently under development.
Conclusion: We demonstrated the feasibility of a blueprint-aligned, dual-mode self-assessment system for medical technologist examination preparation. The platform offers an accessible and extensible alternative to printed materials, and its educational effectiveness will be evaluated in future work.

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P-9-21

一般演題 Education

Evidence-based competency tools with a next-generation digital system

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Objective: As medical technology advances, medical laboratory scientists (MLS) require broader and more complex competencies. In Japan, new MLSs start clinical practice immediately after passing a national written exam, without a standardised training framework. Competency-Based Education (CBE) is effective for workplace training, but competencies for MLSs in clinical settings are not systematically defined, hindering CBE implementation. This study aims to define competencies for MLSs, develop a competency scale, and build a digital support system to promote effective education. **Methods**: We first defined and systematised the competencies needed for novice MLSs in Japan, creating a foundational framework based on over 97% consensus among 95 expert MLS managers. Next, we developed and validated a 40-item competency scale for both self- and supervisory evaluations, ensuring reliability and validity per international guidelines. Based on these results, we began developing a CBE programme. **Results**: At Kobe University Hospital, we are currently developing an electronic educational support system. This system integrates self- and supervisory evaluation within a unified digital platform. Built on a cloud-based architecture, the system stores and manages all evaluation data in a centralised database. To ensure flexibility and adaptability, master data structures have been created for evaluator, department, and assessment item, enabling the system to accommodate changes in personnel and organisational structures. In addition, the system is designed for use on both personal computers and tablet devices, allowing efficient data entry and feedback during routine clinical work and educational activities. **Conclusion**: The system enables visualisation of assessment results, comparison between self- and supervisory evaluation, and continuous feedback, thereby serving as a foundational platform for implementing CBE. Moving forward, we will evaluate the system's educational effectiveness and its impact on competency development through practical operation, with the aim of establishing a standardised model for postgraduate education for MLSs in Japan.

P-9-22

一般演題 Education

Authentic Assessment for Workforce Readiness in Laboratory Medicine

A coherent assessment pathway supporting professional formation and workforce readiness

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Laboratory Medicine placements provide authentic workplace learning within diagnostic pathology laboratories, however, much of this learning remains implicit and difficult for students to recognise, articulate and demonstrate. This presents a challenge for biomedical laboratory science education in preparing reflective, adaptable graduates for evolving workforce demands. To address this, a coherent, career-forming assessment pathway was developed in a final-year Laboratory Medicine work-integrated learning program, making workplace learning explicit, structured and assessable.

Weekly reflections aligned to a structured career development framework (1) guide students to interpret workplace experiences and identify professional actions. Students then evaluate capability development across twelve domains and self-assess readiness for practice. This informs a flexible e-Portfolio, through which students translate learning into authentic professional outputs, including research projects, case study reports, leadership plans and ISO 14001-aligned sustainability artefacts. This integrated model aligns with national competency standards and industry practice. Students are supported to translate workplace experiences into evidence of professional capability, professional identity and career readiness.

Student assessment data, industry feedback and graduate outcomes suggest the pathway supports articulation of professional capability and career readiness. Students have produced authentic outputs, including research dissemination and nationally recognised case study work progressing toward publication. This approach positions assessment as a driver of professional formation and workforce readiness, offering a transferable model for biomedical laboratory science education.

(1) National Careers Institute (2022), *Australian blueprint for career development*.

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P-9-23

一般演題 Education

Modular Master of Health Studies: Stackable Micro-credentials for Postgraduate Pathways

Flexible master's programme combines lifelong learning with continuous academic development

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Background: Healthcare systems are changing due to demographic shifts, digitalization and quality standards, requiring flexible postgraduate education that supports specialization and lifelong professional development.

Objective: To design a modular Master's in Health Studies aligned with European modularization and micro-certificates, enabling stackable pathways and recognition of prior learning.

Programme design: A two-step pathway can be undertaken as standalone qualifications or accumulated towards the degree. Step 1 offers specializations for biomedical scientists as a standalone certificate or as part of the degree. Step 2 develops advanced scientific, strategic and interprofessional skills, with a focus on evidence-based practice, digital health, public health and management. Sequenced outcomes ensure progression from micro-certificates to the Master's degree.

Delivery and Pedagogy: A blended model combines asynchronous online learning with scheduled face-to-face sessions, balancing theory and practice through research-led teaching and partnerships with clinical and laboratory sites.

Outcomes: Early implementation has led to improved access for diverse learners, clearer specialization pathways, and greater alignment with workforce reskilling and upskilling needs. Institutions benefit from flexible short courses that support career transitions and lifelong learning.

Conclusions: The priorities are to admit international cohorts, strengthen transnational partnerships, harmonize recognition across borders, and evaluate graduate outcomes to inform iterative improvement and European adoption.

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P-9-24

一般演題 Education

Competency-Based Curriculum Reform in Biomedical Science Education

Early Laboratory Skills Training and Structured Assessment to Enhance Pracitcal Competence

◎Barbara Kirchknopf[1)]、Michaela Hassler[1)]
University of Applied Sciences Vienna[1)]

Background: Biomedical laboratory education must respond to digital transformation, evolving regulatory frameworks, and workforce shortages. Subject-based curricula often lack transparency and hinder structured competence development, particularly in practical skills.

Objective: To redesign a Bachelor program in Biomedical Science by transitioning to a competency-based curriculum and strengthening early practical skills training to enhance student preparedness.

Program Design: A mixed-methods approach integrated labor market data, student feedback, and expert consultations. A gap analysis mapped modules to regulatory requirements and accreditation standards and defined competence profiles. The curriculum was restructured by explicit learning outcomes and competence levels supported by constructive alignment.

Delivery and Pedagogy: A first-semester "Laboratory Skills" module (10 ECTS credits) focuses on hands-on competencies, including pipetting, microscopy, specimen handling, quality control, and laboratory safety. Teaching is competency-oriented and student-centered, using deliberate practice, checklists, and formative feedback and faculty development. Practical skills are assessed via Objective Structured Clinical Examination (OSCE) with standardized stations and criteria.

Outcomes: The reform reduces redundancy, increases transparency, and establishes clear competence progression. Early structured skills training addresses documented practical skill deficits and is expected to enhance confidence, placement readiness, and safety culture. Planned evaluation includes OSCE scores, supervisor ratings during placements, time-to-independence metrics, and student-reported preparedness.

Conclusion: Integrating competency-based design with early, intensive laboratory skills training and OSCE-based assessment strengthens practical readiness and educational quality. The model is feasible within existing resources, scalable across cohorts, and transferable to comparable programs.

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一般演題 Education

Curriculum Redesign for Part-Time Biomedical Science Education

Blended delivery, simulation and workload alignment in clinical chemistry

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Background: Part-time cohorts juggle employment, study and caregiving. In biomedical science education, inflexible, clustered practical trainings create workload peaks and weak theory–practice alignment, limiting competence development in clinical chemistry.

Objective: Redesign "Clinical Chemical Laboratory Diagnostics 2" to improve studyability, engagement, and learning outcomes for a part-time Biomedical Science cohort.

Methods: Design-based educational intervention using structured student feedback, cohort analytics, and instructor reflections to identify barriers and guide iterative redesign emphasizing constructive alignment, workload smoothing, explicit competency targets, and simulation-enhanced practice.

Delivery and Pedagogy: A blended model combined asynchronous modules with synchronous sessions. Laboratories were reorganized into task-oriented units with objectives, stepwise protocols, and safety checkpoints. Simulation labs provided skills training via low- and medium-fidelity scenarios, checklists, and debriefings. Collaborative learning supported heterogeneous prior knowledge.

Outcomes: Post-implementation feedback indicated improved flexibility, pacing, and workload management. Students reported greater autonomy in knowledge acquisition, higher efficiency during labs, and increased preparedness for workflows. In-course indicators suggested stronger theory–practice integration, consistent competence progression, and a reinforced safety culture. Preliminary quiz and checklist scores improved compared with prior cohort.

Conclusion: A blended, constructively aligned redesign that integrates simulation-based skills training and workload smoothing can enhance studyability and practical competence in part-time laboratory education without diluting standards.

Next Steps: Expand simulation scenarios and asynchronous resources, evaluate learning analytics and practical performance measures, and analyze retention and progression

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P-9-26

一般演題 Education

Shaping the Future: Harmonising Biomedical Laboratory Sciences Education in Portugal

National Council of Biomedical Laboratory Sciences working together for a brighter future!

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Biomedical Laboratory Sciences (BLS) education in Portugal is facing increasing strategic pressure resulting from growing demand for higher education and evolving healthcare needs. In 2025, Portuguese higher education saw 49,595 applicants compete for undergraduate placements, underscoring intensified competition and the need for coherent workforce planning in health professions education. Within this context, BLS training is currently delivered by 11 higher education institutions, seven public and four private, offering a combined total of 400 admission places nationwide.

This study analyses and compares curricular structures, European Credit Transfer System (ECTS) distribution, contact hours, student workload, and clinical training components across Portuguese BLS programmes, between the 7 public higher education institutions. The findings reveal substantial homogeneity between institutions regarding teaching hours, practical training exposure, and workload organisation. While all programmes comply with national regulatory requirements, variations in pedagogical models and training intensity may raise questions concerning educational equivalence, graduate competencies, and professional standardisation. The results demonstrate that clinical placement components remain a central pillar of BLS education, yet disparities in workload distribution and contact hours may influence student preparation, mobility, and alignment with European educational frameworks. In a context of increasing internationalisation of healthcare professions, such variability challenges the establishment of a clearly recognisable professional identity for BLS in Portugal. These findings support the need for strategic national coordination of BLS education, promoting even more harmonised academic standards, transparency in workload expectations, and alignment with European and global benchmarks. Therefore, Associação Portuguesa de Ciências Biomédicas Laboratoriais (BioMedLab) proposed the National Council of Biomedical Laboratory Sciences, where all BLS program directors work together towards strengthening coherence between institutions, which represents a critical step toward ensuring educational quality, professional recognition, and the sustainability of the biomedical laboratory workforce in Portugal's future healthcare system.

Keywords: Public Higher Education, Curricular Standardisation, Workload Distribution, Graduate Competencies, National Coordination

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P-9-27

一般演題 Education

Where Standards Meet Practice Educating - Tomorrow's Biomedical Scientists

Curricular Structures and Professional Standards in Portuguese Private Higher Education

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The private higher education sector in Biomedical Laboratory Sciences (BLS) in Portugal operates within a demanding environment shaped by rising university admission pressures and evolving healthcare workforce requirements. In 2025, nearly 50,000 candidates competed for undergraduate placements nationally, underscoring the urgency of structured and sustainable training pathways in health professions. Three out of four private institutions currently delivering BLS programmes form the analytical focus of this study, representing a meaningful share of national training provision in this field.

This work systematically examines how curricular frameworks, European Credit Transfer System (ECTS) credit allocation, instructional contact hours, learner workload, and supervised clinical exposure are organised across these three institutions. Although the programmes demonstrate broad structural convergence largely attributable to shared regulatory compliance, some differences persist in pedagogical design, practical training intensity, and workload distribution, raising legitimate concerns regarding graduate preparation consistency and professional standardisation within the private sector.

Clinical placement remains an indispensable pillar of professional formation across all three institutions; however, uneven patterns in time allocation and supervised learning contact may affect graduates' workforce readiness and European mobility prospects. Such inconsistencies further complicate the consolidation of a coherent and internationally recognisable professional identity for BLS practitioners in Portugal.

These findings call for deliberate coordination among private BLS providers, advancing harmonised quality benchmarks and alignment with European educational standards. Active engagement within collaborative frameworks such as the National Council of Biomedical Laboratory Sciences, promoted by Associação Portuguesa de Ciências Biomédicas Laboratoriais (BioMedLab), represents a vital step toward ensuring long-term educational quality and professional recognition across Portugal's private biomedical laboratory training landscape.

Keywords: Biomedical Laboratory Sciences, Curricular Harmonisation, Private Higher Education, Clinical Training, Professional Identity

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P-9-28

一般演題 Education

The Importance of Specialized and Standardized Training in Macroscopy

A Proposal for a Competency-Based Educational Model in Biomedical Laboratory Science

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Macroscopic examination constitutes a critical step in the pathology workflow, directly influencing the quality of histological sampling and, ultimately, diagnostic accuracy. Despite its clinical significance, macroscopy training within Biomedical Laboratory Sciences (BLS) curricula remains inconsistent across countries, with considerable variation in depth, duration, and supervisory frameworks dedicated to this competency.

An international review of BLS undergraduate and postgraduate curricula reveals a fragmented landscape: while some European and North American programs integrate structured macroscopy modules with dedicated laboratory hours and formative assessment, others address the topic superficially within broader histopathology course units. This disparity raises concerns about professional readiness and patient safety, particularly as biomedical laboratory scientists assume expanding roles in specimen handling, macroscopic description, and dissection due to the shortage of pathologists and increase in the number and complexity of specimens.

In response to this gap, we propose a competency-based training model specifically designed for macroscopy in BLS education. The model draws on established frameworks - including Entrustable Professional Activities (EPAs) to define progressive levels of autonomy, from supervised observation to independent practice with mandatory assessment. Core competencies encompass specimen identification and orientation, accurate gross description and documentation, systematic dissection technique, and representative sampling. The curriculum further integrates digital tools, such as digital pathology platforms and artificial intelligence (AI)-assisted softwares and contact with innovative automatic technologies to enhance learning in diverse institutional settings.

Standardizing macroscopy training across BLS programs would not only strengthen the technical and cognitive preparedness of graduates but also foster greater professional recognition of the Biomedical Laboratory Scientists (BLSs) contribution to pathological diagnosis. International collaboration through bodies such as IFBLS is essential to harmonize educational standards and develop shared assessment benchmarks.

This proposal aims to stimulate dialogue on curriculum reform and the elevation of macroscopy as a defined, examinable, and professionally valued competency within BLS education worldwide.

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一般演題 Education

Bridging the Future of Biomedical Laboratory Science Through International Training

Insights from the 2024 TMER Overseas Training Program

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International training experiences play an important role in advancing biomedical laboratory science (BLS) by promoting knowledge exchange, professional development, and cross-cultural understanding across global laboratory communities. In 2024, I participated in the Tsukuba Medical Laboratory of Education and Research (TMER) Overseas Training Program in Japan, in collaboration with the International Federation of Biomedical Laboratory Science (IFBLS), representing Canada. This one-week hematology program provided hands-on learning across academic, clinical, and industrial laboratory settings, demonstrating how international training connects current practice with the future of BLS.

I participated in lectures, laboratory-based learning, and site visits. Topics covered included hematology case discussions, bone marrow specimen preparation, flow cytometry, quality assurance practices, and emerging diagnostic technologies. Visits to industry partners provided insight into reagent development and diagnostic manufacturing. I also learned about COVID-19–related public health innovations, including mobile laboratory units and drone-assisted specimen transport systems, improving diagnostic capacity and emergency response.

The TMER program serves as a model for connecting countries through shared learning and innovation, illustrating a more globally integrated laboratory profession. The experience strengthened my technical knowledge, expanded my understanding of international laboratory practice, and reinforced collaboration in laboratory medicine. It also broadened my professional networks and supported integration of innovative practices into laboratory education and workflow.

P-9-30

一般演題 Education

The BLS Academy

An International Academy of Biomedical Laboratory Sciences

©Gry Sjoholt[1)]、Mario Maia-Matos[2)]、Anniina Friman[3)]、Fernando Mendes[4)]、Stephanie Meli[4)]、Line Wergeland[1)]
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The BLS Academy has been established as a society for BLS educational programs throughout Europe, sharing knowledge and best practice of the BLS education.

Our web page, hosted by the European Association of Biomedical Scientists (EPBS), function as the virtual site of the academy. Further on, a biannual European Conference on Biomedical Laboratory Sciences Education (ECBLSE) has also established, whereas the 2nd ECBLSE was completed in Bergen, Norway in 2025 and is planned to be organized in Vienna, Austria in 2027. In this way physical and virtual meeting points for the BLS Academy has been established for blended (both virtual and physical) collaborations.

The BLS Academy aim to enhance innovation of the BLS education through joint development of research based knowledge and sharing of teaching- and learning resources. Partners in the BLS Academy are invited to webinars, BIPs (blended intensive programs), COIL (collaborative on-line international learning), student mobility agreements and international courses and seminars of post graduate students. Extending the society of BLS Academy, we are now inviting other BLS study programs to be part of our international network.

P-10-1

一般演題 Genetics

Urinary Liquid Biopsy for Nuclear and Mitochondrial Genomics in Practice

Urinary Liquid Biopsy for Nuclear and Mitochondrial Genomics in Practice

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[Purpose] Urine is increasingly recognized as a practical non-invasive specimen for liquid biopsy in clinical laboratory settings. Compared with blood sampling or tissue biopsy, urine collection is simple, low-cost, and suitable for repeated testing, supporting routine workflows and longitudinal patient monitoring. Advances in molecular diagnostics have underscored the clinical relevance of genomic analysis, including nuclear DNA (nDNA) and mitochondrial DNA (mtDNA), which are implicated in a wide range of inherited and acquired diseases. This study evaluated the feasibility of extracting and detecting nDNA and mtDNA from trace cellular components in urine samples from healthy individuals, with emphasis on clinical laboratory implementation.

[Methods] Spot urine samples were collected from six healthy volunteers in their twenties. After centrifugation and washing, urinary cell pellets were lysed using a Proteinase K–containing 10% NaCl solution followed by heat treatment. DNA was purified by ethanol precipitation and resuspended in TE buffer. The presence of nDNA and mtDNA was assessed by PCR amplification of the FGFR3 gene and mitochondrial HV1/HV2 regions, respectively, with specificity confirmed by DNA sequencing.

[Results] Extractable DNA was obtained from five of six samples, with Qbit3.0 Fluorometer. PCR amplification of nDNA was observed in five samples, while mtDNA amplification was detected in all six samples.

[Conclusion] Urine specimens can serve as a reliable source of nuclear and mitochondrial DNA using simple procedures compatible with routine clinical workflows. Urine-based liquid biopsy represents a promising non-invasive and implementable genomic testing approach in biomedical laboratory science.

P-10-2

一般演題 Genetics

Transcriptomic endotype-dependent mortality risk associated with mitochondrial gene expression

Evidence from a large sepsis whole-blood transcriptomic cohort

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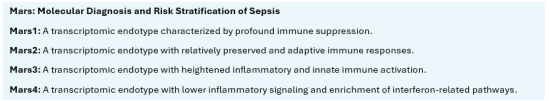
Sepsis is a highly heterogeneous syndrome characterized by diverse host-response states and variable clinical outcomes. Transcriptomic profiling has identified reproducible sepsis endotypes associated with mortality; however, mechanisms underlying outcome heterogeneity within these endotypes remain incompletely understood. Mitochondrial dysfunction has been implicated in sepsis pathophysiology, yet the prognostic significance of mitochondrial gene expression remains inconsistent. We performed and analysis of a large publicly available whole-blood transcriptomic sepsis cohort GSE65682. Patients were classified into four transcriptomic endotypes (Mars1–4) using established molecular signatures. Mitochondrial gene expression was quantified using single-sample gene set enrichment analysis with the MitoCarta gene set. Associations between endotypes, mitochondrial gene expression, and 28-day mortality were evaluated using Kaplan–Meier analysis and Cox proportional hazards models adjusted for age and sex, including endotype-stratified analyses.

Our result show that transcriptomic endotypes were strongly associated with 28-day mortality, with Mars1 exhibiting the highest risk of death. Mitochondrial gene expression differed significantly across endotypes. Higher mitochondrial gene expression was associated with increased mortality risk in the immunosuppressed Mars1 and Mars2 endotypes, but with reduced mortality risk in the immune-competent Mars3 endotype. These opposing associations indicate an endotype-dependent relationship between mitochondrial biology and clinical outcomes.

In conclusion, mitochondrial gene expression demonstrates endotype-specific, rather than uniform, associations with sepsis mortality. A transcriptomic endotype framework reveals prognostic relationships not apparent in unstratified analyses.



P-10-3

一般演題 Genetics

Standardizing RNA Extraction and RNA-Seq Library Prep Using LabDroid MAHOLO

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Introduction: Next-generation sequencing (NGS) has become an essential technology with the advancement of genomic medicine. To enhance research support, our facility introduced the NextSeq 500 in 2016. However, upstream processes of NGS, including RNA extraction and library preparation, involve highly complex workflows and require advanced technical expertise. Manual operation presents several challenges, including workflow complexity, inter-operator variability, susceptibility to human error, and prolonged hands-on time. In this study, we evaluated process standardization and data reliability in preparation for introducing the versatile humanoid robot LabDroid "MAHOLO" into clinical laboratory services. **Samples:** Number of samples: ~8,000.Total operational steps: ~700,000.Main processes:RNA purification (55 steps): >2,500 samples.RNA selection (103 steps): >2,800 samples.Library purification (96 steps): >2,800 samples. **Methods:** Total RNA (100 ng) extracted from mouse brain tissue was used for library preparation. Libraries were prepared using an rRNA depletion method with the NEBNext Ultra II RNA Library Prep Kit. Using MAHOLO, the entire workflow from RNA extraction to library purification was automated. The resulting sequencing data were evaluated in terms of expression profiles and reproducibility. **Results:** Expression consistency: Housekeeping gene expression showed no significant differences between runs.Reproducibility: Scatter plot analysis and replicate experiments demonstrated high correlation (r = 0.99).Operational robustness: Across approximately 700,000 automated steps, the system demonstrated stable performance suitable for practical use. — **Discussion:** Robotic automation improves precision and standardization of NGS workflows, reducing operator variability and errors while increasing throughput. **Conclusion:**Large-scale validation using actual biological samples demonstrated successful standardization of NGS library preparation using MAHOLO. Automation enhances workflow efficiency and supports standardized procedures to ensure data reliability.

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P-10-4

一般演題 Genetics

UGT1A1 Result Documentation and Subsequent Irinotecan Use in Solid Tumors

Insights Into the Real-World Use of UGT1A1 Results

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Objective: UGT1A1 genotyping supports irinotecan dose selection and safety management. This study evaluated how UGT1A1 results were documented in progress notes according to subsequent irinotecan use in patients with solid tumors.

Methods: We retrospectively reviewed 591 patients with solid tumors who underwent UGT1A1 testing between December 2020 and November 2025. Patients were classified as receiving irinotecan-containing therapy, having no subsequent irinotecan use, or having unknown treatment status. UGT1A1 phenotype, chemotherapy records, testing-to-treatment interval, and progress-note descriptions containing "UGT1A1" or "irinotecan/IRI" were analyzed.

Results: Among 591 patients, 426 received irinotecan-containing therapy, 136 had no subsequent irinotecan use, and 29 were unknown. In treated patients, the median interval from testing to administration was 14 days (IQR, 6–35). UGT1A1 and irinotecan were documented in the same clinical context in 221 treated patients; 219 had documentation referring to dose adjustment or adverse-event explanation. Among 28 treated poor metabolizers, 15 had documentation linking UGT1A1 results to dose reduction or toxicity risk. In the no-use group, UGT1A1-related descriptions were identified in 82 patients, whereas irinotecan-related descriptions were identified in 23. No description explicitly stated that irinotecan was avoided because of UGT1A1 results.

Conclusion: In treated patients, UGT1A1 results were commonly documented in association with dose adjustment and toxicity risk, suggesting that testing was incorporated into real-world irinotecan management. In non-treated patients, documentation rarely linked UGT1A1 results to non-use. Thus, UGT1A1 testing appeared useful for supporting safer irinotecan administration and real-world clinical decision support, whereas its role in excluding irinotecan or guiding alternative treatment choices was not evident from routine documentation.

P-10-5

一般演題 Genetics

Detection of Genetic Mosaicism using cfDNA

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Introduction: Genetic mosaicism is the coexistence of distinct genotypes within an individual. This phenomenon arises from somatic mutations and accumulates with age. Mosaicism is thought to occur across diverse tissues and may trigger various diseases, including cancer. Therefore, the early detection of genetic mosaicism facilitates early disease screening. However, identifying genetic mosaicism in specific organs requires invasive tissue biopsies. Cell-free DNA (cfDNA) —DNA fragments released into the circulation via— offers a potential solution. In healthy individuals, although most cfDNA originates from hematopoietic cells, it also contains small fractions derived from other organs. Therefore, cfDNA analysis enables non-invasive detection of genetic mosaicism across multiple tissues, potentially facilitating whole-body screening. In this study, we aimed to evaluate the feasibility of detecting genetic mosaicism by analyzing single-nucleotide variants in specific genes using cfDNA from healthy individuals.

Methods: 12 healthy individuals (6 males and 6 females, aged 10-69 years) were enrolled in this study. cfDNA was extracted from EDTA-plasma samples. Three target genes (*ZFP36L2*, *PPM1D* and *FAT1*) were analyzed using PCR. Target regions (147bp) with histone modifications were selected using ChIP-Atlas. Genetic mosaicism was evaluated by Sanger sequencing.

Results: No definitive genetic mosaicism was detected across the 12 samples; however, regions with a VAF below 20% were detected in *ZFP36L2* across several individuals, suggesting the existence of low-level somatic mutations.

Conclusion: cfDNA is predominantly derived from the hematopoietic system, with only trace amounts originating from solid organs. Since the current method is limited by 20% VAF threshold likely lacked the sensitivity to capture low-level genetic mosaicism. Future studies utilizing high-sensitivity digital PCR are required to precisely evaluate single-nucleotide variants. This approach holds great promise for non-invasive, multi-organ genetic screening.

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P-10-6

一般演題 Genetics

Impact of pre-analytical procedures on plasma microRNA expression

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[Objective] MicroRNAs (miRNAs) in biofluids such as plasma, serve as diagnostic and prognostic markers in various diseases. Despite recommendations for double centrifugation in miRNA extraction protocols, plasma is often processed using single centrifugation in clinical settings. To address this gap, we investigated two inflammation-related miRNAs to assess how pre-analytical procedures affect expression levels and to determine whether alternative pretreatment methods can replace double centrifugation.

[Methods] We recruited 28 healthy subjects. Total RNA, including miRNAs, was extracted from plasma using three protocols: double centrifugation (standard), single centrifugation (clinical practice), and single centrifugation followed by re-centrifugation after thawing (modified). miRNA expression levels were quantified by real-time PCR and normalized using a spike-in control (cel-miR-39) with the ΔΔCt method.

[Results] Bland-Altman analysis showed a proportional bias for miR-155-5p in the single centrifugation protocol and a fixed bias in the modified protocol. For miR-125b, both alternative protocols showed a fixed bias. To identify predictors of expression levels obtained with the standard protocol, correlation analyses were performed using miRNA expression levels and peripheral blood cell counts. For miR-155-5p, few variables were correlated, although a weak correlation was observed with the modified protocol ($r = 0.272$). In contrast, miR-125b showed correlations ($r > 0.3$) with several variables, including expression levels from the alternative protocols and blood cell counts. Linear regression with AIC-based variable selection failed to establish a reliable model for miR-155-5p. In contrast, miR-125b expression could be predicted by a combination of red blood cell count and expression levels from the modified protocol.

[Conclusion] These findings suggest that the modified protocol may serve as a practical alternative to the standard protocol for miR-125b when combined with red blood cell counts, but not for miR-155-5p.

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P-10-7

一般演題 Genetics

Migraine-Related Autonomic Changes Associated with *ASTN2* Polymorphism

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Background: Migraine is a common primary headache disorder; however objective diagnostic tools remain unavailable. Diagnosis relies largely on clinical interviews, as neuroimaging and laboratory tests have limited utility. Autonomic dysfunction and genetic susceptibility have been implicated in migraine, suggesting that integrating single nucleotide polymorphism (SNP) analysis with heart rate variability (HRV) may provide a novel approach to improve diagnostic accuracy.

Methods: The participants included 56 students and staff members from Shinshu University with complete SNP and HRV data. Five migraine-related SNPs (*ASTN2*, *MEF2D*, *PHACTR1*, *PRDM16*, and *SUGCT*) were genotyped using PCR and direct sequencing. HRV was recorded during 5-minute seated sessions, and RMSSD, SDNN, LF power, HF power, and the LF/HF ratio were analyzed following quality control. Migraine diagnosis was based on the ICHD-3 beta criteria. Univariate analyses and multivariable logistic regression (with AIC-based selection) were performed, with $p < 0.05$ considered statistically significant.

Results: Of the 56 participants, 13 had migraines and 43 did not. No significant differences were observed between groups in terms of age, BMI, family history, or HRV parameters. None of the five SNPs showed significant associations in the univariate analyses. However, in multivariable logistic regression, *ASTN2* carrier status (odds ratio [OR] 8.64), male sex (OR 0.12), family history (OR 6.32), and the LF/HF ratio (OR 0.10) were significant predictors of migraine. The final model demonstrated good discriminatory ability, with an AUC of 0.818, a cutoff of 0.210, sensitivity of 84.6%, and specificity of 69.8%.

Conclusion: This study suggests that combining *ASTN2* with the LF/HF ratio and HF power may provide a novel objective method for differentiating migraine. The *ASTN2* risk allele appears to be associated with a lower LF/HF ratio, indicating reduced sympathetic activity. Despite methodological limitations, this approach may enhance diagnostic accuracy and support more appropriate treatment selection.

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一般演題 Genetics

A NOVEL SLC4A3 VARIANT IDENTIFIED IN DILATED CARDIOMYOPATHY

PREDICTION ASSESSMENT OF SLC4A3 PATHOGENICITY USING A ZEBRAFISH MODEL

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[background] *SLC4A3* encoding anion exchanger 3 (AE3), a plasma membrane Cl-/HCO3- exchanger of cardiomyocytes regulates intracellular pH(pHi). Variants in this gene have been reported to contribute to short QT syndrome and to confer resistance to hypertrophic cardiomyopathy. However, the mechanisms by which *SLC4A3* influences these phenotypes remain poorly understood. In this study, we identified a novel *SLC4A3* variant in a patient with dilated cardiomyopathy (DCM) and aimed to investigate its potential pathogenic role.

[Methods and Results] Targeted sequencing of 180 genes associated with arrhythmias and cardiomyopathies identified a novel nonsense variant in *SLC4A3*: c.662C>G, p.Ser221Ter in a 62-year-old male patient diagnosed with DCM and atrial fibrillation/flutter. According to the ACMG/AMP guidelines, this variant was initially classified as a variant of uncertain significance (VUS). To assess its functional impact, we generated *slc4a3* knockout zebrafish using CRISPR/Cas9 and evaluated cardiac phenotypes in homozygous embryos. Compared with wild-type (WT) controls, homozygous mutants exhibited a significantly reduced ventricular ejection fraction, indicating impaired systolic function. In contrast, ventricular calcium transients showed no significant differences between WT and mutants. Unexpectedly, action potential duration in mutant ventricles was comparable to that in WT. However, ventricular conduction velocity was significantly reduced in mutants. These findings from functional analyses in the *slc4a3* knockout model support reclassification of this variant from VUS to likely pathogenic.

[Conclusions] The *slc4a3* knockout zebrafish model demonstrates ventricular systolic dysfunction and impaired conduction, supporting a pathogenic role of the *SLC4A3* variant in DCM. Further studies are warranted to elucidate the molecular mechanisms underlying *SLC4A3*-associated cardiac phenotypes.

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P-10-9

一般演題 Genetics

Evaluation of SNaPshot for detecting *BCR*::*ABL1* mutations

Comparison between SNaPshot and Sanger sequencing methods for detecting drug-resistant tyrosine kinase domain mutations

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Background: Some patients with Philadelphia chromosome–positive acute lymphoblastic leukemia (Ph+ ALL) or chronic myeloid leukemia develop resistance to tyrosine kinase inhibitors due to single nucleotide variants (SNVs) in the tyrosine kinase domain (TKD) of the *BCR*::*ABL1* gene. Sanger sequencing is widely used for mutation detection; however it is relatively labor intensive and time consuming. Therefore, this study used the SNaPshot Multiplex System (Thermo Fisher Scientific, Waltham, MA, USA) (SNaPshot) as an alternative approach and evaluated its performance.
Methods: Plasmid DNA containing the TKD from the minor *BCR*:*ABL1* gene (approximately 1.5 kb) derived from a patient with Ph+ ALL was used as a template. A total of 21 SNVs associated with high resistance and/or frequency were selected as targets. SNaPshot was evaluated using PCR and SNaPshot target primers previously optimized in-house. Detection performance was assessed using plasmids carrying individual target SNVs (mutant type, MT). Analytical sensitivity was evaluated using samples containing 0, 1, 5, 10, 25, 50, and 100% MT. Both SNaPshot and Sanger sequencing were used for the analysis.
Results: SNaPshot detected all target mutations in the MT samples except for several SNVs with mutations near the 3′ end of the primer binding site that interfered with primer binding. The analytical sensitivity ranged from 5–25%, which is comparable to that of Sanger sequencing.
Discussion: SNaPshot demonstrated sensitivity comparable to that of Sanger sequencing; however, it had a shorter processing time. These findings suggest that SNaPshot is a practical and efficient method for detecting clinical mutations. However, further improvements in analytical sensitivity and validation using patient-derived samples are required.

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P-10-10

一般演題 Genetics

G-banding decolorization XY FISH in secondary MDS detection: a case

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Introduction: Secondary myelodysplastic syndrome (MDS) is defined as MDS that develops following prior cancer therapy. We report a case in which XY FISH after G-banding decolorization was useful for detecting secondary MDS following hematopoietic stem cell transplantation for acute lymphoblastic leukemia.
Case presentation: A woman in her 50s was referred to our hospital with suspected acute leukemia and was diagnosed with minor *BCR*::*ABL1*–positive acute lymphoblastic leukemia. She received induction and consolidation therapies including dasatinib, achieved molecular remission, and subsequently underwent sex-mismatched allogeneic hematopoietic stem cell transplantation.
Cytogenetic and Molecular Analyses: Short tandem repeat (STR) PCR was performed to evaluate minimal residual disease after transplantation. On day 33, no recipient peak was detected; however, recipient peaks increased to 2.5% on day 112 and 11.6% on day 202 relative to donor peaks. Bone marrow examination on day 202 showed no apparent dysplasia, and minor *BCR*::*ABL1* PCR remained negative. G-banding analysis revealed a small number of abnormal metaphases with a complex karyotype, in which determination of sex chromosomes was difficult. The coordinates of abnormal metaphases on the G-banded slide were recorded, and the slide was subsequently decolorized for XY FISH analysis. Re-examination of the same metaphases demonstrated that all abnormal cells exhibited an XX signal pattern, indicating recipient origin. The karyotype was determined as 46,add(X)(p11.1),add(X)(q11),-2,add(3)(p25),add(4)(q21),add(7)(p22),add(9)(p11),-13,-15,+4–6mar[cp4]//46,XY[16].
Conclusion: In this case, XY FISH after G-banding decolorization was useful for confirming that the complex karyotype cells detected by G-banding were of recipient origin. Combined with the STR-PCR findings, these results contributed to the diagnosis of secondary MDS.

P-10-11

一般演題 Genetics

Simplification and Utility of Urine DNA Extraction Protocol

Aiming for a Lower-cost and Simpler Method

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[Background] Urine is a complex biological matrix with PCR inhibitors and low cellular concentrations, presenting challenges for nucleic acid extraction. However, recent liquid biopsy advances demonstrate the potential for detecting tumor-associated gene abnormalities in urinary DNA. As personalized medicine increases the demand for non-invasive sampling—moving beyond invasive tissue biopsies and minimally invasive blood or oral samples—urine emerges as a repeatable, entirely non-invasive alternative. This study focuses on establishing a simplified DNA extraction protocol from urine to evaluate its feasibility for clinical genetic diagnostics, providing a practical platform for disease risk prediction and hereditary syndrome diagnosis.

[Methods] Urine samples were obtained from three healthy volunteers in their 20s (one male, two females). Subsequently, after initial processing including centrifugation and washing with phosphate-buffered saline (PBS), each sample was randomly assigned a number from (1) to (3) and subjected to the corresponding DNA treatment: (1) no additional treatment (control), (2) thermal lysis at 95°C, and (3) mechanical homogenization using a Biomasher. DNA was extracted and subsequently amplified via PCR targeting specific genomic regions. The resulting amplicons were analyzed using 3% agarose gel electrophoresis to confirm presence and relative yield.

[Results] Agarose gel electrophoresis revealed distinct bands of the target molecular weight in both the control and the 95°C heat-treated samples. In particular, higher-concentration bands (those with more amplified products) were observed in heat-treated samples. Notably, the heat-treated group exhibited higher band intensity, indicating a superior yield of amplified DNA compared to the control.

[Conclusion] Thermal processing at 95°C effectively facilitates cell lysis and DNA elution, increasing concentrations. Although homogenization yielded no amplification due to insufficient cell recovery during aspiration, our simplified protocol successfully recovered detectable DNA from healthy urine. This non-invasive method offers significant clinical utility for future genetic testing and personalized molecular diagnostics.

P-10-12

一般演題 Genetics

Standardization and Clinical Evaluation of Circulating microRNAs

Quantitative Assessment of Atrial Remodeling in Atrial Fibrillation

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Background: Quantitative assessment of atrial remodeling in atrial fibrillation (AF) is important for early diagnosis and evaluation of disease severity, but current clinical tools, including electrocardiography and echocardiography, cannot accurately measure remodeling extent. Circulating microRNAs (miRNAs) have emerged as biomarkers that reflect atrial remodeling, such as fibrosis and electrical abnormalities, because they are stable in serum and compatible with standard real-time PCR analysis. Reliable quantification requires appropriate endogenous controls.

Objective: To standardize serum miRNA quantification by comparing candidate endogenous controls in healthy subjects and AF patients, and to assess the clinical utility of miRNAs associated with atrial remodeling in AF.

Methods: We analyzed serum samples from 22 AF patients (60.5 ± 14.2 years; M/F = 16/6) and 17 healthy controls (42.9 ± 9.8 years; M/F = 10/7). miRNAs from control participants were isolated from serum immediately following blood collection, whereas miRNAs from patients were extracted after eight months of storage at -80℃. After cDNA synthesis, qPCR was performed for four candidate endogenous controls (miR-30b, miR-30c, miR-191, and let-7d) and two AF-related miRNAs (miR-1 and miR-486). The Mann–Whitney U-test was used ($P < 0.05$).

Results: All four candidate endogenous controls yielded significantly higher Ct values in the AF group, indicating a lower miRNA abundance compared with controls. Among them, let-7d showed the least variation and was selected as an endogenous control for normalization. Normalized miR-1 expression was significantly downregulated in patients with AF.

Conclusion: The differences observed in endogenous control likely reflect extraction conditions, suggesting that long-term serum storage (eight months at −80°C) may contribute to miRNA degradation. Optimization of serum storage and preprocessing conditions is thus essential for reliable miRNA analysis. Our findings also suggest that miR-1 may serve as a potential biomarker for clinical assessment of atrial remodeling in AF.

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P-10-13

一般演題 Genetics

Cellular Deconvolution Methods for Cell-Free RNA in Liver Cancer

Cellular Deconvolution Methods for Cell-Free RNA in Liver Cancer

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Liver cancer remains one of the leading causes of cancer-related mortality worldwide. To solve issues with *cost, accessibility, and their ability to detect disease at an early stage,* l**iquid biopsy using circulating cell-free RNA (cfRNA)** has emerged as a promising minimally invasive alternative for cancer detection, disease monitoring, and treatment response assessment.

A major challenge in cfRNA analysis is its *cellular heterogeneity*, causing the cellular source of observed gene expression signals is often *unclear*, complicating biomarker discovery and biological interpretation. We hypothesize that **cellular deconvolution can improve the interpretation of cfRNA profiles** by estimating cell-of-origin contributions and identifying of cell-specific biomarkers for liver cancer.

To investigate this, we **utilized and benchmarked three tissue deconvolution approaches**: **BayesPrism**, a reference-based Bayesian framework; **nuSVR**, a reference-based machine learning method; and a **deep learning-based deconvolution model**, a reference-free approach.

Reference-based analyses revealed that **cfRNA profiles were predominantly composed of blood-derived signals**, whereas **liver-associated cell types contributed substantially smaller fractions**. Across two independent datasets, hepatocytes and cholangiocytes accounted for approximately 0.10–0.85% and 0.01–0.08% of the estimated cellular composition, respectively.

We also utilized **a neural network-based deconvolution framework** using tissue-specific RNA expression derived from a 22 healthy tissue atlas. **Semi-independent validation demonstrated strong predictive performance**, achieving Pearson correlation coefficients approaching 0.99.. **Independent validation further confirmed accurate tissue fraction estimation for most tissues, except for bladder and stomach**.

Overall, our findings demonstrate that **cellular deconvolution methods can recover biologically meaningful cell-of-origin signals from cfRNA** and provide a promising framework for *improving cell-of-origin inference* and *facilitating biomarker discovery in liver cancer liquid biopsy applications*.

P-10-14

一般演題 Genetics

Detection Rate of Trisomy 21 in AMA Pregnancies Undergoing Amniocentesis

A Five-Year Retrospective Study

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Background: Trisomy 21 (Down syndrome) is strongly associated with advanced maternal age (AMA). While non-invasive prenatal testing (NIPT) has become widely used, amniocentesis remains the gold standard for definitive prenatal diagnosis. This study evaluated the detection rate of Trisomy 21 in AMA pregnancies undergoing amniocentesis over a five-year period. Methods: A retrospective analysis was conducted on all amniocentesis procedures performed at our institution from January 2020 to December 2024. Only pregnancies in women of AMA (≥34 years) were included. Chromosomal analysis was performed using standard karyotyping techniques. Annual detection rates of Trisomy 21 were calculated. Results: A total of 7,306 amniocenteses were performed, with 5,282 (72.3%) involving AMA pregnancies. The annual detection rate of Trisomy 21 among AMA pregnancies ranged from 0.9% to 1.6%, with a slight decrease observed in 2022. Overall, detection rates remained stable, with no consistent temporal trend. Conclusion: Between 2020 and 2024, the detection rate of Trisomy 21 in AMA pregnancies undergoing amniocentesis remained stable. These findings reaffirm the continued relevance of amniocentesis as a definitive diagnostic tool and its essential role in genetic counseling for high-risk pregnancies.

Keywords: Trisomy 21; Down syndrome; advanced maternal age; amniocentesis; chromosomal analysis; non-invasive prenatal testing

P-10-15

一般演題 Genetics

Comprehensive Analysis of Genomic Alterations for Precision Oncology

Comparison Across Specimens and Sequencing Platforms

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Objective: Comprehensive genomic profiling (CGP) may produce different genomic alteration profiles depending on specimen type and sequencing platforms. This study aimed to compare genomic alterations across specimens and sequencing platforms using Genexus Oncomine Comprehensive Assay v3 (OCAv3) and the NCC Oncopanel system (NCC-OP). **Methods:** Sixteen patients with solid tumors (colorectal, pancreatic, lung, and breast cancers; n=4 each) were enrolled. Primary FFPE specimens submitted for clinical testing (NCC-OP or AmoyDx Pan Lung Cancer PCR Panel) and separate non-submitted FFPE specimens were analyzed using OCAv3. In the 12 non-lung cancer cases, OCAv3 results were compared with NCC-OP results. Concordance of genomic alterations was evaluated between paired specimens and sequencing platforms. **Results:** Comparison between paired specimens identified 42 genomic alterations. Among these, 24 alterations were shared between specimens, whereas 13 alterations were detected only in primary specimens and 5 only in secondary (non-submitted) specimens. Concordant alterations frequently involved ARID1A, BRAF, EGFR, ERBB2, KRAS, MYC, PIK3CA, RAD51, RB1, and TP53. Complete concordance across paired specimens was observed for ARID1A, BRAF, ERBB2, RAD51, and RB1. Comparison with NCC-OP demonstrated that 21 alterations were concordantly detected, whereas 17 alterations were identified only by NCC-OP and 11 only by OCAv3. Overall concordance, sensitivity, and specificity were 70.2%, 55.3%, and 80.4%, respectively. **Conclusions:** Major driver mutations were largely conserved between primary and secondary specimens, although several alterations showed discordant detection between specimens. In addition, platform-dependent differences likely reflected differences in target gene coverage and analytical characteristics. These findings highlight the importance of considering both specimen selection and sequencing platform characteristics in comprehensive genomic profiling.

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P-10-16

一般演題 Genetics

Evaluation of Exosome Isolation Methods

Comparison Between Serum and Plasma and the Impact of Freeze Storage

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Exosomes are extracellular vesicles secreted into the bloodstream via endosomal pathways and contain proteins and nucleic acids that reflect the physiological and pathological states of their cells of origin. In recent years, they have attracted considerable attention in cancer research as a promising source for “liquid biopsy” and the identification of novel biomarkers.

Although ultracentrifugation has traditionally been used for exosome isolation, its procedural complexity and requirement for specialized equipment limit its clinical applicability. Since 2015, various commercial kits for isolating exosomes from serum, plasma, and cell culture supernatants have been developed. In our previous study, we evaluated several extraction methods for exosomal RNA (ExoRNA) and demonstrated that ExoRNeasy (QIAGEN) provides high extraction efficiency (Morita K. et al., Igaku Kensa, 2022).

For clinical application of blood-based biomarkers, it is essential to evaluate factors that may affect extraction efficiency, including specimen type and storage conditions. In this study, we compared ExoRNA extraction efficiency between serum and plasma, and between samples stored at −80°C and those analyzed immediately after blood cell separation.

Blood samples from healthy individuals were used. Exosome marker proteins (CD9, CD63, and CD81) were analyzed by Western blotting, and RNA expression was evaluated using RT-qPCR.

RNA analysis showed no significant difference between fresh and frozen samples, while plasma yielded higher values for CD9 and CD63 than serum. Protein analysis also confirmed exosome markers under all conditions.

These findings support the feasibility of using frozen clinical samples for exosome-based biomarker studies and provide a basis for future identification of candidate biomarker genes from patient samples and cell culture supernatants.

P-10-17

一般演題 Genetics

Brushing lavage detects red complex bacteria better than mouth rinse

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Background: Molecular screening for periodontal pathogens is vital for the early prevention of both oral and systemic diseases. While collecting mouth rinse fluid is the standard non-invasive sampling method, its ability to harvest bacteria embedded deep within biofilms is often limited. This study aimed to evaluate whether a "brushing lavage" method could improve detection sensitivity compared to the conventional mouth rinse method.

Methods: The study involved four male subjects in their 50s (three with self-reported periodontitis and one asymptomatic control). Two types of specimens were collected from each subject using 10 mL of DNase/RNase-free water: (1) conventional mouth rinse and (2) brushing lavage, obtained by lightly brushing the periodontal pockets. DNA was extracted from all samples, and PCR analysis was performed targeting the Red Complex bacteria: Porphyromonas gingivalis, Treponema denticola, and Tannerella forsythia. All PCR products were sequenced and identified using NCBI BLAST to verify species homology.

Results: The brushing lavage method demonstrated significantly higher detection sensitivity than the mouth rinse method. In subjects with periodontitis, brushing samples consistently yielded clear PCR bands for the target bacteria, whereas mouth rinse samples often showed faint or negative results. Sequence analysis confirmed that all amplicons originated from the targeted bacterial species, validating the specificity of the method.

Conclusion: Our findings indicate that brushing lavage is superior to simple mouth rinsing for the genetic detection of periodontal pathogens. By physically disrupting the biofilm, brushing facilitates the collection of bacteria that are otherwise difficult to obtain, making it a more reliable and effective tool for non-invasive clinical screening.

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P-10-18

一般演題 Genetics

Role of Medical Technologists in Comprehensive Genomic Profiling in Japan

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Background In Japan, comprehensive genomic profiling (CGP) tests have been reimbursed under the national health insurance since June 2019. Medical technologists (MTs) play a pivotal role in ensuring the success rate of CGP tests. This study evaluated the clinical outcomes of CGP tests at Kansai Medical University Hospital.

Methods We retrospectively analyzed 486 cases who requested for CGP testing between January 2020 and March 2026. Data included cases demographics, cancer types, test modalities-tissue panels (FoundationOne CDx (F1CDx), OncoGuide NCC Oncopanel (NOP), and GenMineTOP) and liquid panels (FoundationOne Liquid CDx (F1LCDx), and Guardant360 CDx (G360CDx), expert panel (EP) assessment rates, turnaround time (TAT), and the proportion of patients who reached targeted therapies.

Results Of the 486 cases, 418 underwent CGP tests, while 68 were judged ineligible for the CGP tests by the Cancer Board, mainly because of the poor general condition. The submitted panels included F1CDx (n=283), G360CDx (n=59), GenMineTOP (n=42), F1LCDx (n=27), and NOP (n=7) cases. Four cases were switched to liquid biopsy following the failure of tissue-based CGP tests. Notably, sample failure occurred in only 4 cases (1.0%), demonstrating excellent pre-analytical management by pathologists and MTs. One case died before the EP. Consequently, 413 cases (98.6%) were reviewed by the EP. Among these cases, 111 were recommended for genomically matched therapies, and 20 subsequently received such treatments. Nine cases could not receive their CGP results because of death or hospitalization at another facility. Updated data will be presented at the meeting.

Conclusions The low sample failure rate (1.0%) highlights the crucial role of MTs in rigorous sample quality assessment for CGP tests.

P-10-19

一般演題 Genetics

Genetic Variation Analysis of the G6PD

Genetic Variation Analysis of G6PD in Neonate

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Congenital hypothyroidism (CH) is a common neonatal endocrine disorder that may interact with metabolic and oxidative stress pathways. Glucose-6-phosphate dehydrogenase (G6PD) plays a crucial role in maintaining redox homeostasis, and genetic variations in the G6PD gene have been implicated in several neonatal conditions. However, data regarding G6PD genetic variation in neonates with CH remain limited. This study aimed to analyze genetic variations of the G6PD gene in neonates diagnosed with congenital hypothyroidism using Sanger sequencing and bioinformatics analysis. Genomic DNA was extracted from peripheral blood samples of two neonates diagnosed with congenital hypothyroidism. PCR amplification targeting a ~700 bp fragment of the G6PD gene was performed using specific primers, followed by bidirectional Sanger sequencing. Sequence quality assessment, assembly, BLAST analysis, multiple sequence alignment, and phylogenetic reconstruction were conducted using standard bioinformatics tools. PCR amplification and Sanger sequencing were successfully performed for both samples. BLAST analysis showed 100% query coverage, 100% sequence identity, and E-value of 0.0 when compared with reference *Homo sapiens* G6PD sequences. Multiple sequence alignment demonstrated no nucleotide variation across the analyzed region. Phylogenetic analysis using the Neighbor-Joining method clustered both samples tightly with reference *Homo sapiens* G6PD sequences, confirming complete genetic conservation within the sequenced fragment. No genetic variation was detected in the analyzed region of the G6PD gene among neonates with congenital hypothyroidism in this study. These findings suggest that common G6PD sequence variants are unlikely to contribute to congenital hypothyroidism through this genomic region. Further studies involving larger cohorts and full-length gene sequencing are warranted.

Keywords: Congenital hypothyroidism, G6PD, genetic variation, neonates, Sanger sequencing

P-10-20

一般演題 Genetics

Application of Cytogenetic Biodosimetry in Radiation Workers

Enhancing Occupational Safety Tracking in Biomedical Laboratory Science

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Introduction: Occupational radiation monitoring is essential for nuclear medicine and radiology personnel. Physical dosimeters quantify exposure but not biological effects. Dicentric chromosome assay (DCA) and electron paramagnetic resonance (EPR) provide complementary biodosimetric information. This study evaluated their laboratory application for occupational radiation surveillance.

Materials and Methods: Peripheral blood and fingernail samples from 20 hospital radiation workers were analyzed under ethical approval. DCA calibration curves (0–5 Gy) were established using Co-60 irradiated blood, while EPR calibration curves (0–20 Gy) were generated from fingernails. Biological dose estimates were compared with longitudinal physical dosimetry records.

Results: Both DCA and EPR demonstrated strong dose-response relationships and technical feasibility. Radiation workers showed low-dose exposure within national safety limits. Although minor discrepancies existed between physical and biological measurements, both methods exhibited good reproducibility and readiness for routine laboratory use.

Discussion: Biodosimetry complements physical monitoring by providing biological evidence of radiation exposure. Biomedical laboratory scientists are central to specimen processing, quality assurance, and screening. Standardized DCA and EPR protocols may strengthen emergency preparedness, improve individualized risk assessment, and enhance occupational radiation protection.

Keywords: Biodosimetry; Dicentric Chromosome Assay; Electron Paramagnetic Resonance; Radiation Safety; BLS.

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P-10-21

一般演題 Genetics

Preliminary study of a novel *BRAF* V600E detection method

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[Introduction] BRAF is a key factor involved in cell proliferation and differentiation. *BRAF* gene mutations have been identified in a variety of tumors, including lung cancer, malignant melanoma, and thyroid cancer, with many of these mutations known to cluster at *BRAF* c.1799T>A p.Val600Glu (*BRAF* V600E) mutation. Current detection methods such as immunohistochemistry and PCR using commercial kits have limitations, including nonspecific staining reactions and high cost. Therefore, we conducted a preliminary study aimed at developing a novel, highly sensitive, and cost-effective method for detecting *BRAF* gene mutations.

[Materials and methods] We synthesized an artificial gene fragment harboring the *BRAF* V600E mutation and constructed a detection system based on an allele-specific PCR method, incorporating custom-designed fluorescent probes and primers. We evaluated the performance of this method for detecting the *BRAF* V600E mutation. We applied this method to 20 cases in which the presence or absence of the *BRAF* V600E mutation had been confirmed by immunohistochemistry or PCR using kits, and calculated the sensitivity and specificity for each.

[Results] Using the allele-specific PCR method with synthetic gene fragments, a fluorescent signal was detected only in samples harboring the *BRAF* V600E mutation. This method could be performed at a cost of approximately 1,000 yen per sample, making it more affordable than existing testing methods. In the detection limit assessment, the method detected mutant alleles at a frequency as low as 0.1% against a 99.9% wild-type allele background. In the evaluation of sensitivity and specificity, excellent results were obtained with 100% sensitivity and 100% specificity for both immunohistochemistry and PCR using kits.

[Discussion] Through this study, we established a highly sensitive and cost-effective *BRAF* V600E detection method capable of detecting as little as 0.1% of the mutant allele. Compared to existing detection methods, we obtained favorable results for both sensitivity and specificity.

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P-10-22

一般演題 Genetics

Culture-Negative Microsporidial Endophthalmitis Diagnosed by PCR and Electron microscopy

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【 Introduction 】 Microsporidia are obligate intracellular eukaryotic pathogens that primarily cause keratoconjunctivitis and myositis in immunocompromised hosts. Endophthalmitis caused by Microsporidia is rare, with particularly few cases reported in Japan. We describe such a case caused by Anncaliia algerae.

【Case Report】An 80-year-old immunocompromised woman (WBC 1,500/μL) with diffuse large B-cell lymphoma, rheumatoid arthritis on corticosteroids, and right-eye uveitis was referred for persistent inflammation and a white pupillary mass-like lesion after cataract surgery.

Microscopic examination and culture were performed on an intraocular mass, vitreous fluid, and perfusion fluid. Microscopy of the intraocular mass and perfusion fluid revealed organisms suspected to be yeast-like fungi, but culture results were negative. Based on the microscopic findings, a fungal infection was suspected; therefore, genetic analysis targeting the 28S rRNA D1/D2 region was performed. As a result, Anncaliia algerae, a species of Microsporidia, was identified by BLAST analysis with 99% sequence identity. Identification was confirmed using Microsporidia-specific SSU rRNA primers reported by Masafumi Uematsu et al.Transmission electron microscopy was then performed for definitive diagnosis. Polar tube structures characteristic of Microsporidia were confirmed in tissue attached to the posterior surface of the iris. Numerous ovoid spores approximately 3 μm in size were observed on the surface of the extracted intraocular lens. Based on these findings, the patient was diagnosed with endophthalmitis caused by Microsporidia.

【 Discussion and Conclusion: 】 Sequencing and electron microscopy established the diagnosis of microsporidial endophthalmitis caused by Anncaliia algerae.

PCR and electron microscopy are essential when Microsporidia infection is suspected, as standard fungal cultures fail to detect them.

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P-10-23

一般演題 Genetics

Molecular analyses of GALNT6 in luminal breast cancer

Subtype-specific transcriptomic association with estrogen receptor-related epithelial programs

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Purpose: Altered protein glycosylation is a hallmark of cancer and has been implicated in the regulation of tumor cell behavior and tissue organization. N-Acetylgalactosaminyltransferase 6 (GALNT6), an initiating enzyme of mucin-type O-glycosylation, has been associated with breast cancer progression. However, the subtype-specific molecular characteristics of GALNT6 in breast cancer remain unclear. This study aimed to investigate GALNT6-associated transcriptional programs in breast cancer using TCGA-BRCA datasets.

Methods: TCGA-BRCA transcriptomic datasets were analyzed using PAM50 subtype classification. Co-expression and functional enrichment analyses, including Gene Ontology, Reactome, and Hallmark analyses, were performed to characterize GALNT6-associated molecular pathways.

Results: GALNT6 expression was significantly elevated in luminal A breast cancer compared with basal-like tumors and normal breast tissue. GALNT6 positively correlated with luminal differentiation–associated genes, including ESR1, FOXA1, GATA3, AGR2, and SPDEF. Functional enrichment analyses demonstrated significant enrichment of mammary epithelial development, gland morphogenesis, apical membrane organization, and estrogen response pathways. Reactome and Hallmark analyses additionally exhibited enrichment of ESR-mediated signaling and estrogen-dependent transcriptional programs.

Conclusion: These findings indicate that GALNT6 is closely associated with luminal epithelial differentiation and ER-related transcriptional networks in luminal A breast cancer. This study highlights the subtype-specific molecular characteristics of GALNT6 and provides a transcriptomic framework linking glycosylation-associated pathways to luminal breast cancer biology.

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P-10-24

一般演題 Genetics

Analytical Validation of a Solid Tumor Comprehensive Genomic Profiling Assay

Analytical Performance of an NGS-Based Comprehensive Genomic Profiling Assay for Solid Tumors

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Background: Comprehensive genomic profiling (CGP) is the cornerstone of precision oncology. For laboratory-developed tests (LDTs), rigorous analytical validation and clinical concordance are essential before clinical implementation. This study evaluated an in-house CGP workflow utilizing the AVENIO Tumor Tissue CGP Assay, assessing its performance against established FoundationOne® CDx (F1CDx).

Methods: The assay interrogates 324 cancer-related genes to detect single-nucleotide variants (SNVs), small insertions/deletions (Indels), copy number alterations (CNAs), and rearrangements. It also reports complex biomarkers including tumor mutational burden (TMB), microsatellite instability (MSI), and loss of heterozygosity (LOH). Analytical sensitivity (LoD) was defined using HD753 reference standards. Clinical accuracy was assessed using 20 FFPE specimens previously characterized by F1CDx. Performance was summarized by positive/negative percent agreement (PPA/NPA) and overall concordance, with a predefined acceptance threshold of >90%.

Results: The assay demonstrated high sensitivity, with an LoD at allele frequency (AF) ≥5% for SNVs, Indels, and fusions, and ≥4.5 copies for CNAs. Clinical validation across 20 samples showed overall concordance exceeding 90% for all variant classes. For SNVs with allele frequency >5%, overall concordance was 99.9%, with PPA of 98.5% and NPA of 100.0%. Fusion and LOH exhibited 100.0% concordance, while CNA reached 99.5% agreement. Notably, although the initial MSI overall concordance was 90.9% (PPA=100.0%, NPA=87.5%), the single discordant case was adjudicated using an orthogonal 5-STR (Short Tandem Repeat) method, which confirmed MSI-high status and supported the AVENIO result. Furthermore, TMB showed near-perfect correlation with F1CDx (R^2=0.9994) across a range of 0 to >350 mut/Mb. Inter-operator and inter-run reproducibility were consistently 100.0%.

Conclusions: Our findings establish that the AVENIO CGP Assay provides the analytical rigor required for high-complexity clinical diagnostics. The exceptional concordance with FDA-cleared comparators and the ability to resolve complex discordant cases through orthogonal adjudication demonstrate that this in-house workflow is a robust, reliable solution for delivering actionable genomic insights in precision oncology.

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P-10-25

一般演題 Genetics

BRCA2 LOH Drives Melphalan Sensitivity in Vaginal Clear Cell Carcinoma

A Genomic Case Study on Melphalan Efficacy in Cisplatin-Refractory Clear Cell Carcinoma

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Background
Vaginal clear cell carcinoma is an aggressive malignancy lacking standard treatments after platinum failure. Melphalan generates DNA interstrand crosslinks (ICLs) requiring Fanconi anemia/homologous recombination (FA/HR) pathways for repair. We elucidate the genomic basis of an exceptional Melphalan response in a cisplatin-refractory patient.

Materials and Methods
We analyzed whole-exome sequencing (WES) data from matched germline blood, primary vaginal tumor, and a cisplatin-refractory lung metastasis. Our pipeline integrated somatic variant filtering, DNA damage response (DDR) prioritization, and LOH/HRD-proxy scoring.

Results
We identified a rare germline *BRCA2* missense variant (c.A1568G:p.H523R). Variant allele frequency elevated from the germline (0.52) and primary tumor (0.48) to the lung metastasis (0.71), confirming somatic loss of heterozygosity (LOH). Consequently, the metastasis exhibited profound genomic instability: a 5.1-fold higher LOH fraction, a genomic scarring index of 4, and a doubled tumor mutational burden. Pure-somatic analysis lacked DDR enrichments, proving the vulnerability was germline-driven.

Conclusion
Melphalan efficacy was strictly driven by biallelic *BRCA2* inactivation—a germline variant completed by somatic LOH exclusively in the metastasis. Disabling the FA/HR axis sensitized the tumor to Melphalan, overcoming prior cisplatin resistance. Integrated germline-plus-LOH WES analysis is crucial for uncovering precision medicine opportunities in rare malignancies.

Keywords
BRCA2, Whole Exome Sequencing, Melphalan, Loss of Heterozygosity

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P-10-26

一般演題 Genetics

A case of left craniofacial overgrowth with a *PIK3CA* variant

localized to the right buccal mucosa

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Introduction: *PIK3CA*-related Overgrowth Spectrum (PROS) is a mosaic disorder characterized by segmental overgrowth. Next generation sequencing (NGS) based ultra-deep sequencing and samples from affected regions have been recommended in previous reports. We report a case in which NGS-based analysis revealed a pathogenic *PIK3CA* variant only in buccal mucosa.

Case presentation: The patient was a 9-month-old girl born at 39 weeks of gestation with a birth weight of 3,566 g and a head circumference of 37.0 cm. She was referred to the Division of Medical Genetics for molecular diagnosis of PROS due to segmental overgrowth of the left craniofacial region and cutaneous capillary malformations. At referral, her weight was 10.1 kg (+2.1 SD) and head circumference was 46.3 cm (+1.7 SD). Whole exome sequencing (WES) did not identify pathogenic variants. Subsequently, WES using genomic DNA obtained from right buccal mucosa revealed a pathogenic *PIK3CA* variant (p.Arg115Pro). Additional ultra-deep sequencing demonstrated mosaicism, with variant allele frequencies (VAFs) of 29.6% in the right buccal mucosa and 7.0% in the left, whereas no variant was identified in the blood.

Discussion: Previous reports documented the importance of a combinational tissue-based approach and fresh samples from affected tissues for improving the diagnostic yield of PROS. Consistent with previous reports, our findings suggested the importance of a combinational tissue-based approach beyond blood samples for the molecular diagnosis of PROS. Notably, in contrast to previous recommendations, the pathogenic *PIK3CA* variant localized to the right buccal mucosa obtained from less affected side.

Conclusion: Our findings highlight the importance of NGS-based ultra-deep sequencing and a combinational tissue-based approach, including samples from less affected tissues, to improve the molecular diagnostic yield in mosaic disorders presenting segmental overgrowth.

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P-10-27

一般演題 Genetics

Implementation of Droplet Digital PCR for Circulating Tumor DNA Detection

Establishing a clinical testing platform for novel cancer markers at Oslo University Hospital

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Introduction

Many of today's tumor markers have limited use, and there is a need for improved biomarkers to evaluate treatment response and support more personalized cancer care. Circulating cell-free DNA (cfDNA) consists of double-stranded DNA fragments that can be detected in the blood of both healthy individuals and cancer patients. cfDNA is believed to be released actively into the bloodstream from cells and as a result of apoptosis and necrosis. Circulating tumor DNA (ctDNA) is a fraction of cfDNA that originates from cancer cells and reflects the genetic profile of the tumor, making it a promising biomarker. At the Department of Medical Biochemistry, Oslo University Hospital, we have implemented a Droplet Digital PCR (ddPCR) method to detect ctDNA in cancer patients.

Methods

Sixteen patients were included in this pilot study, and blood samples were collected in Streck Cell-Free DNA BCT® tubes at up to three different time points. Plasma was isolated by double centrifugation and frozen at –80 °C until further use.

cfDNA will be extracted from 4 mL of plasma using the EZ1&2 ccfDNA Kit for Automated cfDNA Extraction on the EZ2 Connect MDx (Qiagen) and analyzed using the Automated Droplet Generator and QX600 Droplet Reader (Bio-Rad Laboratories). Based on previously identified mutations in each patient's tumor, cfDNA will be analyzed using four different ddPCR Mutation Detection Assays from Bio-Rad: KRAS G12C, KRAS G12D, KRAS G13D, or the KRAS G12/G13 Screening Kit. In addition, cfDNA will be analyzed with a multiplex quality-control assay developed in Denmark to assess the quality of the samples. Results will be evaluated using the QX Manager Software.

Results and conclusion

The ddPCR experiments will be performed during the summer of 2026, and the results will be presented at the conference.

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P-10-28

一般演題 Genetics

Quantitative methylation analysis of LINC01869 for colorectal cancer diagnosis

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Background and Objectives: Colorectal cancer (CRC) ranks third in morbidity and second in mortality among all cancers worldwide, yet it is potentially curable when detected early. The fecal occult blood test, widely used for CRC screening, requires self-collection of stool samples, and the cumbersome nature of stool collection has led to suboptimal screening participation worldwide. Consequently, a simple and non-invasive screening method is desirable, and liquid biopsy based on blood collection has attracted attention as a promising alternative. We previously identified LINC01869, a long non-coding RNA (lncRNA) associated with CRC. This study aimed to identify informative CpG methylation sites within the LINC01869 promoter region using tissue specimens, and evaluate their utility for CRC detection in serum cell-free DNA (cfDNA).

Materials and Methods: DNA was extracted from paired tumor and non-tumor tissue specimens from four CRC patients. Bisulfite sequencing measured methylation levels at eight CpG sites (CpG #1–#8) in the LINC01869 promoter. Cell-free DNA (cfDNA) from serum of 37 CRC patients (cancer group) and 38 non-cancer patients was then analyzed using the combined restriction digital PCR assay (CORD assay) to quantify methylation rates.

Results: In tissue specimens, CpG #8 showed significantly higher methylation in the cancer group ($p = 0.034$), and co-methylation of CpG #2-3 trended higher ($p = 0.063$). In cfDNA, both markers showed significantly higher methylation in the cancer group (both $p < 0.0001$), with AUC values of 0.843 and 0.823, respectively. Methylation levels of CpG #8 and CpG #2-3 showed a strong positive correlation ($r = 0.94$, $y = 1.18x + 2.56$).

Conclusion: LINC01869 is a promising biomarker for CRC liquid biopsy. The strong correlation between the two methylation markers suggests that either marker alone may suffice, enabling assay simplification for large-scale screening. Further case accumulation is needed to confirm clinical utility.

P-10-30

一般演題 Genetics

Haplotype selection improves chimerism quantification accuracy

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Background: Chimerism quantification is essential for monitoring engraftment and relapse after allogeneic hematopoietic stem cell transplantation. SNP-based NGS assays enable sensitive chimerism analysis. However, single-SNP markers are susceptible to PCR and sequencing errors. Haplotypes with SNP clusters may reduce these errors and improve accuracy. We developed a haplotype-based chimerism assay and investigated factors affecting quantitative performance.
Methods: Sequencing was performed using the Ion GeneStudio S5 Plus System with the MH-74 Plex Research Panel (74 regions, 227 SNPs), and haplotypes containing 2–5 SNPs were analyzed. Three mixtures containing 1% recipient DNA were analyzed to evaluate the effect of donor–recipient SNP differences within informative haplotypes. Recipient proportions were calculated for each haplotype, and relative deviation from expected values was assessed. Haplotypes differing by a single SNP were compared with those differing by ≥2 SNPs. Subsequently, 26 post-transplant samples from 10 patients were analyzed using haplotypes with ≥2 SNP differences. Relative deviation was further evaluated according to SNP count per haplotype, donor/recipient zygosity, and shared donor–recipient alleles.
Results: In the 1% recipient DNA mixtures, 132 haplotypes were analyzed. Haplotypes differing by ≥2 SNPs showed significantly lower relative deviation and more stable quantification than those differing by a single SNP ($p < 0.001$). In clinical samples, 423 haplotypes were analyzed. Haplotypes containing shared donor–recipient alleles tended to yield higher estimated recipient proportions, whereas non-shared haplotypes tended to yield lower proportions. SNP count per haplotype and donor/recipient zygosity had no significant effect on quantitative accuracy.
Conclusion: Restricting analysis to haplotypes differing by ≥2 SNPs improved quantitative accuracy and stability, supporting reliable post-transplant chimerism assessment.

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P-10-32

一般演題 Genetics

Relationship Between Mutant Ataxin-3 Protein and Mitophagy in SCA3 Patients

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Neurodegenerative diseases are conditions that progressively damage the structure and function of the nervous system. These conditions usually develop slowly, and the effects and symptoms tend to appear later in life. Spinocerebellar ataxia type 3 (SCA3), also known as Machado-Joseph Disease (MJD), is an autosomal dominant neurodegenerative disease. MJD often begins as progressive symptoms accompanied by motor incoordination, dysarthria, infrequent blinking, and cognitive decline. SCA3 is the most prevalent subtype of SCAs in Taiwan, accounting for approximately 45% of all SCAs patients. In the study, we focus on the difference between the gene and protein expression in two SCA3 patients (MJD07, MJD08) and a healthy person (LCL). PCR analysis show an expansion of the CAG repeat in the ATXN3/MJD1 gene on chromosome 14 in SCA3 patients, which leads to the translation of mutant ataxin-3 protein and confirmed the diagnosis of SCA3 in both MJD07 and MJD08 patients. Western blot analysis further demonstrated that the mutant ataxin-3 protein promoted the phosphorylation of mitochondrial proteins ERK1/2 in the lymphoblastoid cells of MJD patients. Mitophagy proteins LC3 I and LC3 II, as well as autophagy related proteins Atg5, Atg7, and Atg12 were significantly upregulated, indicating autophagy activity enhanced in both MJD07 and MJD08 patients. Images from electron microscopy show that autophagosomes in the cytoplasm of MJD07 cells encapsulated abnormally aggregated proteins. The phenomenon suggests that the mutant ataxin-3 protein triggers mitochondrial damage and protein aggregation, which are subsequently cleared through autophagy. The process represents a common cellular protective mechanism in neurodegenerative diseases. Based on these findings, we propose that inhibiting the expression of mutant ataxin-3 protein or regulating mitochondrial autophagy pathways could be potential therapeutic strategies to mitigate the progression of SCA3.

Key words: Neurodegenerative diseases, Spinocerebellar Ataxia Type 3 (SCA3), Mitophagy, Mutant Ataxin-3, ERK1/2 phosphorylation

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P-10-33

一般演題 Genetics

The neuroprotective effect of Caffeic acid phenethyl ester on SCA3

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Spinocerebellar ataxia type 3 (SCA3), also known as Machado–Joseph disease (MJD), is the most common autosomal dominant spinocerebellar ataxia worldwide. Healthy individuals carry 13–36 CAG-trinucleotide repeats in the ATXN3 gene on chromosome 14q24.3-q31, whereas patient with SCA3 possess expanded alleles of 51-79 CAG. Although the detailed pathogenic mechanism remains to be fully elucidated, both ferroptosis and oxidative stress—particularly reactive oxygen species (ROS) released from aggregated mutant proteins play pivotal roles in the disease progression. Caffeic acid phenethyl ester (CAPE) possesses antioxidant, anti-inflammatory, and immunomodulatory activities. The purpose of this study was to investigate the neuroprotective role of CAPE against mutant ataxin-3 induced toxicity in SK-N-SH-MJD78 cells, with a specific focus on its potential anti-ferroptotic mechanisms. Accordingly, we evaluated the effects of CAPE on apoptosis, autophagy, Nrf2/Keap1 pathways, mitochondrial membrane potential, lipid peroxidation, and intracellular labile iron levels. Our results showed that pre-treatment with CAPE significantly attenuated caspase-3 activities and apoptotic nuclear changes in SK-N-SH-MJD78 cells. Moreover, CAPE modulated the Nrf2/Keap1 pathway and increased LC3-II and p62 protein expression. Notably, further investigation into its auxiliary anti-ferroptotic effects revealed that MJD78 cells exhibited a decrease in MitoTracker Red signal accompanied by an elevation in BODIPY 581/591 C11 fluorescence, indicating mitochondrial impairment and lipid peroxidation. Strikingly, treatment with CAPE (50 and 100 nM) effectively reversed these alterations by restoring mitochondrial membrane potential and suppressing lipid ROS accumulation. In conclusion, these findings demonstrate that CAPE exerts robust neuroprotective effects primarily by suppressing cytotoxicity, modulating Nrf2/Keap1-mediated autophagy, and partially alleviating ferroptotic stress, highlighting its therapeutic potential for SCA3.

Keywords: Spinocerebellar ataxia type 3 (SCA3), Caffeic acid phenethyl ester (CAPE), Ferroptosis, Mitochondrial dysfunction, antioxidant, Nrf2/Keap1 pathway

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P-10-34

一般演題 Genetics

Evaluation of miRNA Enhance Buffer for Improving microRNA Recovery Efficiency

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Background: MicroRNAs (miRNAs) are small non-coding RNAs involved in the post-transcriptional regulation of gene expression and are associated with cancer progression and therapeutic resistance. Recently, miRNAs have attracted attention as biomarkers for the diagnosis and monitoring of various diseases, including cancer. Their application to liquid biopsies using blood, urine, and other body fluids is also expected. However, because miRNAs are short RNA molecules, their recovery efficiency can be affected by the sample type and extraction method. Therefore, optimizing the extraction process is essential for stable miRNA analysis. This study evaluated the effect of miRNA Enhance Buffer (KANTO CHEMICAL CO.,INC) on improving miRNA recovery efficiency using several commercially available RNA extraction kits. **Methods:** K562 cells were used for basic evaluation. Cica Geneus RNA Prep Kit (for Tissue) 2 (KANTO CHEMICAL CO.,INC), High Pure miRNA Isolation Kit (Roche), High Pure RNA Isolation Kit (Roche), miRNeasy Mini Kit (QIAGEN), and RNeasy Mini Kit (QIAGEN) were compared using their standard protocols and protocols supplemented with miRNA Enhance Buffer (KANTO CHEMICAL CO.,INC). miR-21 was measured using stem-loop RT-qPCR, and Cp values were compared. To assess the applicability to clinical specimens, miR-16 and miR-21 were also measured in human peripheral blood leukocytes, healthy urine sediment, stool samples, and plasma-derived extracellular vesicles. **Results:** In K562 cells, the addition of miRNA Enhance Buffer decreased the Cp value of miR-21 in several RNA extraction kits, suggesting improved miRNA recovery efficiency. In clinical specimens, decreased Cp values were also observed in peripheral blood leukocytes, urine sediments, stool samples, and plasma-derived extracellular vesicles. Notably, the stool samples showed marked decreases in Cp values for both miR-16 and miR-21. **Conclusion:** The miRNA Enhance Buffer may improve miRNA recovery efficiency in RNA extraction kits and may be applicable to liquid biopsy specimens. This method could be useful as a pretreatment approach for miRNA analyses.

P-10-35

一般演題 Genetics

Polyamine-Based Nucleic Acid Recovery Method

Application to Liquid Biopsy and Methodological Development

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[Background] Liquid biopsy enables minimally invasive disease assessment and monitoring through analysis of cell-free DNA (cfDNA), microRNA (miRNA), and extracellular vesicle-associated molecules in liquid samples. However, these targets are often present at low concentrations, especially in urine and saliva. A simple, low-cost method that can process large sample volumes and concentrate nucleic acids would facilitate broader clinical laboratory applications. We developed a novel polyamine-based nucleic acid recovery method and evaluated its utility as a pretreatment method for liquid biopsy analysis.

[Materials and Methods] K562 culture supernatants and urine samples from healthy individuals were used to evaluate cfDNA and miRNA detection and to examine changes in recovery according to sample volume, up to 40 mL. In this method, one-tenth volume each of polyamine solution and 5 M NaCl was added to the sample, followed by centrifugation. Nucleic acids were extracted from the resulting pellet. cfDNA was extracted using the High Pure PCR Template Preparation Kit (Roche), and miRNA was extracted using the Cica Genius RNA Prep Kit (for tissue) 2 with miRNA Enhance Buffer (KANTO CHEMICAL). The method was also applied to plasma and saliva samples from healthy individuals.

[Results] The polyamine-based method enabled detection and quantification of cfDNA and miRNA from K562 culture supernatants and urine samples. Measured cfDNA and miRNA levels changed with increasing sample volume, indicating that larger-volume processing can enhance recovery from low-concentration liquid samples. cfDNA and miRNA were also detected in plasma and saliva samples.

[Conclusion] The polyamine-based method provides a simple and inexpensive approach for concentrating and recovering cfDNA and miRNA from culture supernatants and body fluids. This method may serve as a practical pretreatment platform for expanding liquid biopsy analysis in clinical laboratory testing.

P-10-36

一般演題 Genetics

xCT expression in astrocytes on glutamate metabolism under hypoxic environment

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Background

Acute symptomatic seizures are thought to result from increased neuronal excitability due to excessive glutamate accumulation in the synaptic cleft during the acute phase of stroke. Astrocytes take up synaptic glutamate via glutamate transporters; however, other pathways involved in glutamate metabolism remain largely unclear. This study aimed to elucidate astrocytic glutamate metabolism under ischemic conditions, with a focus on the cystine/glutamate exchanger (xCT), which maintains intracellular redox homeostasis and protects against reactive oxygen species (ROS)-induced damage.

Methods

The relationship between HIF-1α, a hypoxia-responsive transcription factor, and xCT was examined in cultured astrocytes (SVGp12) under control, low-glucose, hypoxic, and oxygen-glucose deprivation (OGD) conditions using YC-1 and erastin. Cultured astrocytes exposed to each condition for 16 hours were analyzed using RT-qPCR and Western Blotting. Welch's t-test was used for statistical analysis. Statistical significance was set at $P < 0.05$.

Results

The OGD condition increased HIF-1α levels in astrocytes by 9.82-fold compared with controls ($p < 0.05$). Nuclear translocation was also observed. xCT protein expression decreased to 0.56-fold ($p < 0.05$). Consistent with these changes, intracellular glutamate levels increased 2.7-fold ($p < 0.05$). Although HIF-1α protein increased when xCT was inhibited at normal oxygen levels, no nuclear translocation was observed. Also, intracellular glutamate levels didn't increase. Inhibitor analysis suggested that HIF-1α activation and nuclear translocation contribute to intracellular glutamate accumulation via downregulation of xCT.

Conclusion

HIF-1α mediated downregulation of xCT promotes intracellular glutamate accumulation in astrocytes, which may play a protective role under ischemic conditions. These findings suggest that this pathway may serve as a potential therapeutic target.

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P-10-37

一般演題 Genetics

Splicing Analysis of Novel *PROS1* Variant in Protein S Deficiency

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Purpose: We identified a novel variant in *PROS1*, the gene encoding protein S (PS), in a patient with inherited PS deficiency. We aimed to elucidate its pathogenic mechanism, focusing on aberrant RNA splicing.
Case Presentation: The proband was a 60-year-old man with a history of proximal deep vein thrombosis and cerebral infarction at the age of 51. His total PS antigen level was within the normal range at 86%, whereas PS activity was reduced to 25.5%. After obtaining informed consent, direct sequencing analysis of *PROS1* identified a novel heterozygous c.965G>A variant at the 3' end of exon 9.
Methods: (1) A minigene vector was constructed by cloning the *PROS1* genomic region spanning exons 8–10, amplified from genomic DNA extracted from the proband's leukocytes, into pcDNA3.4. After transfection into HEK293 cells, RNA was extracted and analyzed by RT-PCR, electrophoresis, and sequencing to evaluate splicing products. (2) mRNA extracted from leukocytes of the proband and a healthy control was analyzed using the same procedures.
Results: (1) Cells transfected with the wild-type *PROS1* minigene showed a band corresponding to the normally spliced transcript, whereas cells transfected with the mutant minigene showed a shorter band. Sequence analysis confirmed complete skipping of exon 9 in the mutant transcript. (2) RT-PCR analysis of leukocyte-derived mRNA from the proband and a healthy control detected only normally spliced transcripts. Sequence analysis did not detect mutant-derived transcripts.
Discussion: Minigene analysis demonstrated aberrant splicing with exon 9 skipping in the mutant allele. However, aberrant transcripts were not detected in patient-derived mRNA. One possible explanation is that aberrant splicing generated a premature termination codon, possibly leading to degradation of the mutant transcript through nonsense-mediated mRNA decay. These findings suggest that the c.965G>A variant may contribute to PS deficiency through aberrant splicing of *PROS1* transcripts.

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P-10-38

一般演題 Genetics

The expression of stress-related mitochondrial non-cording RNA in hair shaft

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Objective
Psychological stress exacerbates various psychiatric and neurological diseases. However, reliable biomarkers for objectively assessing long-term psychological stress have not yet been established. In this study, we investigated the association between psychological stress and ASncmtRNA-2, a mitochondria-derived long non-coding RNA (ncmtRNA) present in the hair shaft and can be collected non-invasively.
Methods
Ten patients with epilepsy (8 females; aged 23–57 years) and ten healthy controls (10 females; in their 20s) were enrolled in this study. Psychological stress was assessed using the Stress Response Scale-18 (SRS-18) prior to hair sample collection. Total RNA was extracted from the samples, and ASncmtRNA-2 expression levels were analyzed by RT-qPCR.
Results
Subjective psychological stress assessed using the SRS-18 was higher in the patient group than in the control group across all stress categories, with 1.04-fold higher scores for Depression, 1.13-fold for Anger, 1.12-fold for Apathy, and 1.12-fold for Total Stress. Among participants classified as having low-stress, patients exhibited 1.8-fold higher "Apathy" scores and 1.5-fold higher "Total Stress" scores related to hair ASncmtRNA-2 compared with controls. Moreover, in the high-stress group, which included both patients and controls, subjective stress scores were significantly correlated with ASncmtRNA-2 expression for "Depression" (r = 0.83) and "Total Stress" (r = 0.77), suggesting differential regulation depending on stress level. Across four analyses, no significant decrease in expression levels was observed with hair growth, suggesting that ASncmtRNA-2 is a stable molecule.
Conclusion
These findings suggest that ASncmtRNA-2 in the hair shaft may serve as a novel, non-invasive biomarker of assessing psychological stress.
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P-11-a-1

一般演題 Others1 (Physiology)

Developing a Framework for Cognitive Age Estimation.

Using Multidomain Cognitive Scores.

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Background: In a previous study, we developed an original cognitive function assessment encompassing temporal and spatial orientation, memory, delayed recall, calculation, repetition and backward recall, writing, and figure copying, incorporating precise response time measurement. The assessment was administered to 63 cognitively healthy adults aged 21–88 years. Higher total scores were observed among older participants, indicating greater sensitivity to age-related declines in processing speed rather than pathological cognitive impairment.

Objective: Based on these findings, this study aimed to develop a computational program to estimate predicted cognitive age and its associated prediction interval using normative data from healthy adults.

Methods: Using data from the prior study, the relationship between assessment scores and chronological age was analyzed. Isotonic regression with a monotonic increasing constraint was applied to construct a smoothed normative reference curve. Predicted cognitive age was derived from the corresponding position on this curve for each input score. A standardized report template was also developed to provide clear and interpretable feedback.

Results: The program generated predicted cognitive age values with 60% prediction intervals across all input scores. Interval width varied systematically with score level, with narrower intervals in the mid-range and wider intervals at the extremes. Intervals exceeding 90% were substantially broader and considered less suitable for practical user interpretation.

Conclusions: Predicted cognitive age may facilitate intuitive understanding of cognitive status; however, the limited sample size and age distribution bias indicate the need for further validation. Broader implementation will require an integrated digital framework. This feature is intended for educational use only and does not constitute medical diagnosis or treatment.

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P-11-a-2

一般演題 Others1 (Physiology)

Development of a real-time neurofeedback analysis method using magnetoencephalography.

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Post-stroke rehabilitation plays a critical role in functional recovery. Previous studies have demonstrated that rehabilitation following brain injury promotes functional and structural reorganization of the brain, leading to improvement in motor function. Rehabilitation using electroencephalography-based neurofeedback has also shown clinical utility. Magnetoencephalography (MEG) is a noninvasive neuroimaging technique that provides high temporal and spatial resolution for evaluating brain activity and is widely used in clinical and research settings. However, in rehabilitation applications, MEG analysis has primarily relied on off-line mapping of sensory and motor functions. Consequently, brain activity during rehabilitation cannot be evaluated in real time, and no established analytical method currently exists for real-time assessment of brain function using MEG.

To develop an analysis method suitable for real-time neurofeedback systems, we compared the speed and accuracy of three analytical approaches for detecting event-related desynchronization (ERD) and event-related synchronization (ERS) during finger movement tasks in healthy subjects. The evaluated methods included fast independent component analysis with 10 components (ICA_n10), fast independent component analysis with 20 components (ICA_n20), and spatial-spectral decomposition (SSD).

The results showed that ICA_n20 achieved high classification accuracy for ERD and ERS patterns but required the longest processing time (3–5 seconds), limiting its applicability to real-time neurofeedback. Using classification criteria derived from experimental data, ICA_n10 classified the greatest number of trials into ERD and ERS patterns, with an analysis time of approximately 2 seconds or less. These findings indicate that ICA_n10 provides an optimal balance between accuracy and processing speed and is suitable for real-time MEG-based neurofeedback systems, suggesting potential applicability in clinical rehabilitation.

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P-11-a-3

一般演題 Others1 (Physiology)

Motor function assessment using second lumbrical CMAP in CTS

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【Objective】
In severe carpal tunnel syndrome (CTS), compound muscle action potentials (CMAPs) from the abductor pollicis brevis (APB) are frequently unrecordable, limiting evaluation of motor nerve function. This study aimed to assess the clinical usefulness of second lumbrical (2L) CMAP and to compare its electrophysiological characteristics with those of APB CMAP in patients with CTS.
【Methods】
We retrospectively analyzed 123 patients diagnosed with CTS. Motor nerve conduction studies were performed using standard techniques with wrist stimulation, and CMAP amplitudes were recorded from the APB and 2L muscles. Associations between 2L CMAP amplitude and distal motor latency were evaluated to assess its relevance to motor nerve impairment. In patients who underwent carpal tunnel release, pre- and postoperative changes in CMAP amplitudes were analyzed (n = 47). In addition, the recordability of CMAPs was examined on a hand-based level to evaluate their clinical applicability, particularly in severe CTS.
【Results】
2L CMAP amplitude showed a significant negative correlation with distal motor latency ($r = -0.453$, $p < 0.001$), indicating its association with motor nerve dysfunction. In surgical cases, both APB and 2L CMAP amplitudes improved after decompression; however, the magnitude of improvement differed between the two muscles. Notably, in 18 hands with absent APB CMAP, 2L CMAP remained recordable in 17 hands (94.4%). Overall, the recordability rate was significantly higher for 2L CMAP than for APB CMAP (99.4% vs. 88.7%, $p < 0.001$).
【Conclusion】
2L CMAP provides clinically useful complementary information for evaluating motor function in CTS, particularly in severe cases where APB responses are absent. These findings suggest that motor involvement in CTS may not be uniform across distal median nerve branches, and that different muscles may reflect distinct aspects of motor nerve dysfunction.

P-11-a-4

一般演題 Others1 (Physiology)

Changes in Body Composition and the Cardio-Ankle Vascular Index

A Longitudinal Study in Children

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[Aims] The Cardio-Ankle Vascular Index (CAVI) is a noninvasive marker of arterial stiffness widely used in clinical practice. However, its applicability and interpretation in children remain unclear. We have previously reported an inverse cross-sectional association between obesity indices and CAVI in children. This study aimed to evaluate the relationship between longitudinal growth-related changes in body composition and CAVI. **[Methods]** A total of 441 primary and secondary school students (mean age 10.4 years) who underwent CAVI measurements in both 2024 and 2025 were analyzed. CAVI was measured using the VaSera VS-3000TE (Fukuda Denshi, Tokyo, Japan). Body composition was assessed by bioelectrical impedance analysis (MC-780A-N, Tanita, Tokyo, Japan), including body fat percentage, fat mass, lean body mass, and muscle mass. The Rohrer index was used as an indicator of obesity. Associations between one-year changes in body composition and CAVI were examined.

[Results] CAVI showed no significant change over one year. The Rohrer index decreased, while body fat percentage, fat mass, muscle mass, and fat-free mass increased. Changes in CAVI were weakly but consistently inversely correlated with changes in the Rohrer index and BIA-derived indices. **[Discussion]** These findings suggest that increases in adiposity may be associated with lower CAVI values in children, possibly reflecting physiological vascular adaptation or autonomic regulation. From a laboratory perspective, this inverse relationship may affect the interpretation of CAVI as a stiffness marker in pediatric populations. **[Conclusion]** Longitudinal growth-related changes in body composition were inversely associated with changes in CAVI in children. Careful interpretation of CAVI is warranted in obese pediatric individuals, as values may underestimate arterial stiffness.

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P-11-a-5

一般演題 Others1 (Physiology)

Ictal Dynamics on Wide-Band Electroencephalography in Childhood Absence Epilepsy

Direct current shifts and high-frequency oscillations as candidate biomarkers of preictal-to-ictal transition

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Purpose: Conventional scalp electroencephalography (EEG) has primarily assessed signals within the 1–70 Hz range. Recent advances in digital technology have expanded this assessment to include lower-frequency direct current (DC) shifts (< 0.1 Hz) and high-frequency oscillations (HFOs; > 80 Hz), enabling wide-band EEG analysis. However, ictal wide-band EEG findings in childhood absence epilepsy (CAE) remain unclear. We aimed to characterize the ictal dynamics of DC shifts and HFOs using wide-band scalp EEG to identify potential biomarkers for the preictal-to-ictal transition.

Methods: We retrospectively analyzed three typical absence seizures in two girls with CAE (aged 7 and 8 years) recorded during hyperventilation. To isolate specific signal components from the wide-band data, we utilized a 2-second time constant for ictal DC shift identification. Ictal HFOs (80–250 Hz) were assessed using an 80-Hz high-pass filter and time-frequency spectrographic analysis. The temporal relationship among ictal DC shifts, the first generalized spike-and-wave complex (SWC), and ictal HFOs was evaluated across all seizures.

Results: A consistent temporal sequence was observed in all examined seizures. A negative ictal DC shift appeared several hundred milliseconds before the first SWC and deepened at seizure onset. Subsequently, ictal HFOs emerged immediately after the initial SWC and were strictly phase-locked to the spike component. Notably, these HFOs exhibited a characteristic frequency evolution, beginning with an early upward shift followed by a gradual downward evolution. This dynamic pattern was reproducible both within and between patients.

Conclusion: Wide-band scalp EEG may serve as a noninvasive candidate biomarker of early ictal activity in CAE by demonstrating distinct ictal DC shifts and HFOs at seizure onset. This approach may improve the physiological characterization of early seizure dynamics and facilitate the identification of a measurable preictal-to-ictal transition on scalp EEG.

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P-11-a-6

一般演題 Others1 (Physiology)

Validity of Smart Ring-Derived Sleep Parameters Compared With Electroencephalography

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【Objective】
Wearable devices enable convenient assessment of sleep in daily life. Smart rings, in particular, impose minimal burden and facilitate long-term continuous monitoring; however, their validity and agreement with electroencephalography (EEG)-based sleep assessment remain unclear. In the present study, we evaluated the validity of smart ring-derived sleep parameters using simultaneous recordings with a portable EEG device.

【Methods】
In total, 52 university students (mean age 19.2 years; 45 females) underwent simultaneous overnight monitoring with a smart ring (SOXAI Co., Ltd.) and portable EEG device (Proassist Co., Ltd.). Sleep parameters, including total sleep time (TST), sleep onset latency (SOL), wake after sleep onset (WASO), and sleep stages, were compared between devices.

【Results】
The median TST was similar between the smart ring and portable EEG device (315 vs. 343 minutes), demonstrating a strong correlation ($r = 0.70$, $p < 0.01$), but no significant correlations were observed for SOL or WASO. Regarding sleep staging, a modest correlation ($r = 0.45$, $p < 0.01$) was observed for light sleep (N1 + N2), whereas no significant correlations were noted for deep sleep (N3) or rapid eye movement (REM) sleep. In the Bland-Altman analyses, the smart ring systematically overestimated WASO and deep sleep compared with the portable EEG device.

【Conclusions】
Although smart rings provide a reliable estimate of TST and may be useful for long-term sleep monitoring in real-world settings, their limited accuracy for sleep staging and sleep fragmentation metrics warrants cautious interpretation. Further refinement of sleep staging algorithms is needed to improve their clinical applicability.

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P-11-a-7

一般演題 Others1 (Physiology)

Development of a New Predictive Index for Carotid Plaque

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[Purpose] Heart and cerebrovascular diseases, primarily caused by atherosclerosis, cause 21.3% of deaths in Japan. Focusing on carotid ultrasonography, this study investigated whether plaque formation, an advanced atherosclerotic stage, can be predicted.

[Subjects] The study included 377 individuals (138 males, 239 females; mean age 64.2±10.3 years) who underwent carotid ultrasonography during community health screenings conducted in 2019 and from 2022 to 2024.

[Methods] Ultrasonography was performed using the LISENDO 880LE (Fujifilm Medical). We evaluated the diagnostic performance of Wall Shear Stress (WSS), Stiffness Parameter β (β), and mean Intima-Media Thickness (mean IMT). Furthermore, 52 parameters, including demographics, laboratory data, and lifestyle factors, were analyzed for their association with plaque formation to develop a predictive mode.

[Results] ROC analysis was used to evaluate the diagnostic performance of WSS, β, and mean IMT. The diagnostic accuracies were 62.0% for WSS, 52.8% for β, and 58.7% for mean IMT. Subsequently, multivariate analysis was performed on basic, laboratory, and lifestyle data to identify the factors associated with plaque formation. From these results, we developed the following predictive formula: *Plaque Index = -3.180435 + (β × -0.1247942) + (mean IMT × 3.19097053) + (Age × 0.07585882) + (Sex [male=1, female=2] × -0.644576) + (ALP × -0.0071885) + (Brinkman Index × 0.00094332) + (Angina/Myocardial Infarction × 2.30855388)*. ROC analysis of the Plaque Index demonstrated a diagnostic accuracy of 74.7%.

[Conclusion] Our findings indicate that the newly developed Plaque Index achieved a high diagnostic accuracy (74.7%) compared with individual ultrasound parameters. This suggests that the Plaque Index is a valuable tool for predicting carotid plaque formation in clinical and screening settings.

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P-11-a-8

一般演題 Others1 (Physiology)

Segmental beta response evaluation is beneficial for assessing arterial stiffness

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[Aims] The cardio-ankle vascular index (CAVI) is a noninvasive indicator used to assess arterial stiffness and predict atherosclerotic cardiovascular disease (ASCVD). CAVI represents a scale-converted form of the stiffness parameter ß. Both CAVI and ß reflect overall arterial stiffness from the heart to the ankle. However, there are distinct mechanistic pathways underlying the heterogeneous progression of ASCVD across the arterial tree (e.g., elastic and muscular arteries). Thus, the present study aimed to: 1) examine differences in segmental β between elastic and muscular arteries at rest; 2) compare these differences between young and older adults at rest; and 3) further compare them with the segmental β responses observed after exercise.

[Methods] Eighty healthy individuals aged 18–52 years were recruited and divided into two groups: the Young group (18–23 years, n = 54) and the Adult group (31–52 years, n = 26). Cuffs were applied to both upper arms, the left thigh, and the right ankle. Segmental β was measured at rest as well as immediately after exercise using the Master's two-step exercise test.

[Results] At rest, muscular arterial stiffness (thigh-ankle β [taβ]) was higher than elastic arteries (heart-thigh β [htβ]). htβ and heart-ankle β (haβ) were higher in the Adult group than in the Young group ($p < 0.05$), whereas taβ was lower in the Adult group ($p < 0.05$). After exercise, taβ, htβ, and haβ decreased in both groups. In the Young group, exercise-induced β reduction was greatest in taβ, compared with htβ and haβ. This reduction was significantly greater in the Young group than in the Adult group.

[Conclusion] This study demonstrated distinct segmental β values between elastic and muscular arteries, suggesting that the inherent stiffness of the arterial beds should ideally be assessed separately.

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P-11-a-9

一般演題 Others1 (Physiology)

EEG Sleep Variability and Depressive Symptoms

Wearable-Based Assessment in Japanese Workers

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Objectives Irregular sleep–wake patterns associated with contemporary work styles have been implicated in adverse mental health outcomes in Japan. However, much of the existing evidence relies on self-reported data, which may limit measurement accuracy. This study aimed to objectively evaluate the relationship between day-to-day sleep variability and depressive symptoms in a real-world occupational setting.

Methods A total of 32 healthy adults without a history of physical or psychiatric disorders, insomnia, or shift work participation, and working regular weekday schedules (Monday–Friday), were enrolled. Sleep parameters were continuously recorded for seven consecutive days using a wearable electroencephalography device in the home environment. Objective sleep indices were derived, and subjective assessments were conducted using the Pittsburgh Sleep Quality Index (PSQI) and the Beck Depression Inventory-II (BDI-II). All study procedures conformed to the ethical standards of the Nagoya University Ethics Review Committee (approval numbers: 2010–0930, 2019–0105) and the Declaration of Helsinki. Written informed consent was obtained from all participants.

Results Bedtime, wake time, and time in bed were significantly delayed or extended prior to non-working days. During holidays, light sleep duration increased, and sleep latency was prolonged. Greater variability in bedtime was significantly associated with higher BDI-II scores. Median sleep duration and rapid eye movement sleep were correlated with PSQI scores. Sleep disturbances were linked to variability in sleep duration, sleep efficiency, and light sleep proportion. Additionally, absolute social jetlag was associated with higher PSQI.

Conclusion These findings highlight the importance of maintaining consistent sleep patterns for mental health in occupational populations.

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P-11-a-10

一般演題 Others1 (Physiology)

Association Between Sleep Restfulness and Smart Ring Derived Sleep Parameters

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[Objectives]
Sleep restfulness is an important component of sleep health; however, its relationship with objectively measured daily sleep parameters remains unclear. This study examined the associations between self-reported sleep restfulness and smart ring–derived sleep parameters in university students.

[Methods]
A total of 62 university students (mean age: 19.2 years; 87% female) provided 451 nights of sleep data. The dataset included sleep parameters obtained from a smart ring, such as total sleep time (TST), sleep stages, sleep continuity, and sleep timing, as well as a questionnaire-based measure of sleep restfulness. The associations between sleep parameters and sleep restfulness were analyzed using ordinal mixed-effects models. Receiver operating characteristic (ROC) analysis was performed to evaluate discriminative performance.

[Results]
Sleep restfulness was significantly associated with TST (OR = 1.007, $p < .001$) and time spent in light (OR = 1.010, $p < .001$), deep (OR = 1.009, $p < 0.01$), and rapid eye movement (REM) sleep (OR = 1.011, $p < .001$). Sleep timing variables, including bedtime difference, wake-up time difference, and social jetlag, were also associated with sleep restfulness; however, these associations became non-significant after adjustment for TST. On ROC analysis, TST had the highest discriminative performance (AUC = 0.78), with an optimal cut-off value of 392 minutes.

[Conclusion]
Sleep restfulness was primarily associated with sleep duration rather than sleep timing or other sleep parameters, suggesting that increasing the TST is effective at improving perceived sleep restfulness in university students.
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P-11-a-11

一般演題 Others1 (Physiology)

Felt Inversion After Aortic Arch Replacement

A Rare Cause of Mechanical Hemolytic Anemia Diagnosed by Echocardiography

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[Case]
A man in his 50s was emergently transferred to our hospital due to sudden onset of severe back pain. Contrast-enhanced computed tomography (CT) revealed an acute aortic dissection extending from the ascending to the abdominal aorta. Emergency ascending aortic and arch replacement was performed to close the entry. The postoperative course was initially uneventful; however, on postoperative day (POD) 12, the patient developed severe anemia with a hemoglobin level of 6.8 g/dL despite blood transfusion. Peripheral blood smear showed schistocytes, suggesting mechanical hemolytic anemia.
[Echocardiographic Findings]
Transthoracic echocardiography (TTE) demonstrated preserved cardiac function, and no significant valvular disease. However, an isoechoic structure was observed within the prosthetic graft at the proximal anastomosis of the ascending aorta, accompanied by turbulent flow distal to the lesion. The maximum flow velocity was 3.7 m/s, raising suspicion of significant stenosis within the graft at the anastomotic site.
[Clinical Course]
Subsequent contrast-enhanced CT confirmed inversion of the felt material, leading to a definitive diagnosis. Due to progressive anemia and concern for multi-organ failure secondary to ongoing hemolysis, redo graft replacement surgery was performed on POD 29 to relieve the proximal anastomotic stenosis.
[Discussion]
We report a rare case of inverted felt material within a prosthetic graft at the proximal anastomosis following ascending aortic arch replacement. As this extremely rare complication can be life-threatening, early diagnosis is crucial. When performing TTE after ascending arch replacement, it is important not only to assess cardiac function but also to carefully evaluate the proximal anastomosis using multiple imaging planes, whenever possible, to detect abnormal intraluminal structures or turbulent flow.
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P-11-a-12

一般演題 Others1 (Physiology)

Evaluation of respiratory muscles in patients with Duchenne muscular dystrophy

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Introduction/Aims: In patients with Duchenne muscular dystrophy (DMD), progressive respiratory failure usually develops after 10 years of age. Ultrasound studies have shown increased diaphragm thickness in younger children with DMD, which diminishes with age. Intercostal and external oblique muscle thicknesses and echo intensity (EI) have not been documented using ultrasonography for respiratory muscle assessment in patients with DMD. Intercostal muscles cannot be assessed using MRI because of their small size. We aimed to evaluate respiratory muscle thickness using ultrasonography in children with DMD and investigate age-related morphological changes.
Methods: Using B-mode ultrasonography at the apposition zone, we measured the thickness and brightness of the diaphragm, intercostal, and external oblique muscles during maximum expiratory maneuvers at residual capacity in nine males with DMD (mean [SD] age, 15.6 [7.0] years) and a reference group (n = 12; 11.9 [4.2] years).
Results: The mean thicknesses of the diaphragm (mean [SD], 2.1 [0.8] mm), intercostal muscles (4.2 [1.2] mm), and external oblique muscles (4.6 [2.5] mm) were significantly greater in the DMD group than in the reference group (1.5 [0.2], 2.8 [0.6], and 2.5 [1.2] mm; $p = 0.038$, $p = 0.007$, and $p = 0.043$, respectively). The external oblique muscle EI was greater in the DMD group (88.1 [22.4]) than in the reference group (56.0 [18.2]; $p = 0.003$). No significant differences were observed in the EI of the diaphragm (56.9 [25.5]) and intercostal muscles (74.7 [33.5]) relative to that of the reference group (49.2 [7.2], 54.8 [13.0]).
Discussion: Ultrasound imaging enabled measurement of the EI along with the thicknesses of the diaphragm, intercostal muscles, and external oblique muscles. Changes in diaphragmatic thickness in the DMD group suggested a trajectory from compensatory hypertrophy to structural deterioration.
Conclusion: Ultrasonographic evaluation of age-related changes in the respiratory muscles may improve the management and prognosis of DMD.

P-11-a-13

一般演題 Others1 (Physiology)

Telemedicine-Assisted EEG Simulation for Legal Brain Death Determination

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Background: In Japan, organ transplantation has increased annually, resulting in more frequent legal brain death determinations for organ donation after brain death. However, expertise in electroencephalography (EEG) during legal brain death determination is not uniformly available across institutions, particularly in facilities with limited experience. Therefore, establishing a remote support framework may improve preparedness and procedural reliability.

Methods: A simulation was performed between Facility A, where training for legal brain death determination was conducted, and Facility B, which remotely monitored the procedure using the telemedicine system Taladoc HEALTH. The simulation evaluated two points: (1) whether an EEG checklist developed for legal brain death determination could be visually and audibly confirmed from Facility B, and (2) whether bidirectional communication between the two facilities was feasible. After the simulation, participants—primarily Biomedical Laboratory Scientists (BLS)—completed a questionnaire. Responses were classified as successful aspects, unsuccessful or concerning aspects, and areas requiring improvement.

Results: From the questionnaires, seventeen successful aspects, seventeen unsuccessful or concerning aspects, and twelve areas requiring improvement were identified. Successful aspects included stable communication, clear audio and video quality via Taladoc HEALTH, confirmation of equipment placement, and verification of EEG examination procedures. Unsuccessful or concerning aspects involved the examination environment, equipment availability, technical skills or knowledge of BLS, and patient-related factors. Areas requiring improvement included the development of operation manuals, regular simulation training, and strategies for managing urgent requests.

Conclusion: Telemedicine-based simulation may enable institutions with limited experience in legal brain death determination to receive direct guidance from experienced facilities, thereby reducing anxiety and improving preparedness for EEG examinations conducted by BLS. (Tel:+81 58 230 6000)

P-11-a-14

一般演題 Others1 (Physiology)

Invasive EEG versus Stereo-EEG for Epileptogenic Zone Localization

A Comparative Analysis of Invasive Monitoring Techniques in Presurgical Epilepsy Evaluation

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Background
Precise localization of the epileptogenic zone is essential for successful surgical treatment in drug-resistant epilepsy. When non-invasive evaluations are inconclusive, invasive electroencephalography (EEG) becomes necessary. Subdural grid/strip-based invasive EEG and stereo-electroencephalography (S-EEG) are the two principal approaches currently in use.

Objective
To compare subdural invasive EEG and S-EEG with respect to clinical utility, safety, spatial resolution, and suitability for presurgical evaluation.

Methods
A comparative analysis was performed focusing on surgical approach, electrode configuration, complication profiles, and effectiveness in identifying epileptogenic networks. Clinical indications favoring each modality were also reviewed.

Results
Subdural invasive EEG provides extensive coverage of cortical surfaces and allows precise functional mapping, particularly in eloquent cortex. However, it requires craniotomy and is associated with higher morbidity. In contrast, S-EEG employs depth electrodes inserted through minimally invasive burr holes, enabling three-dimensional exploration of deep and bilateral brain structures with lower complication rates. S-EEG is particularly advantageous in cases involving deep-seated lesions, multilobar epilepsy, or poorly localized seizure onset zones.

Conclusion
S-EEG offers a less invasive and more versatile approach for evaluating complex epileptogenic networks, especially those involving deep structures. Nevertheless, subdural invasive EEG remains indispensable for detailed cortical mapping. Optimal modality selection should be individualized based on anatomical hypotheses and clinical context.

P-11-a-15

一般演題 Others1 (Physiology)

Cross-sectional area of the tibial and fibular nerves using ultrasound

Investigation of reference values and evaluation of reproducibility

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Introduction: Nerve cross-sectional area (CSA) measured with ultrasound is used to evaluate peripheral nerve disorders. In Japan, standard CSA values are known for the upper extremities but not for the lower extremities. This study determined tibial and fibular nerve CSA values and assessed their reproducibility.

Methods: Eleven healthy Japanese adults (mean age ± SD, 21.5 ± 0.5 years), without neurological disorders, participated: two males and nine females. Anthropometric data were recorded. Tibial and fibular nerve CSAs were measured using ultrasound (ARIETTA 60; HITACHI, Japan) with a 12-2 MHz linear array transducer. The probe was placed at the ankle to record the tibial nerve, and at the popliteal crease to record the tibial and fibular nerves. For each participant, reproducibility and right lower limb CSA measurements were assessed by two students after one month of training. A Bland-Altman plot was used to assess reproducibility. Pearson's correlation was used to assess the relationship between anthropometric data and the CSA of each nerve.

Results: Mean tibial nerve CSA values at the ankle and the popliteal crease were 5.5 ± 1.5 mm^2 and 21.0 ± 2.9 mm^2, respectively. The mean fibular nerve CSA at the popliteal crease was 6.2 ± 2.4 mm^2. The Bland-Altman plot of the tibial nerve CSA at the ankle revealed high reproducibility. A negative correlation was observed between height and tibial nerve CSA at the ankle ($r = -0.52$, $p = 0.01$).

Discussion: Variability in CSA measurements of tibial and fibular nerves at the popliteal crease may identify nerve epineurium defects due to tissues such as subcutaneous fat. The association of smaller CSA with greater height may reflect elongation of the tibial nerve together with skeletal growth.

Conclusions: This study established normative CSA values for the tibial and fibular nerves. Tibial nerve CSA values at the ankle were highly reproducible.

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P-11-a-16

一般演題 Others1 (Physiology)

Clinical and Sonographic Features Differentiating ICPN from Gallbladder Carcinoma

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Purpose: Intraductal papillary neoplasm of the bile duct (ICPN) is a newly defined entity in the 2019 WHO classification. It is a rare tumor, accounting for approximately 0.4–0.5% of all cholecystectomy cases, and its imaging diagnostic criteria remain unclear. Preoperative differentiation between ICPN and gallbladder carcinoma (GBC) is clinically challenging but important for surgical planning. This study aimed to identify clinical and imaging features distinguishing these two entities.

Methods: Patients with pathologically confirmed ICPN (n=6) and GBC (n=9) were retrospectively analyzed. Evaluated parameters included age, sex, tumor location (neck/body/fundus), attachment side (hepatic/ventral), morphological type (pedunculated/sub-pedunculated/sessile), and vascular assessment using high-resolution ultrasound with microvascular flow imaging.

Results: The median age was 64.5 years in the ICPN group and 73 years in the GBC group. Females predominated in the ICPN group (83.3%) compared to the GBC group (44.4%). Pedunculated polyps were observed in 33.3% of ICPN cases, whereas all GBC cases (100%) were sub-pedunculated or sessile, showing a significant difference (p=0.0418). In vascular assessment, the number of vessels entering the tumor from the gallbladder wall was a significant differentiator; 50% of ICPN cases had a single vessel, whereas all GBC cases exhibited multiple vessels (p=0.0440). Additionally, 77.8% of GBC cases demonstrated a dendritic (tortuous) flow pattern. ICPN cases showing dendritic flow were pathologically diagnosed as high-grade dysplasia.

Conclusions: Morphological type and the number of intratumoral vessels are useful indicators for differentiating ICPN from GBC. Multiple intratumoral vessels strongly suggest GBC over ICPN. However, ICPN with high-grade dysplasia may also exhibit dendritic vascular patterns, suggesting microvascular architecture may reflect histological grade.

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P-11-a-17

一般演題 Others1 (Physiology)

Wide-Band Scalp Electroencephalography Analysis in Infantile Epileptic Spasms Syndrome

Analysis of ictal direct current shifts during a seizure cluster of spasms

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Purpose: Recent advances in digital electroencephalography (EEG) have enabled the recording of a broad spectrum of signal components, ranging from low to high frequencies, beyond the conventional frequency band (Wide-band EEG). However, ictal wide-band EEG findings in infantile epileptic spasms syndrome (IESS) remain poorly understood. Wide-band scalp EEG analysis was performed in a single case of IESS to investigate lower-frequency direct current (DC) shifts (<0.1 Hz) during the pre-ictal to ictal transition of spasms within a seizure cluster.

Case history: The patient, a 2-year-old boy, was diagnosed with IESS at 6 months and is undergoing follow-up at our hospital. Although spasms had been resolved after adrenocorticotropic hormone therapy, readmission was required due to recurrence of 5-8 seizure clusters per day, with each cluster consisting of approximately 10 spasms. EEG recorded at readmission captured a seizure cluster of spasms at approximately 10-second intervals.

Methods: EEG data obtained at readmission, including a seizure cluster of spasms, was analyzed. To extract specific signal components from wide-band data, a 2-second time constant was applied for the identification of ictal DC shifts. The temporal relationship between the onset of ictal DC shifts and spasms was evaluated for all individual spasms within a seizure cluster.

Results: Ictal DC shifts were observed in 24 of 34 spasms within a seizure cluster. These ictal DC shifts, characterized by an initial negative potential change, appeared several hundred milliseconds before seizure onset and deepened thereafter. A sharp negative deflection was followed by a gradual downward shift, with the entire potential change lasting approximately 3 seconds. This pattern was reproducible within a seizure cluster.

Conclusion: Ictal DC shifts, characterized by distinct changes at seizure onset in IESS, may serve as a noninvasive candidate biomarker of early ictal activity. Furthermore, these findings may facilitate the identification of the pre-ictal to ictal transition.

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P-11-a-18

一般演題 Others1 (Physiology)

EEG in Neuro emergencies : Role of Biomedical Laboratory Scientists

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【Introduction】
In Japanese emergency care, about 10% of neuro emergency cases with impaired consciousness remain unexplained by CT or MRI. EEG is essential for evaluating brain function and guiding diagnosis, treatment, and prognosis. However, the shortage of EEG specialists—fewer than 0.4% of physicians, with about 85% of facilities lacking on-site experts—limits timely use in emergencies. In this context, biomedical laboratory scientists （BLSs） play a crucial role by ensuring accurate EEG acquisition and supporting interpretation, thereby sustaining the quality of neuro emergency care. This presentation highlights their importance through cases from our institution.

【Data Collection method】
EEG is performed in the exam room and ICU. In emergencies, a reduced-electrode setup is used with 5–10 min recording. Tests are done on weekdays (including after hours). During long holidays, one technologist works every 3 days for testing and preliminary reads. Final reads are by ER doctors, neurosurgeons, and part-time neurologists. Brain death EEG is handled on call.

【Results】
In a 2022 survey covering the previous 2.5 years, 209 EEG requests were made from the emergency department, with epileptiform discharges found in about half of the cases. Among these, 50% were nonconvulsive status epilepticus (NCSE) without visible seizures—diagnosed only by EEG—highlighting the need for rapid EEG assessment.

【Discussion】
Early EEG and initial screening by BLSs facilitate accurate diagnosis and appropriate treatment. Their specialized role in neuro emergencies improves diagnostic accuracy and overall emergency care quality. Even with the introduction of AI interpretation, acquiring high-quality EEG recordings remains essential. Examples will be presented and explained.

P-11-a-19

一般演題 Others1 (Physiology)

The relationship between tinnitus pitch and hearing loss.

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Background and aim: Tinnitus is a major complaint among older adults and the patients with ear disease. The mechanism of developing tinnitus remains unclear. The patients often complain a prevention of tinnitus from hearing in testing audiometry. However, this interaction also remains unclear. Therefore, we assessed the association of tinnitus pitch with frequency of hearing loss.

Materials and methods: The subjects with tinnitus were recruited from 2022 to 2025 at a department of otorhinolaryngology and head and neck surgery in Kyushu university hospital. Audiometry and tinnitus test (pitch-match) were conducted to 221 ears of them with pure tone tinnitus. Pitch of tinnitus was compared with audiometric patterns.

Results: The pitch frequency of tinnitus was 8kHz in 69 ears, 6kHz in 29 ears and 4kHz in 26 ears, while that was non-octave frequency in 77 ears. The pitch frequency matched a frequency of highest threshold in 75 ears (33.9%). The patients with high-tone hearing loss as usually seen in aging showed that 44.3% of ears had the same frequency of tinnitus as that of highest threshold in audiogram. Those of low-tone hearing loss showed that 33.3% of ears had the same frequency of tinnitus as that of highest threshold.

Discussion and Conclusions: The pitch frequency of tinnitus was not always consistent to the frequency of worst threshold. Clinical guideline for tinnitus suggests to divide tinnitus with two groups: pulsatile and non-pulsatile. Therefore, clinical guidelines do not discuss the tinnitus pitch frequency. These results suggest that the frequency of tinnitus may not play a role of detection of lost frequency.

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P-11-a-20

一般演題 Others1 (Physiology)

The reliability of Ultrasound measurements in Knee Tendon Thickness

Effect of Measurement Distance from Tendon Insertion

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Background: Musculoskeletal ultrasound (MUS) is widely used in clinical practice owing to its non-invasive nature, accessibility, and cost-effectiveness. However, evidence regarding its agreement with magnetic resonance imaging (MRI), particularly across different measurement locations, remains limited.

Objective: This study aimed to evaluate the agreement between fusion MUS and MRI in measuring knee tendon thickness and to investigate the influence of measurement distance from the tendon insertion on reliability.

Methods: Twenty-five healthy adults (14 men and 11 women; mean age, 30.9 ± 17 years) underwent MRI and fusion MUS examinations with the knee positioned at 30° flexion. Tendon thickness was measured at the quadriceps tendon and patellar tendon at the patellar and tibial insertions. Measurements were obtained at 0, 0.5, and 1.0 cm from the insertion site. Agreement between modalities was assessed using intraclass correlation coefficients (ICC) and Bland–Altman analysis.

Results: High agreement was observed across all measurement sites (ICC range, 0.872–0.997; all $p < 0.001$). The highest agreement was found at 0.5 cm from the tibial insertion of the patellar tendon (ICC = 0.997). In the quadriceps tendon, ICC values decreased as the measurement point moved farther from the insertion. A significant difference between MRI and MUS measurements was identified only at 1.0 cm in the quadriceps tendon ($p < 0.05$). Bland–Altman analysis demonstrated increasing bias and wider limits of agreement with greater distance from the insertion, whereas the patellar tendon exhibited minimal bias and narrow limits of agreement.

Conclusion: Fusion MUS showed excellent agreement with MRI for tendon thickness assessment. However, measurement error increased with distance from the insertion, particularly in the quadriceps tendon. Standardization of measurement location is therefore essential, and measurements within 0–0.5 cm of the insertion appear to provide the greatest reliability.

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P-11-a-21

一般演題 Others1 (Physiology)

Exclusion marker of pulmonary embolism on transthoracic echocardiogram.

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[Background and aim]
Pulmonary embolism (PE) is a critical disease to diagnose rapidly. Enhanced CT and D-dimer is often used as tools to diagnose PE. Transthoracic echocardiogram (TTE) is non-invasive rapid tool to test cardiac function. The overload of right heart is well-known as a clinical marker on the diagnosis of PE while this echocardiogram is not sufficient. Therefore, a novel marker on TTE is necessary to increase the diagnostic rate of PE.
[Materials and Methods]
Retrospective study from electric medical records. The 24 admitted patients with PE were recruited from 2021 to 2025. All of them received TTE on the same or the day before enhanced CT. The diameter of right atrium (RA), left atrium (LA) and right ventricle (RV), the diameter of inferior vena cava (IVC), D-shaped LV, McConnell's sign, Tricuspid valve regurgitation velosity (TRV), LA volume index (LAVI) and RV outflow tract velosity-time integral (RVOT-VTI) were collected from TTE records. This study was approved by the institutional ethical committee.
[Results]
TTE study showed dilated RA diameter in 33%, dilated RV diameter in 46%, D-shaped LV in 58%, McConnell's sign in 58% and dilated IVC in 17%. TRV could be measured in 88% and that was over 2.8 m/sec in 67%. All patients had normal LA diameter, small LAVI and normal RVOT-VTI. Fifteen patients could be suspected as PE by only TTE.
[Conclusion]
This study indicates that the triad including dilated LA, high LAVI and high RVOT-VTI may be a useful marker to exclude PE on TTE. Further study is needed by addition of more patients.
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P-11-a-22

一般演題 Others1 (Physiology)

Maximizing Biomedical Laboratory Scientists' Value

Phase-Free Activities for Preventing Disaster-Related and Sudden Deaths

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【Purpose】Preventive medicine depends on detecting health risks before symptoms appear. Biomedical laboratory scientists play a central role in this process because they can perform examinations, generate objective data, and identify early abnormalities. This report describes phase-free activities by biomedical laboratory scientists in both disaster and non-disaster settings, focusing on the prevention of disaster-related deaths and sudden deaths.
【Methods】We implemented mobile laboratory activities using ultrasound and point-of-care testing in two settings. In disaster shelters after the Noto Peninsula earthquake, screening for deep vein thrombosis was performed using interviews, lower-limb venous ultrasound, and additional blood testing when necessary. In non-disaster settings, screening activities were conducted for workers and community residents to visualize vascular conditions and detect asymptomatic risks. The activities were evaluated from the perspective of how biomedical laboratory scientists could contribute to early detection and prevention.
【Results】In disaster settings, mobile screening enabled early identification of individuals at risk of deep vein thrombosis and pulmonary embolism. The activities supported timely medical referral and may contribute to the prevention of disaster-related deaths. In non-disaster settings, vascular screening helped identify asymptomatic abnormalities that are usually difficult to recognize through subjective symptoms alone. These findings suggest that laboratory testing can provide actionable evidence for preventing sudden health events.
【Conclusion】Biomedical laboratory scientists are essential professionals in preventive medicine. Their ability to detect abnormalities in asymptomatic individuals allows them to contribute not only during disasters but also in everyday health management. Phase-free laboratory activities can expand the role of biomedical laboratory scientists and may help reduce both disaster-related deaths and sudden deaths.

P-11-a-23

一般演題 Others1 (Physiology)

Home-based sleep EEG assessment of exercise effects in young women

Effects of resistance exercise during the luteal phase

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Introduction : Menstrual cycle–related changes in body temperature are known to affect sleep quality in women. Home-based electroencephalography (EEG) has gained attention as a practical method for assessing sleep in daily living environments. This study investigated whether daytime resistance training (RT) enhances heat dissipation and improves sleep quality, as assessed using home-based EEG, during the follicular phase (FP) and luteal phase (LP).

Methods : Twelve young women participated in four experimental conditions: FP non-exercise, FP exercise, LP non-exercise, and LP exercise. Participants performed 40 minutes of moderate-intensity RT during the daytime. Overnight sleep was assessed at home using home-based EEG and skin temperature monitoring. Subjective sleep evaluations were assessed using a visual analogue scale (VAS) before sleep and after awakening. Heat dissipation was evaluated using the distal–proximal skin temperature gradient (DPG). This study was approved by the Ethics Committee of Saitama Prefectural University (Approval No. 25211).

Results : In the LP exercise condition, RT significantly increased pre-sleep and nocturnal DPG and was associated with an increase in Stage N3 sleep (p=0.028). Stage N3 sleep was maintained during the latter half of the night, accompanied by increases in delta power (p=0.043) and nocturnal DPG (p=0.046). Subjective evaluations showed reductions in difficulty organizing thoughts and eye fatigue compared with the LP non-exercise condition (p=0.039 and p=0.041, respectively). Greater pre-sleep heat dissipation was positively correlated with feeling refreshed (r=0.829, p=0.042) and improved mood (r=0.812, p=0.049), and negatively correlated with physical fatigue (r=-0.883, p=0.020).

Conclusion : These findings suggest that daytime RT during the luteal phase enhances heat dissipation and promotes deeper sleep, particularly slow-wave sleep, as assessed using home-based EEG. Home-based EEG may be a useful tool for evaluating exercise-related sleep changes in young women under daily living conditions. (Momo Fushimi, E-mail: fushimi-momo@spu.ac.jp)

P-11-a-24

一般演題 Others1 (Physiology)

Embolic Events and Clinical Echocardiographic Findings in Cardiac Myxoma Patients

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Background and Objective: Cardiac myxoma is the most common primary benign cardiac tumor and may cause serious embolic events, including cerebral infarction. Tumor morphology is considered an important determinant of embolic risk; however, the impact of concomitant atrial fibrillation (AF) remains unclear. In this study, we retrospectively evaluated the associations among echocardiographic findings, clinical characteristics, and embolic events in patients with cardiac myxoma.

Methods: We retrospectively reviewed 12 patients who underwent surgical resection at our institution between April 2016 and March 2026 and were histopathologically diagnosed with cardiac myxoma. Clinical characteristics, including the prevalence of AF, echocardiographic findings (tumor size, mobility, surface characteristics, and attachment site), laboratory data, and the CHA_2DS_2-VASc score were compared between the embolic and non-embolic groups using the Mann–Whitney U test and Fisher's exact test. Multivariate analysis was not performed because of the small sample size.

Results: Preoperative embolic events were observed in 5 of 12 patients (41.7%). The prevalence of AF did not differ significantly between the embolic and non-embolic groups (20% vs. 29%, p = 1.00). Echocardiography showed a trend toward larger tumor size in the embolic group (median, 50 mm vs. 25 mm; p = 0.17), although the difference was not statistically significant. All patients in the embolic group had irregular tumor surfaces (100% vs. 43%; p = 0.08); however, this also failed to reach statistical significance. No significant differences were observed in mobility, attachment site, or other variables.

Discussion and Conclusion: These findings suggest that embolic events in patients with cardiac myxoma may be more closely associated with tumor size and surface characteristics than with AF. Although statistical significance was not achieved, patients with large myxomas and irregular tumor surfaces may warrant consideration for early surgical resection to reduce the risk of embolic complications.

P-11-a-25

一般演題 Others1 (Physiology)

Vascular Function and Subjective Sleep Characteristics in Young Adults

Sex Differences in Sleep-Vascular Associations

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[Objective]
Sleep characteristics are increasingly recognized as important determinants of cardiovascular health. However, little is known about the relationship between subjective sleep characteristics and vascular function in healthy young adults. Therefore, this study aimed to investigate associations between physiological indices of vascular function and subjective sleep characteristics, with consideration of sex differences.

[Methods]
114 healthy university students (75 females, 39 males) participated in this study. Participants completed questionnaires on lifestyle habits, including sleep habits, diet, bedtime/wake-up times, and the Epworth Sleepiness Scale (ESS). Intima media thickness (IMT) was measured using carotid ultrasonography. Pulse wave velocity (PWV), arterial velocity pulse index (AVI), arterial pressure volume index (API), and blood pressure were also assessed. A 60-minute polysomnography study and subjective sleep assessments after waking were also obtained using a visual analogue scale (VAS). This study was approved by the Saitama Prefectural University Ethics Committee.

[Results]
Men showed significantly higher values for blood pressure, API, AVI, IMT, and PWV than women (all $p < 0.05$). Regarding subjective sleep assessments upon waking, pulse wave velocity (PWV) showed a significant negative correlation with sleep depth and subjective rest in both the overall population and women (both $p < 0.05$). In men, IMT showed a significant positive correlation with the ESS score ($p < 0.05$). In addition, PWV showed a significant positive correlation with irregular bedtime and awareness of nutritional balance, and a significant negative correlation with alcohol consumption frequency (all $p < 0.05$). Similar associations were observed in women (all $p < 0.05$).

[Conclusion]
Subjective sleep characteristics were associated with vascular function in healthy young adults, and these associations differed between men and women. Subjective sleep characteristics, particularly perceived sleep depth, were more strongly associated with vascular function in women, whereas daytime sleepiness was associated with early vascular changes in men.

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P-11-a-26

一般演題 Others1 (Physiology)

Vascular Function and Sleep EEG Architecture in Women

Comparisons Between Young Adult and Menopausal Women

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【Introduction】 Vascular function and sleep are important determinants of cardiovascular health. The menopausal transition is associated with reduced estrogen levels, vascular dysfunction, and sleep disturbances. However, the association between vascular function and sleep EEG architecture in women remains unclear across reproductive stages. Therefore, this study investigated associations between arterial stiffness indices and sleep EEG architecture in young adult and menopausal women.
【Methods】 This study was approved by the Ethics Committee of Saitama Prefectural University. Twenty-nine healthy women (13 young adult women and 16 menopausal women) participated in the study. Ankle-brachial index (ABI), pulse wave velocity (PWV), arterial velocity pulse index (AVI), and arterial pressure volume index (API) were measured, followed by overnight polysomnography (PSG). Sleep stages were classified according to international criteria, and spectral analysis of EEG signals was performed.
【Results】 Menopausal women had significantly higher AVI and PWV values than young adult women (all $p<0.05$). In young adult women, significant negative correlations were observed between arterial stiffness indices, including AVI and PWV, and slow-wave activity (SWA) (both $p<0.05$). In menopausal women, a significant positive correlation was observed between API and wake after sleep onset (WASO) ($p= 0.044$), and a significant negative correlation was observed between API and sleep efficiency ($p=0.041$). However, no significant correlations were found between arterial stiffness indices and SWA.
【Conclusion】 In young adult women, lower arterial stiffness was associated with greater slow-wave activity. In contrast, among menopausal women, sleep fragmentation was associated with vascular function. This suggests that changes in the hormonal environment during menopause may influence the relationship between sleep and vascular function.

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P-11-b-1

一般演題 Others2 (Miscellaneous)

Tableau Monitoring Optimizes Blood Draw for Rehabilitation Bus Patients

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Wheelchair and rehabilitation bus patients frequently waited over 30 minutes at blood draw counters due to lack of priority routing. This study implemented a dedicated smart ticketing workflow to reduce wait times for mobility-impaired patients.A 6-month prospective intervention (n=200) at a regional teaching hospital. A "Wheelchair/Rehabilitation Bus" button was added to the ticketing interface, routing patients to three barrier-free lanes via a real-time FIFO algorithm. IoT sensors and Python triggered music alerts when queues exceeded 10. A Tableau dashboard visualized wait-time trends, KPIs, and peak-flow predictions. Pre/post periods (3 months each) were compared using t-tests and ANOVA; target: 50% wait reduction.

Average wait dropped from 35.2 min to 3.8 min. Green channel utilization reached 92%; dedicated lane capacity 85% with no peak-hour congestion. Alert response time averaged 1.5 min (~3×/day). Patient satisfaction rose from 3.4 to 4.7($p<0.001$). Tableau achieved 95% alert accuracy and supported proactive staffing in 28 instances/month. The green channel, dedicated lanes, and Tableau monitoring improved care for vulnerable patients and optimized resource allocation. Future enhancements — AI-based detection and big-data prediction — will further advance health equity.

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P-11-b-2

一般演題 Others2 (Miscellaneous)

Healthcare Needs Assessment in Uzbekistan

Preliminary field survey for future laboratory collaboration

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Purpose: To identify baseline healthcare, laboratory, and public health challenges in Uzbekistan and to explore feasible entry points for future international collaboration in biomedical laboratory science and healthcare support.

Methods: A two-week exploratory field survey beginning on 21 November 2025 was conducted in Uzbekistan, mainly in Tashkent and Bukhara. Direct field observations were combined with discussions with healthcare personnel, public health officials, and local stakeholders. The survey focused on environmental conditions, hygiene and sanitation, barriers to healthcare access, variation in medical infrastructure, workforce development needs, and possible areas for technical and educational collaboration.

Results: Recurrent concerns regarding urban air pollution were noted, particularly in Tashkent and Bukhara, where air quality appeared markedly poorer than that in Tokyo during the same period. Hygiene and sanitation challenges appeared more pronounced in regional areas than in the capital, suggesting unequal public health conditions. Although advanced medical facilities supported by foreign investment were present, substantial variation in infrastructure, operational capacity, and service quality was observed across settings. The coexistence of highly modern facilities and uneven basic conditions suggested persistent disparities within the healthcare environment.

Social barriers affecting women and children were also identified, indicating restricted access to healthcare in some situations. In addition, local stakeholders expressed strong interest in Japanese medical technology, safe medical devices, laboratory quality improvement, and professional collaboration, including opportunities for training in Japan.

Conclusion: Uzbekistan appears to be a meaningful setting for phased international collaboration, particularly in laboratory quality management, human resource development, safety, and improvement of healthcare access. These findings clarified priority problems and led us to begin considering targeted support in these areas, providing a practical foundation for future collaborative projects.

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P-11-b-3

一般演題 Others2 (Miscellaneous)

Application of Artificial Intelligence in Preanalytical Phaseof Clinical Laboratory

Promoting Quality Assurance Stewardship

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Application of Artificial Intelligence in Preanalytical Phase of Clinical Laboratory

Background
Accessing laboratory procedures from extensive documents is time-consuming and increases the risk of pre-analytical errors. Large Language Models (LLMs) with Retrieval-Augmented Generation (RAG) can improve rapid access to accurate information.

Aim
To develop and evaluate LabMate, an AI assistant providing instant, structured laboratory guidance.

Methods
Validated laboratory documents (≈17,000 words) were used as the knowledge base. A RAG-based application was built using Python, Streamlit, Google Cloud, and Vertex AI. Documents were chunked, embedded, and queried using a Google Gemini LLM. A feedback system supported quality improvement.

Results
LabMate delivers real-time, structured responses on specimen requirements, storage, and turnaround times. It is ISO 15189 compliant, secure, and scalable, with an integrated audit and feedback loop.

Conclusion
LabMate improves efficiency, supports compliance, and reduces pre-analytical errors, enhancing patient care.

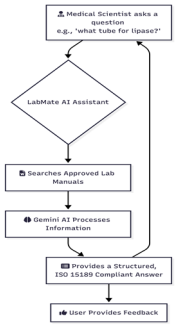

Figure 1: Labmate architectural diagram

P-11-b-4

一般演題 Others2 (Miscellaneous)

Multidisciplinary CKD Intervention Triggered by Laboratory Data Extraction

Role of Medical Laboratory Technologists in Early Dialysis Prevention

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Objective: Chronic Kidney Disease (CKD) is a global health challenge which, if it progresses to end-stage renal disease, necessitates dialysis therapy. However, many inpatients do not receive nephrology consultation despite laboratory abnormalities. At our institution, medical laboratory technologists (MLTs) extract laboratory data to identify intervention candidates and recommend nephrology referral through a multidisciplinary CKD round. This study evaluated whether this round contributes to dialysis prevention.

Methods: This retrospective observational study analyzed cases from February 2021 to December 2025. Weekly inpatient data were extracted by MLTs, who identified patients aged under 80 years with an estimated glomerular filtration rate (eGFR) below 45 mL/min/1.73 m² from the previous week and shared the data with the team. Candidates were discussed at a weekly conference to determine intervention appropriateness. For necessary cases, recommendations including nephrology referral, medication adjustment, and dietary therapy review were communicated to the attending physician via the medical records.

Results: A total of 241 patients were enrolled. Outcomes were: 19.2% attending our nephrology outpatient clinic, 8.9% managed under a CKD collaborative care pathway, 14.6% referred to other institutions or discharged, 14.2% deceased, 0.8% initiating dialysis, and 42.3% with other outcomes. Of the patients who received intervention, 42.7% were continuously followed up at an appropriate medical institution. Annual dialysis initiations were 83 (2021), 80 (2022), 58 (2023), 52 (2024), and 68 (2025).

Conclusion: A multidisciplinary CKD round triggered by MLTs who centrally manage clinical laboratory data facilitates the timely and efficient selection of target patients. These results suggest that early multidisciplinary intervention leads patients to continuous kidney disease management and may contribute to the reduction of dialysis initiation. Contact: +81-564-21-8111

P-11-b-5

一般演題 Others2 (Miscellaneous)

Human Factors Redesign Improves Laboratory Workflow Efficiency

Enhancing Risk Management and Patient Safety in High-Volume Health Screenings

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Objective The pre-analytical phase in laboratory medicine is particularly prone to errors in high-volume settings such as health screenings. This study applied Human Factors Engineering to redesign the Laboratory Information System (LIS) workflow, aiming to effectively reduce cognitive load, improve overall efficiency, and enhance patient safety without increasing manpower or cost.

Methods A retrospective pre–post study evaluated workflow efficiency and error reduction. Two key optimization strategies were implemented: (1) workflow automation (batch logging), allowing personnel to simply scan a medical record number to trigger automatic test order entry and barcode generation, replacing manual selection; and (2) system alerts for time-sensitive tuberculosis (TB) culture specimens, which trigger warnings as elapsed time approaches a critical threshold to prevent delays and ensure safe, timely processing.

Results In 2025, an average of 17,417 tubes were processed monthly. After implementation, preparation time per patient decreased from 120 to 30 seconds (a 75% reduction). Missed tube preparations declined from 10 cases annually to zero, and delayed TB culture processing was eliminated. These improvements strengthened patient safety by preventing specimen-related errors, reducing cognitive burden, and enhancing overall system reliability, thereby ensuring consistent and stable workflow performance. Overall, these findings highlight the effectiveness of system-based interventions in improving laboratory safety and reducing human-dependent variability.

Conclusion In summary, our Human Factors Engineering–based LIS redesign significantly improved efficiency, standardization, and patient safety without the need for any additional resources. This scalable and cost-effective approach demonstrates a strong real-world impact and provides a practical and reproducible model for broader implementation in clinical laboratories.

Keywords: Human Factors Engineering, Laboratory Information System, Patient Safety, High-volume health screening

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P-11-b-6

一般演題 Others2 (Miscellaneous)

Cerebrovascular Modulation by Spinal Cord Stimulation in Stroke

Insights into Perfusion Dynamics and Recovery in a Mouse Model

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Spinal cord stimulation (SCS) is an established intervention for chronic pain that also augments tissue perfusion and mitigates ischemic injury. Prior studies indicate cervical SCS exerts profound cerebrovascular effects, notably enhancing cerebral blood flow and potentially facilitating motor recovery after ischemic stroke. Although its safety is well-recognized, the comprehensive therapeutic efficacy and underlying neurobiological mechanisms remain incompletely elucidated. This study investigates the neuroprotective effects and mechanistic pathways of SCS in ischemic stroke.

Utilizing a murine model of middle cerebral artery occlusion (MCAO), we applied clinically approved spinal cord stimulators to evaluate the impact of SCS on cerebral morphology and functional outcomes.

Our preliminary findings demonstrate that SCS significantly promotes functional recovery and preserves brain tissue integrity post-MCAO. Mechanistically, SCS was observed to regulate the expression of transient receptor potential vanilloid 1 (TRPV1) within the cervical spinal cord. Concurrently, it modulated the cerebral expression of calcitonin gene-related peptide (CGRP), substance P, and nitric oxide synthase (NOS). These molecular alterations culminated in an immediate and substantial elevation in cerebral blood flow, a concomitant reduction in infarct volume, and a marked amelioration of sensorimotor deficits.

This research provides novel mechanistic insights into the neuroprotective role of SCS in ischemic stroke, with a specific focus on its capacity to modulate cerebral perfusion. These findings significantly advance the current understanding of cerebrovascular dynamics in post-stroke recovery, thereby highlighting the translational potential of SCS as a viable therapeutic strategy for stroke rehabilitation.

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P-11-b-7

一般演題 Others2 (Miscellaneous)

Progress of Task Shifting and Sharing Among Medical Technologists

A Multi-Institutional Survey Following the 2024 Work-Style Reform in Tama, Tokyo

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Background: Following the enforcement of the “Work-Style Reform for Doctors” in April 2024, promoting task shifting and task sharing has become essential in Japanese healthcare settings. The Tama district of Tokyo includes a diverse range of institutions, from advanced tertiary hospitals to community-based clinics. However, regional differences in the progress of implementation and the challenges associated with these reforms have not been sufficiently clarified.

Methods: A questionnaire survey was conducted in March 2026 across multiple medical institutions in the Tama district. Survey items included completion of the Ministry of Health, Labour and Welfare (MHLW)-designated training course and the status of currently implemented or planned task-shifted/shared responsibilities among medical technologists.

Results: Responses were obtained from 10 institutions, ranging from small clinics to large hospitals with more than 500 beds. Overall, 64% of medical technologists had completed the MHLW-designated training course. Tasks already implemented included patient instruction and management for continuous glucose monitoring (CGM), ward-based phlebotomy, evoked potential testing, and assistance with endoscopic procedures. In addition, two institutions were preparing to introduce responsibilities related to venous access. These findings indicate that the transfer of key duties is progressing across institutions, while further expansion will depend on access to specialized technical training.

Conclusion: Although no established benchmark is currently available, the completion rate of the MHLW-designated training course was considered favorable. Initial steps in task shifting and sharing appear to include both relatively accessible duties that improve resource utilization, such as ward phlebotomy and CGM management, and roles that make effective use of the expertise of medical technologists, including endoscopic assistance and venous access preparation.

P-11-b-8

一般演題 Others2 (Miscellaneous)

Mitochondrial adaptation mechanisms regulated by caveolin-1 C-terminal region

Toward molecular markers for assessing atherosclerotic plaque vulnerability

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Atherosclerotic plaque vulnerability is a major determinant of acute cardiovascular events; however, methods to directly assess vascular instability remain limited. Vascular smooth muscle cells (VSMCs) contribute to vascular homeostasis by adapting to environmental stimuli, and dysregulation of these responses has been implicated in vascular aging and plaque destabilization. Caveolin-1 (Cav1), a principal component of caveolae, is abundantly expressed in VSMCs and is involved in the regulation of signaling pathways; however, the role of its C-terminal region remains unclear. In this study, we investigated the role of the Cav1 C-terminal region in mitochondrial dynamics and metabolic adaptation in VSMCs.

Human VSMCs were transduced with full-length Cav1 or a 19-amino-acid C-terminal truncation mutant (Cav1ΔC). Mitochondrial respiration, dynamics, and DRP1 phosphorylation were evaluated using Seahorse analysis, time-lapse imaging, and western blotting, respectively.

Cav1ΔC-expressing VSMCs exhibited reduced maximal respiration under basal conditions and showed attenuated increases in maximal respiration in response to platelet-derived growth factor-BB (PDGF-BB). Furthermore, PDGF-BB-induced mitochondrial fission was suppressed. DRP1 suppresses mitochondrial fission when phosphorylated at Ser637 and promotes fission when phosphorylated at Ser616. In Cav1ΔC-expressing VSMCs, phosphorylation at Ser637 was elevated under basal conditions. In addition, phosphorylation at both Ser616 and Ser637 failed to respond to PDGF-BB stimulation, suggesting impaired switching of DRP1 phosphorylation states.

In conclusion, the C-terminal region of Cav1 regulates mitochondrial dynamics and respiratory adaptation by modulating DRP1 phosphorylation, thereby contributing to signal responsiveness in VSMCs. Disruption of this mechanism may contribute to VSMC dysfunction associated with plaque vulnerability and may provide a mechanistic basis for identifying molecular markers to assess plaque vulnerability.

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P-11-b-9

一般演題 Others2 (Miscellaneous)

Insights into Internal Quality Control in Veterinary Biochemistry Using Chiritrol

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Background：Clinical laboratory testing is essential in veterinary diagnosis. Although in-clinic biochemical testing is widely used in veterinary practice, routine internal quality control (IQC) remains less established than in human medicine. This study evaluated the short-term precision and stability of a dry chemistry analyzer using a general-purpose serum control and assessed the cost and time required for IQC implementation.
Methods：Chiritrol was used as the control serum. A FUJI DRI-CHEM NX500V analyzer was used to measure a routine 20-analyte biochemistry panel. A Hitachi 3100 analyzer was used as a comparator. Measurements on the dry chemistry system were performed approximately once weekly over 30 days. Mean, standard deviation, and coefficient of variation were calculated for each analyte. Reagent cost and hands-on time per IQC run were also recorded. Inter-system agreement was not defined as a primary endpoint.
Results：The dry chemistry system showed generally low CV values, although precision varied among analytes. The highest CV was observed for total bilirubin at 6.8%. No clear temporal trend or shift was detected during the study period. Each IQC run required approximately JPY 4,000 and 20 minutes.
Conclusions：IQC using a general-purpose serum control may be feasible for in-clinic biochemical testing. Practical implementation in veterinary hospitals may require prioritization of key analytes rather than equal monitoring of all parameters. A stepwise introduction, starting with a low testing frequency, may be a realistic approach for facilities without an established IQC program. （Tel：+81-478-82-3161）

P-11-b-10

一般演題 Others2 (Miscellaneous)

Multidimensional Sleep Characteristics and Arterial Stiffness in Older Adults

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Aim: Sleep is a multidimensional behavior encompassing duration, quality, and behavioral patterns. The associations between sleep characteristics and arterial stiffness remain unclear. This study aimed to investigate the associations between multidimensional sleep characteristics and arterial stiffness in older adults.
Methods: This cross-sectional study included 243 community-dwelling adults aged ≥65 years. Arterial stiffness was assessed using the cardio-ankle vascular index (CAVI). Sleep parameters—including time in bed (TIB), sleep duration, sleep latency, sleep restfulness score (SRS), daytime sleepiness assessed by the Japanese version of the Epworth Sleepiness Scale, and nocturia—were evaluated using standardized self-administered questionnaires. Multivariable linear regression analyses were performed to assess independent associations between sleep characteristics and CAVI after adjustment for potential confounders.
Results: The mean age was 76.4 years, and the mean CAVI was 8.90 ± 1.03. CAVI differed significantly across TIB, SRS, and nocturia categories, with higher values observed in participants with prolonged TIB (≥8 h), poorer sleep restfulness, and more frequent nocturia ($p < 0.05$). In contrast, sleep duration, sleep latency, and daytime sleepiness were not significantly associated with CAVI. In multivariable analyses, SRS remained independently associated with CAVI in both the overall population and the 7–8 h TIB group ($\beta \approx -0.13$ to -0.20, $p < 0.05$). Nocturia was also positively associated with CAVI.
Conclusions: In older adults, sleep restfulness, nocturia, and behavioral sleep patterns such as TIB may be associated with arterial stiffness, whereas sleep duration alone was not. These findings support the importance of multidimensional sleep assessment in the evaluation of vascular health.

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P-11-b-11

一般演題 Others2 (Miscellaneous)

TLA Improves TAT and Workflow Efficiency

Under High-Demand Emergency Conditions

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Background:
Rapid laboratory turnaround time (TAT) is crucial in emergency, where delays directly affect clinical decision-making and patient outcomes. With increasing emergency department visits in an aging society, laboratories face growing challenges, including high sample volumes and limited staffing. Optimizing workflow while maintaining TAT has therefore become a key priority. This study evaluated the impact of implementing Total Laboratory Automation (TLA) on TAT and workflow efficiency in an emergency laboratory.
Methods:
A before-and-after study was conducted under routine clinical conditions. Key performance indicators included the 30-minute reporting rate, defined as the proportion of results reported within 30 minutes from sample receipt, and the 90th percentile TAT for potassium (K^+) and troponin I (TnI). Workflow changes were further analyzed using process mapping and spaghetti diagrams.
Results:
Following TLA implementation, laboratory performance improved significantly. The 30-minute reporting rate increased from 80.8% to 89.7%. The 90th percentile TAT decreased from 42 to 29 minutes for K^+ and from 50 to 31 minutes for TnI ($p < 0.005$). These tests represent critical assays frequently requested in emergency settings. Additionally, 62.5% of manual processing steps were eliminated, reducing 9,984 manual movements per day. Notably, the greatest improvements were observed during peak workload periods, demonstrating enhanced system efficiency under operational stress.
Conclusion:
The implementation of TLA significantly improved reporting timeliness and reduced high-percentile TAT for critical emergency tests. By streamlining workflow and minimizing manual handling, laboratory staff were able to focus more on ensuring accurate and timely results. Automation reduced delays where clinical risk is highest, reinforcing its role in high-acuity laboratory settings.

P-11-b-12

一般演題 Others2 (Miscellaneous)

Automated Reagent Expiry Warning System

Improving management efficiency in clinical biochemistry laboratories

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Background: Clinical biochemistry laboratories rely on numerous reagents, calibrators, and quality control (QC) materials. Manual monitoring may result in expiration oversight, testing interruptions, and delayed QC parallel testing, affecting laboratory efficiency and patient safety.

Objective: To develop and evaluate an AI-assisted automated expiry warning system for proactive reagent management.

Methods: An integrated database was established to track item names, lot numbers, expiration dates, and consumption rates. Tiered warning thresholds were applied: 90 days for imported materials, 30 days for QC materials, and 7 days for reagents/calibrators. Notifications were delivered through LIS pop-up alerts, color-coded dashboards, and daily emails. AI-based machine learning algorithms predicted reagent consumption trends and dynamically adjusted reorder points according to usage patterns and supplier lead times.

Results: After implementation, reagent expiration incidents were reduced to 0%, testing interruptions caused by expired materials were eliminated, and 100% of QC parallel testing was initiated on schedule. Manual inventory inspection time decreased by approximately 75%, improving operational efficiency.

Conclusion: The AI-driven automated warning system significantly reduced human error, optimized inventory turnover, and maintained stable laboratory operations. Low-cost digital integration combined with AI prediction effectively enhanced laboratory efficiency and patient safety.

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P-11-b-13

一般演題 Others2 (Miscellaneous)

Multilingual Audio Vision Testing System

Enhancing communication in driver license vision examinations

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Background: Health management centers frequently serve examinees from diverse nationalities for physical examinations and driver's license testing. Communication barriers are common when examinees speak non-mainstream languages or have limited English proficiency, especially during vision-related examinations requiring precise instructions.
Objective: This study aimed to develop a multilingual audio-assisted support system to improve communication, testing efficiency, and examinee satisfaction.
Methods: One year of demographic data identified the five most common non-native language groups: Japanese, Indonesian, Thai, Filipino, and Vietnamese. Standardized testing instructions were first translated into written form; however, some examinees had difficulty understanding written content due to limited literacy. Therefore, standardized audio instructions were recorded in the five target languages. QR codes linked to each audio file were generated, allowing staff to instantly play the appropriate instructions during examinations.
Results: After implementation, the average duration of driver's license vision testing decreased by 50%, from 10 minutes to 5 minutes per person. The audio-assisted approach effectively overcame literacy barriers and improved comprehension among examinees. Anxiety during testing was reduced, while overall satisfaction with the examination process increased. In addition, repetitive verbal explanations by staff were minimized, resulting in improved workflow efficiency.
Conclusion: The multilingual QR code-based audio support system effectively reduced communication barriers in multicultural healthcare settings. By replacing text-only instructions with accessible audio guidance, the system enhanced testing efficiency, examinee understanding, and patient-centered service quality. This low-cost and scalable model may be widely applied in international health screening and diagnostic environments.

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P-11-b-14

一般演題 Others2 (Miscellaneous)

Meeting Patient Expectations: A Survey for Enhancing Blood Collection Services

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Background:
In competitive healthcare environments, service quality and patient satisfaction are critical. Implementing structured satisfaction assessments enables healthcare providers to identify service gaps and improve patient-centered care.

Objective:
This study aimed to evaluate patient satisfaction at a blood collection station through a structured survey system and to identify key factors influencing the quality.

Methods:
A cross-sectional survey was conducted from December 8 to 18, 2025, using a QR code generated via Microsoft forms. The questionnaire collected demographic data and utilized a Likert scale.
Responses were integrated into SharePoint via Power Automate for real-time data capture. An automated alert system flagged negative responses for immediate follow-up.Data were analyzed using statistics, including reliability analysis and t-tests. Results were visualized using Power BI for interactive exploration.

Results:
A total of 235 valid responses were collected. Most respondents were patients (89.8%) and returning visitors (86.4%), primarily aged 36–55 years (50.2%), with blood testing as the main purpose (74.5%). All 11 evaluated indicators of service quality and environment achieved satisfaction rates exceeding 95%. Following spatial redesign and equipment upgrades, overall satisfaction reached 97.9%, while the comprehensive satisfaction rate was 99.6%.

Conclusion:
The blood collection station demonstrated consistently high patient satisfaction and service quality. Continuous optimization of service processes and environments is essential to sustain high-quality, patient-centered care and enhance long-term loyalty.
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P-11-b-15

一般演題 Others2 (Miscellaneous)

AI-Driven Intelligent Document Processing in Laboratory Medicine

Transforming ISO 15189 Documents into Standardized Patient-Readable Information Sheets

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Purpose: The study aims to develop and validate an AI-driven platform that automatically converts technical ISO 15189 laboratory Standard Operating Procedures (SOPs) into structured, patient-centered information sheets. By integrating textual and graphical elements, the system bridges communication gaps between healthcare providers and patients while ensuring laboratory quality consistency.

Methods: A six-phase system development framework was implemented: (1) Document Processing: Importing ISO 15189 PDFs and using OCR for de-identified text extraction. (2) AI Analysis: Utilizing fine-tuned Large Language Models (LLMs) for semantic and layout analysis to extract key clinical fields. (3) Validation: Applying rule-based normalization and a human-in-the-loop interface for expert review. (4) Image Integration: Linking a specimen container imagery repository to specific test items. (5) Platform Development: Building a web-based interface with API access for retrieval of structured test information. (6) Field Evaluation: Assessing performance through quantitative metrics and user satisfaction surveys.

Results: Preliminary pilot testing demonstrated a 60–70% reduction in document conversion time and significant improvements in data consistency. The system successfully achieved high-granularity extraction of over 12 critical parameters directly from unstructured SOPs, including specimen volumes, container requirements, and biological reference ranges. The platform enables real-time updates aligned with ISO 15189 quality requirements while enhancing patient comprehension through visual workflows.

Conclusion: The AI-based intelligent document processing system provides a feasible approach to transforming complex laboratory documents into accessible patient information. It supports continuous quality improvement, enhances transparency, and serves as a scalable model for digital transformation and smart healthcare in clinical pathology.

Keywords: ISO 15189, Artificial Intelligence, Laboratory Medicine, Large Language Model

P-11-b-16

一般演題 Others2 (Miscellaneous)

Reliable POCT: Risk Defense and Smart Monitoring

A PDCA-Based Model for Enhancing Patient Safety and Clinical Quality

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Background: Point-of-Care Testing (POCT) plays a critical role in clinical decision-making and patient safety. However, decentralized testing environments,diverse operators, and manual data entry processes increase the risk of patient misidentification and quality control failures, thereby affecting diagnostic reliability and healthcare quality. To comply with ISO 15189 and hospital accreditation requirements, a traceable and data-driven POCT management system is essential.

Objective: This study aimed to establish a reliability POCT system by integrating risk-based strategies and smart monitoring tools.

Methods: A cross-departmental framework was implemented via the PDCA cycle: 1) Risk-Based Management: Barcode scanning replaced manual data entry to eliminate patient identification risks. User authorization was dynamically linked to the Training Management System (TMS) for deactivation. Furthermore, system-level optimizations were coordinated with vendors following the analysis of identified non-conformities. 2) Digitalization: A QR code-based system integrated Level 1 and 2 maintenance records. 3) Smart Monitoring: A Power BI dashboard was utilized to visualize key quality indicators, including user authorization status, EQA performance,and incident rates.

Results: Following implementation, the EQA failure rate was maintained at 0.3% in 2025. Manual identification errors decreased from 4 cases in 2025 to 0 cases in Q1 2026. Level 2 maintenance compliance reached 100%. All 2025 internal audit non-conformities were fully corrected (100% rate). Finally, a digitalized management system for equipment calibration and maintenance was established, featuring automated notifications and a Power BI smart dashboard for visualized monitoring.

Conclusion: A data-driven POCT model integrating risk defense, digitalized maintenance, and Power BI monitoring significantly improves diagnostic quality and patient safety.

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P-11-b-17

一般演題 Others2 (Miscellaneous)

Optimizing Cross-Departmental Administrative Efficiency via Knowledge Management

A SharePoint-based Approach in a Clinical Laboratory

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Background: Administrative workflows between clinical laboratories and hospital departments often face friction due to manual, once-daily paper delivery. Requests submitted after the noon pickup are delayed until the following day. A 247-case simulation estimated the average turnaround time at 18.7 hours (1122 minutes), accounting for transit and weekend constraints. This study implements a SharePoint-based Knowledge Management (KM) system to eliminate these delays and transition toward a paperless environment.
Methods: A "Low-code" strategy enabled laboratory supervisors to autonomously design digital workflows without specialized IT programming. The system integrates structured fields with Power Automate for real-time notifications and feedback. We analyzed 247 application records and conducted a post-implementation satisfaction survey (n=26). The Top-Two Box method quantified user acceptance, focusing on system reliability, audit traceability, and ISO 15189 standards.
Results: Implementation yielded transformative gains: (1) Mean processing time plummeted from 1122 minutes to 1 minute (>99.9% increase); (2) Paper consumption fell from 247 to 0 sheets (100% paperless); (3) Overall satisfaction rose from a 65% baseline to 93% (Top-Two Box score); (4) 100% of participants recognized the system’ s superiority in audit traceability and document loss prevention, reducing handling risks to < 1%.
Conclusion: The SharePoint KM system ensures high-level security through Permission Control and digital archives. Bypassing traditional development barriers, this model empowers laboratory professionals to lead digital transformation efforts. This scalable framework enhances administrative resilience and serves as a benchmark for hospital-wide ESG initiatives and sustainable institutional management.

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P-11-b-18

一般演題 Others2 (Miscellaneous)

Utility Evaluation of Dedicated On-site Pre-Analytical Laboratory in Clinical Trials

Reducing pre-analytical errors and improving research outcomes by implementing specialized on-site sample handling units

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Background: The pre-analytical phase is critical for sample integrity in clinical trials. Large-scale hospital laboratories may encounter challenges related to complex logistics such as transport delays and procedural inconsistencies that risk compromising sample quality. To address these issues, a dedicated on-site pre-analytical laboratory was established at the Oslo Myeloma Center, Oslo University Hospital. This facility was designed to manage the entire workflow from blood collection to staging and dispatching samples. This prospective observational study (Jan 2025 – Jan 2026) evaluated the clinical and logistical utility of the facility while handling twenty-five high-volume protocols simultaneously.

Methods: Processing efficiency was measured by tracking “vein-to-freeze” intervals using precision timers. Environmental stability was ensured through continuous 24/7 digital temperature logging of all storage units, supplemented by a rigorous schedule for equipment calibration. Quality control and procedural adherence were evaluated through sponsor audit findings and systematic feedback collected from various central laboratories.

Results: Average processing times were maintained within 30 minutes for plasma and within 90 minutes for serum, in accordance with protocol requirements. All protocols adhered to predefined standards for temperature monitoring and calibration. No discrepancies were identified during sponsor audits. Twenty-two of twenty-five protocols have been completed to date without recorded pre-analytical errors. The overall error rate was 0.10%, with most discrepancies intercepted on-site before shipment. Only in 3 protocols 4 errors occurred across 3,910 samples (two unnecessary shipments, one incorrect urine collection, and one missing sample).

Conclusion: An on-site pre-analytical laboratory ensures high sample quality and minimal error rates, providing a robust framework for optimizing sample handling in complex trials.

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P-11-b-19

一般演題 Others2 (Miscellaneous)

Establishing progastrin-releasing peptide cut-off in lymph node biopsies

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Background:
Ultrasound-guided fine-needle aspiration biopsy (FNAB) is central to the diagnosis and follow-up of thyroid cancer. Measurement of progastrin-releasing peptide (ProGRP) in FNAB washout fluid from cervical lymph nodes is a valuable adjunct in the detection of medullary thyroid carcinoma (MTC). In suspected metastatic disease, FNAB-ProGRP results are typically interpreted qualitatively as either detectable or undetectable. However, the variations in sampling protocols may introduce variability in test results and complicated clinical interpretation.
Objective:
To evaluate whether a cut-off value can reliably distinguish negative from positive FNAB-ProGRP results across different sampling procedures.
Methods:
FNAB-ProGRP results obtained between 2015 and 2025 were retrospectively retrieved from the laboratory information system, including samples from both internal and external institutions. Internal data were analyzed to characterize result distribution and identify a suitable cut-off value to distinguish negative and positive results. The cut-off validity was subsequently assessed using external samples.
Results:
A total of 189 samples were included (169 internal, 20 external). Among internal samples, 67% were <90 ng/L and 30% were >250 ng/L, with only 3% between 100–250 ng/L. A cut-off value of 150 ng/L provided clear discrimination between negative and positive results. External samples were either <90 ng/L (90%) or >1000 ng/L (10%), supporting the validity of the proposed threshold.
Conclusion:
In this dataset, a cut-off value of 150 ng/L reliably differentiates negative FNAB-ProGRP results from positive results and appears robust despite variability in sampling protocols.

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P-11-b-20

一般演題 Others2 (Miscellaneous)

Incremental learning framework for adapting shared blood sampling prediction models

A cross-institutional framework for efficient model adaptation and deployment

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Objective: Predicting the number of daily blood collections is helpful for the efficient operation of blood collection rooms. This study evaluated an incremental learning (IL) framework designed to learn transferable patterns from external base models and adapt them to different clinical environments with minimal data. We applied this framework to reduce outpatient blood collection congestion, a common problem that lowers patient satisfaction and operational efficiency. While machine learning can address this, building models from scratch is resource-intensive, and "dataset dependency" often prevents simple model sharing. Our approach efficiently overcomes these barriers by adapting shared models to our specific workflow.
Methods: We used blood collection logs, outpatient counts, and weather data. Data from January to December 2024 were used for initial training and IL, while January to August 2025 and November 2025 were used for retrospective and prospective validation, respectively. A base model (XGBoost) built at Hospital A (average: 1,300 outpatients/day) was adapted to Hospital B (average: 2,600 outpatients/day) through the IL process to assess its transferability for daily patient count prediction.
Results: Direct application of the Hospital A model to Hospital B showed poor predictive performance, yielding an R2 of -14.074 for daily patient counts due to the significant difference in outpatient volume. However, after applying the IL framework, the R2 greatly improved to 0.745. Prospective validation using future data further confirmed its robustness, achieving an R2 of 0.807. These results demonstrate that the IL process successfully adapted the external model to our unique environment, providing sufficient accuracy for practical use.
Conclusion: The IL framework is an effective approach to sharing AI models as intellectual assets across institutions. It allows facilities to achieve highly accurate, localized predictions for daily operations with much lower costs than starting from scratch, offering a scalable solution for global hospital management.

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P-11-b-21

一般演題 Others2 (Miscellaneous)

Process-based Analysis of Endoscopy Room Workflow

Impact of Endoscopist Experience, Assistant Competency, and Patient Age

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Background and Aim: Endoscopy unit efficiency depends not only on procedure time but also on overall workflow, including preparation and post-procedure processes. This study aimed to evaluate workflow by decomposing total room time and examining the impact of endoscopist experience, assistant competency, and patient age.

Methods: We retrospectively analyzed consecutive upper gastrointestinal endoscopy cases over one year. Total room time was divided into preparation (entry to insertion), procedure (insertion to removal), and post-procedure time (removal to exit). Endoscopists were categorized as experienced or junior based on years of practice. Assistants were classified into three competency levels. Univariate analysis was followed by multivariate regression including age, day of the week, endoscopist category, and assistant competency.

Results: A total of 7,616 cases were analyzed. Median total room time was 10 minutes. In multivariate analysis, junior endoscopists were associated with longer total room time (+2.90 minutes, p<0.001) and longer procedure time (+1.01 minutes, p<0.001). Age was also associated with prolonged total room time (+0.06 minutes per year, p<0.001). Assistant competency showed limited impact on total room time; however, novice assistants were associated with shorter post-procedure time (−0.45 minutes, p=0.038).

Conclusion: Total room time is influenced by endoscopist experience and patient age, while the impact of assistant competency appears dependent on case mix and workflow structure. Process-based workflow analysis may help optimize efficiency and improve operational stability in endoscopy units.

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P-11-b-22

一般演題 Others2 (Miscellaneous)

Obesity and Hyperlipidaemia Correlation with Chronic Chlorpyrifos Exposure Workers

Correlation Analysis of Obesity and Hyperlipidaemia with Long-Term Chlorpyrifos Exposure in Pest Control Workers

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Introduction: Cardiovascular disorders are the leading cause of mortality contributing to one third of global deaths. Dyslipidemia and obesity are the major contributing factors of concern. Exposure to pesticides is often linked to increased risk of cardiovascular disease. Chlorpyrifos (CP), a broad-spectrum chlorinated organophosphate, widely used by the pest control workers and is known to impair lipid metabolism. The pilot study performs Pearson correlation analysis of the lipid levels and obesity with years of CP exposure in these workers to assess temporal associations.

Material and Methods: Forty-nine pest control workers and 23 non-exposed controls were recruited. CP levels were estimated in serum using GC-MS. Eighteen of 49 exposed workers tested positive for CP and were included in the analysis. Ten of 23 non-exposed controls were selected based on lipid profiles. Years of CP exposure, age, height, weight and BMI were recorded. Lipid levels were analyzed from Blood samples. Data were presented as mean ± SD. Groups were compared by unpaired two tailed t-test. Pearson correlation coefficients (ρ) were calculated (two-tailed, with p-values).

Results: Mean age was 39.8 ± 8.1 years for exposed workers (n=18) and 31.4 ± 8.7 years for controls (n=10). Mean CP levels were 39.9 µg/kg in exposed workers vs. 11.57 µg/kg in controls. Exposed workers had higher BMI (27.4 ± 3.1 vs. 21.4 ± 2.1 kg/m2), weight (75.13 ± 9.11 vs. 60.19 ± 8.2 kg), triglycerides (237.7 ± 89.24 vs.103.4 ± 31.6 mg/dl) and LDL (145.3 ± 43.3 vs. 73.78 ± 11.3 mg/dl). The Pearson correlation coefficient (ρ) for triglycerides vs. years of exposure is 0.801 and for LDL levels vs. years of exposure is 0.837. Similarly, the Pearson correlation coefficient (ρ) for BMI vs. years of exposure is 0.816.

Conclusion: Despite age differences, CP-exposed individuals showed higher weight, BMI, deranged lipid levels vs. non-exposed controls, indicating long term CP exposure may increase risk of cardiovascular and metabolic disorders.

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P-11-b-23

一般演題 Others2 (Miscellaneous)

Impact of Missing Data in Real-World Data Analysis

An Example Using Risk Factors for Anemia

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[Objective] The use of real-world data (RWD) has increased in laboratory medicine. As these data are not primarily collected for research purposes, missing values are frequently present in laboratory measurements. Although missing data can influence estimation, studies evaluating its impact remain limited. This study compared two common approaches for handling missing data—complete case analysis (CCA) and multiple imputation (MI)—in an analysis of anemia risk factors, and aimed to provide practical guidance for handling missing data in RWD analyses.
[Methods] We analyzed publicly available data from the National Health and Nutrition Examination Survey (NHANES 2017–2018), including individuals aged ≥65 years (n=1,336). Variables included age, sex, body mass index (BMI), smoking status, C-reactive protein (CRP), estimated glomerular filtration rate (eGFR), ferritin, and albumin. We first assessed the extent of missingness and identified predictors of missingness. We then applied CCA and MI and performed logistic regression analyses with anemia as the outcome. We compared the estimated odds ratios and 95% confidence intervals (95% CIs) obtained by each method.
[Results] Missing values were observed in BMI, CRP, eGFR, ferritin, and albumin, and approximately 6.4% of cases were excluded in CCA. Missingness was related to observed variables rather than being completely at random. Estimated odds ratios were broadly similar between CCA and MI. For most variables, the 95% CIs were slightly narrower with MI than with CCA.
[Conclusion] Differences between CCA and MI were limited, likely because the overall proportion of missing data was relatively low and missingness showed no clear association with anemia. Appropriate handling of missing data may help reduce bias due to missingness and provide more appropriate interval estimates by accounting for uncertainty. After careful evaluation of the mechanism and characteristics of missing data, MI should be considered alongside CCA rather than relying solely on CCA.

P-11-b-24

一般演題 Others2 (Miscellaneous)

Verifying Third-Party Control Materials for Hormone and Tumor Marker Testing

Comparative evaluation with dedicated controls using patient R-values from the even check method

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Background In clinical laboratory internal quality control, the introduction of third-party controls independent of measurement system manufacturers is recommended to detect potential bias. Hormone and tumor marker analytes are particularly susceptible to reagent lot changes, where even minor shifts may affect clinical decision-making. This study aimed to verify the clinical utility of a third-party control by comparing its performance with manufacturer-dedicated controls, using R-values retrospectively derived from the even check method based on patient data (patient-R-values) as an objective indicator. **Methods** Using cobas 8000 e801 with ECLIA, eight analytes including FT4, FT3, TSH, CEA, ferritin, CA19-9, CA125, and PSA were measured in parallel with the third-party control and dedicated controls at the same time points. Shifts around specific events and trends during evaluation periods were analyzed, with patient-R-values serving as the objective indicator. **Results** For FT4, FT3, and CEA, the third-party control detected measurement system shifts with sensitivity equivalent to the dedicated controls, showing generally good agreement with patient-R-values. For PSA, both controls demonstrated concordant significant upward trends, detecting subtle system changes at an early stage before any impact appeared in patient-R-values. For ferritin, a specific upward trend was observed only in the third-party control while patient-R-values and dedicated controls remained stable. The remaining analytes showed no notable changes in either controls or patient-R-values. **Conclusion** The third-party control showed potential as an early-warning tool, demonstrating detection capability equivalent to the dedicated controls for both shifts and early trends. For ferritin, the observed trend resolved after reagent replacement, supporting early detection of reagent drift rather than a matrix effect. However, distinguishing true reagent drift from matrix effects remains challenging. Since third-party controls may occasionally detect changes whose interpretation is not straightforward, parallel use with patient data-based real-time quality control is recommended for comprehensive verification.
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P-11-b-25

一般演題 Others2 (Miscellaneous)

Borrelia burgdorferi detection in Iceland

Detection of Borrelia burgdorferi (s.l.) in Ixodes ricinus ticks collected in Iceland

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Ixodes ricinus is the most widespread tick species in Europe and a known vector of several zoonotic pathogens, including *Borrelia burgdorferi* sensu lato (s.l.) and tick-borne encephalitis virus (TBEV). Its presence in Iceland has raised concerns regarding its potential role in pathogen transmission to humans and animals. This study aimed to assess whether *I. ricinus* ticks collected in Iceland carry *B. burgdorferi* (s.l.), and in a limited number of samples, other pathogens of public health relevance.

Ticks were collected from birds at the South East Iceland Bird Observatory between 2018 and 2019. All specimens were screened for *B. burgdorferi* (s.l.). Additionally, 133 ticks collected prior to 2018 and preserved in the Natural Science Institute of Iceland were analyzed for *B. burgdorferi* (s.l.), TBEV, *Coxiella burnetii*, *Francisella tularensis*, and *Rickettsia* spp. Positive *Borrelia* samples underwent sequencing and BLAST analysis.

In total, 1,209 *I. ricinus* ticks were screened for *B. burgdorferi* (s.l.), with a prevalence of 9.9% (86/866). Sequencing of 28 positive samples identified three genospecies: *B. garinii* (82.1%), *B. valaisiana* (14.3%), and *B. afzelii* (3.6%). No other pathogens were detected in the archived specimens.

This study provides the first molecular evidence of *B. burgdorferi* (s.l.) in *I. ricinus* ticks in Iceland. Although Lyme borreliosis is not considered endemic and *I. ricinus* is not yet considered established, the presence of infected ticks indicates a potential risk of tick-borne disease. Ongoing surveillance and public health awareness are essential to mitigate future risk.

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P-11-b-26

一般演題 Others2 (Miscellaneous)

Avian Influenza screening in Iceland

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Highly pathogenic avian influenza viruses (HPAIVs) of hemagglutinin type H5 and clade 2.3.4.4b have widely spread within the northern hemisphere since 2020 and threaten wild bird populations, as well as poultry production.

Although low pathogenicity avian influenza virus (AIV) strains have been detected in sea birds around Iceland, outbreaks of HPAIV were not reported from Iceland until spring 2022.

Despite an appeal from the Icelandic Food and Veterinary Authority (MAST) in Iceland to the public to report finding of sick or dead wild birds only 17 birds came to be sampled in the first 9 months of 2021 where AIV was tested, and all samples were AIV negative. In the beginning of 2022, MAST enhanced passive surveillance through reports from the public of sick or dead wild birds. In mid-April, a common raven (Corvus corax) and a pink-footed goose (Anser brachyrhynchus) tested HPAIV H5N1 positive.

Surveillance for HPAIV in wild birds, found deceased or exhibiting signs of illness, is ongoing. In 2023, the first detection of HPAIV H5N5 in a white-tailed sea eagle was reported. Since the initial detection of HPAIV in Iceland, MAST has closely monitored the virus's spread within wild bird populations.

Each year, a limited number of samples from poultry have been tested for AIV, all yielding negative results until December 2024. During this time, a poultry farm reported birds exhibiting clinical symptoms consistent with avian influenza. Diagnostic screening confirmed the presence of HPAIV H5N5 in the samples.

In late December 2024, HPAIV H5N5 was detected in a domestic kitten that died after a short illness and had undergone a post-mortem examination at Keldur. This finding prompted expanded screening for IAV in domestic cats and wild mammals, leading to the detection of H5N5 in two additional cats, two foxes, and a mink.

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P-11-b-27

一般演題 Others2 (Miscellaneous)

Vitamin-D status and metabolic risk markers in Icelandic youth

A longitudinal cohort study

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Background:
Low vitamin D status has been associated with insulin resistance, type 2 diabetes, and other metabolic disturbances. These associations may be particularly relevant during childhood and adolescence, a critical period for metabolic development. However, it remains unclear whether vitamin D plays a causal role or primarily reflects confounding factors such as adiposity and lifestyle, particularly in populations living at northern latitudes.
Objectives:
To investigate the longitudinal association between serum 25-hydroxyvitamin D [25(OH)D] levels in childhood and subsequent changes in body mass index (BMI) and markers of glucose metabolism during adolescence.
Methods:
This study is based on secondary analysis of data from the *Health Behaviour of Icelandic Youth* cohort, a longitudinal study including approximately 230–250 participants followed from 2006 to 2017. The dataset includes repeated measurements of serum 25(OH)D, fasting glucose, insulin, and HbA1c, as well as data on body composition and lifestyle factors such as physical activity and sleep. Statistical analyses will assess associations between early vitamin D status and later metabolic outcomes, with adjustment for relevant covariates including adiposity and lifestyle factors.
Results:
Data analysis is currently ongoing. Preliminary analyses will examine longitudinal associations between childhood 25(OH)D levels and adolescent BMI and metabolic markers.
Conclusion:
This study will provide insight into the potential role of vitamin D in early metabolic regulation and its association with later metabolic risk. The findings may contribute to a better understanding of whether vitamin D status represents an independent factor or a marker of underlying metabolic risk in children and adolescents.

P-11-b-28

一般演題 Others2 (Miscellaneous)

Data-driven management of outpatient blood collection crowding

Integrating AI prediction with clinical capability

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Objective: Outpatient blood collection rooms often face severe morning congestion, leading to patient dissatisfaction and high staff workload. At Gifu University Hospital, a facility managing approximately 1,320 daily outpatients, operational decisions traditionally relied on reactive staff intuition. This study established a proactive, data-driven management system using an AI-based congestion prediction application to optimize resource allocation and improve patient flow.
Methods: We developed a prediction engine using the XGBoost algorithm, integrating real-world data such as historical collection logs, calendar variables, and meteorological data from the Japan Meteorological Agency. Clinical laboratory scientists led the development by performing critical feature engineering, incorporating domain knowledge such as the specific impact of rainy days and post-holiday patient surges. The system was deployed as a user-friendly application for frontline staff to visualize predicted waiting times and time-slot-specific reception counts.
Results: Implementation enabled the proactive activation of a tenth temporary collection lane when predicted waiting times exceeded 30 minutes. On Fridays, this intervention successfully maintained average waiting times within 30 minutes. On Wednesdays, the combination of the tenth lane and a 10-minutes earlier 8:05 start time led to significant improvements in patient throughput. Recognizing that internal resources were reaching physical limits, predicted congestion data was disclosed to patients to encourage arrivals after 9:30. This "Patient Partnership" approach effectively dispersed peak demand and balanced service needs.
Conclusion: Sustainable laboratory management relies on the integration of predictive technology, agile staffing, and data transparency. Empowering clinical experts to lead AI development through domain-specific feature engineering is essential for creating high-precision, practical tools for healthcare operations.

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P-11-b-29

一般演題 Others2 (Miscellaneous)

Advancing Efficiency and Safety in RIA via Fully Automated Instruments

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Background : In Taiwan, most of clinical laboratories use semi-automated methods to perform RIA (Radioimmunoassay) tests, and our laboratory is no exception. However, manual steps carry a substantial risk of manual errors and manual handling between instruments leads to significant timing variability. Additionally, with the increasing number of specimens and the difficulty of increasing manpower, the shift toward comprehensive automation has become imperative to maintain diagnostic quality. **Methods :** Take our laboratory as an example. To address the aforementioned challenges, we are the first RIA clinical laboratory in Taiwan to introduced the MESSIAH R-4200, a fully automated instrument featuring true walk-away capability. **Results :** The MESSIAH R-4200 is an integrated system that automates the entire workflow, from barcode scanning, sample aliquoting, and tracer addition to incubation, washing, and radioactivity counting. Consequently, staff members no longer need to move samples manually through each experimental stage, allowing for a more efficient and standardized workflow. By significantly reducing the frequency of manual radioactive material handling, the system effectively minimizes occupational health risks and ensures a safer working environment in compliance with ALARA principles. Moreover, in handling a 27% increase in sample numbers over five years, this equipment has proven to be a tremendous asset, greatly enhancing throughput without requiring additional full-time equivalents (FTEs). This transition allows laboratory professionals to shift their focus from repetitive manual labor to more critical tasks, such as data analysis and quality control. **Conclusion:** Implementing fully automated RIA systems minimizes manual errors, enhances occupational safety, and optimizes laboratory throughput. This transition is essential for modern laboratories to ensure standardized diagnostic quality amidst increasing workloads.

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P-11-b-30

一般演題 Others2 (Miscellaneous)

MAP-Derived Compounds: Animal Studies to Human Pathological Insights

Translational Pathological Assessment of MAP-Derived Compounds from Animal Models to Human Health

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Medicinal and Aromatic Plants (MAPs) have long been recognized as a valuable source of bioactive compounds with therapeutic potential. In recent years, increasing attention has been directed toward the scientific validation of MAP-derived leads using experimental animal models to bridge the gap between traditional knowledge and modern clinical applications. Research work in our laboratory emphasis on pre-clinical development to explore the role of MAP-derived phyto-constituents in modulating pathological conditions in experimental animals, with an emphasis on their translational relevance for human health. A wide range of plant-derived compounds, were evaluated for their pharmacological efficacy in small animal models exhibiting inflammatory, metabolic, neurological, and infectious disorders. Pathological investigations, including histopathology, immuno-histochemistry, biochemical assays, and molecular analyses, were employed to assess tissue-specific responses, mechanisms of action, and safety profiles. These investigations provided critical insights into disease progression, cellular alterations, and therapeutic outcomes following treatment with MAP-derived compounds.

These scientific validation studies, conducted under physiological conditions in animal models, provide a foundation for subsequent regulatory studies and clinical validation in end users, i.e., humans.

Keywords: MAPs, Experimental Animals, Pathology,

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P-11-b-31

一般演題 Others2 (Miscellaneous)

Unmasking Occult CKD via Selective Cystatin C Testing

An Interpretable Routine Data Model for Prioritized Detection Under Resource Constrains

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Background: Creatinine-based estimated glomerular filtration rate (eGFRcr) can overestimate kidney function in older adults and individuals with reduced muscle mass, leading to underrecognized chronic kidney disease (CKD). Cystatin C-based assessment can reveal this occult CKD, but routine measurement is often limited by cost and reimbursement constraints. We developed an interpretable prediction model to prioritize cystatin C testing for detecting occult CKD using routinely available laboratory variables.

Methods: This retrospective study used laboratory data from Gifu University Hospital (August 2022 to October 2025). Adults with same-day serum creatinine and cystatin C measurements were included (n = 6,914). Occult CKD was defined as eGFRcys < 60 with eGFRcr ≥ 60 mL/min/1.73 m². Data were split temporally into development (n = 2,085) and validation (n = 1,029) cohorts restricted to eGFRcr ≥ 60. An L2-regularized logistic regression model was developed using six routine variables: age, sex, serum creatinine, blood urea nitrogen, serum albumin, and hemoglobin. Performance was compared with eGFReq5 and individualized eGFRcr (eGFRindiv) in a resource-constrained screening scenario where cystatin C testing was limited to a fixed proportion of highest-risk patients.

Results: Occult CKD prevalence was 31.0% (319/1,029) in the validation cohort. The proposed model achieved an AUC of 0.816 (95% CI: 0.789 to 0.843), outperforming all comparators. In the resource-constrained screening analysis, the model consistently detected more occult CKD cases than eGFReq5 and eGFRindiv. At a 20% flagging rate, the model achieved 43.4% sensitivity, representing relative improvements of 19% over eGFReq5 (36.6%) and 40% over eGFRindiv (30.9%). Advantages were most pronounced among older adults and those with lower serum albumin.

Conclusions: An interpretable model using six routine laboratory variables may help prioritize cystatin C testing under resource constraints and may improve detection of occult CKD that may be underrecognized by creatinine-based screening alone.

P-11-b-32

一般演題 Others2 (Miscellaneous)

Roles and Duties of medical technologists in the Emergency Department

A Report on Task-Shifting Implementation

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[Introduction] In May 2012, our hospital established a new emergency ward, leading to the permanent assignment of medical technologists (MTs) to the emergency department (ED). Furthermore, following the promotion of work-style reforms for physicians, the scope of practice for various healthcare professionals are expanding through task-shifting and task-sharing. A legal amendment in October 2021 further facilitated a working environment for MTs to perform specialized clinical duties more efficiently.

[Background and Objectives] At our hospital, MTs are assign to the ED to provide active clinical support as integral members of the medical team. Although the number of facilities employing MTs in emergency settings is increasing due to task-shifting, widespread adoption remains in its early stages. This report introduces the specific duties of MTs in our ED.

[Methods and Duties] MT duties in our ED primarily consist of statutory tasks, such as blood collection, specimen sampling and performing electrocardiograms. Additionally, under the task-shifting framework, they also engage in clinical support beyond traditional laboratory work, including assisting with chest compressions during cardiopulmonary resuscitation, and securing peripheral intravenous access.

[Results and Discussion] The primary advantage is the ability to participate in patient care through close multidisciplinary collaboration. Conversely, challenges include staffing coordination with the central laboratory and the need for continuous standardization of clinical duties.

[Conclusion] We hope these insights contribute to discussions regarding promoting the placement and expanding the professional roles of MTs in emergency medical settings.

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P-11-b-33

一般演題 Others2 (Miscellaneous)

ChA induces ROS-mediated apoptosis via HAS in HCC cells

Apoptotic effects of ChA via the ROS/HAS axis in HCC cells

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Hepatocellular carcinoma (HCC) is one of the most common and lethal malignancies worldwide. Chaetoglobosin A (ChA), a metabolite isolated from the endophytic fungus Chaetomium globosum Km1226, exhibits antitumor effects; however, its anticancer mechanisms in HCC remain unclear. In this study, ChA significantly inhibited HCC cell growth and proliferation and induced G2/M phase arrest through downregulation of p-Cdc2/Cyclin B1 and upregulation of γ-H2AX. ChA also promoted apoptosis, mitochondrial dysfunction, and ROS accumulation, accompanied by increased HO-1 and reduced Keap1 expression. Treatment with N-acetylcysteine (NAC) or HO-1 knockdown attenuated ChA-induced apoptosis and mitochondrial dysfunction, indicating that activation of the ROS–HO-1 axis plays a critical role in these effects. RNA sequencing further identified HAS2, a gene associated with hyaluronan synthesis and tumor progression, as a downstream target suppressed by ChA. ChA-induced downregulation of HAS2 and RSK1 was restored by NAC treatment, suggesting regulation through a ROS-dependent mechanism. Moreover, MG132 treatment reversed RSK1 suppression, indicating that ChA promotes ubiquitin–proteasome-mediated RSK1 degradation, thereby contributing to HAS2 inhibition. Collectively, these findings demonstrate that ChA exerts potent anticancer activity in HCC cells through activation of the ROS–HO-1 axis and suppression of the RSK1–HAS2 pathway, highlighting its therapeutic potential for HCC treatment.

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P-11-b-34

一般演題 Others2 (Miscellaneous)

Occupation-specific burnout pathways among Korean healthcare workers

Moderated mediation through job satisfaction using Korea Veterans Health Service data

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Background This cross-sectional secondary analysis examined whether job satisfaction mediates the association between emotional labor and burnout, and whether the mediation pathway differs by occupation among hospital-based healthcare workers.
Methods We analyzed data from a standardized self-administered survey conducted in July 2022 across six hospitals under the Korea Veterans Health Service. Of 570 eligible healthcare workers, 290 responded (response rate 50.9%), including clinical laboratory scientists, radiologic technologists, physical therapists, and dental hygienists. We applied generalized structural equation modeling to test an occupation-specific moderated mediation model (emotional labor → job satisfaction → burnout), adjusting for age, sex, employment status, weekly working hours, self-rated health status, and hospital.
Results Dental hygienists showed the highest mean emotional labor and burnout levels. In the overall mediation model, higher emotional labor was associated with lower job satisfaction (a = − 0.765; 95% CI − 0.857 to − 0.674) and higher burnout both directly (c′ = 0.340) and indirectly via job satisfaction (indirect effect = 0.096), corresponding to 22.1% mediation of the total effect (total effect = 0.436). In occupation-specific models, the indirect effect through job satisfaction was significant for clinical laboratory scientists and radiologic technologists, whereas the direct effect of emotional labor on burnout remained significant across all four occupations.
Conclusion The mediation pathway differed by occupation, suggesting that burnout mitigation strategies may benefit from occupation-tailored approaches, with particular attention to strengthening job satisfaction where mediation is evident.

Keywords Burnout, Emotional labor, Healthcare workers, Job satisfaction, Moderated mediation, Structural equation modelling.

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P-11-b-35

一般演題 Others2 (Miscellaneous)

Enhancing Clinical Laboratory Internship Training Through an Intelligent Learning System

Application to Sperm Counting and Morphological Analysis in Microscopic Examination

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Background:

Integrating AI into clinical laboratories can address training challenges in manual semen analysis, which is time-consuming and prone to inter-observer variability. Interns often lack sufficient hands-on practice, leading to inconsistent skills and low confidence.

Method:

We developed an AI-assisted teaching platform using the YOLO object detection algorithm. The system integrates an optical microscope, a high-resolution CMOS camera, and an AI processing unit to analyze real-time video feeds. Interns perform manual microscopic examination, then immediately compare their results with the AI-generated report (count, motility, and morphology).

Results:

Preliminary validation showed good accuracy (AUC > 0.87). The platform provides immediate objective feedback and enables a “practice-feedback-reflection” cycle, which improved interns’ operational consistency and interpretation confidence.

Discussion and Conclusion:

This AI-enhanced platform reduces inter-observer variability, optimizes teaching resources, and standardizes training. Limitations include the need for broader morphological recognition and long-term outcome studies. Future work will extend the system to motility grading and other microscopic analyses, promoting deeper AI integration in laboratory medicine education.

Keywords: *AI-assisted teaching, Image recognition, Clinical laboratory education, Sperm analysis*

P-11-b-36

一般演題 Others2 (Miscellaneous)

The Ethics Game

Exploring Ethical Awareness Through Guided Group Reflection

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The Ethics Game is a structured, discussion-based learning tool designed to help small groups reflect on ethical dilemmas commonly encountered in the work environment. Initially introduced at the Scandinavian BLS Congress (BIO 2023), the game has since been implemented across Norwegian BLS educational programs, medical laboratory workplaces, and among union representatives. Its primary aim is to strengthen ethical awareness through guided reflection, dialogue, and value exploration.

Central to the game is the **Game Master**, a facilitator with ethical competence who creates a safe and stimulating environment for discussion. The Game Master—typically a teacher, ethics committee member, or organizational leader—receives dedicated training to ensure they can effectively guide participants through the game’s structure and support meaningful ethical conversations.

Participants navigate an “ethical landscape” where they are introduced to ethical theories, underlying values, and practical dilemmas. No prior knowledge of ethics is required for the participants, making the game accessible to diverse professional groups. Each group works with its own board and can select dilemma categories relevant to their specific context, ensuring that discussions remain meaningful and applicable.

The Ethics Game encourages open dialogue, respectful challenge, and active listening. By articulating personal viewpoints and engaging with differing perspectives, participants gain deeper insight into their own reasoning and broaden their ethical understanding. The game fosters a collaborative learning atmosphere where values are examined, motivations are clarified, and ethical awareness is strengthened collectively.

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P-11-b-37

一般演題 Others2 (Miscellaneous)

Menstrual blood stem cells in wound healing

Comparison of regeneration of stem cells derived from women with and without premenstrual syndrome

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Stem cells derived from menstrual blood (MenSCs) represent a promising alternative in regenerative medicine to established sources such as umbilical cord blood and bone marrow, mainly due to their non-invasive and repeatable collection. In addition, MenSCs exhibit high regenerative potential, making them particularly relevant for wound healing applications. Since cyclic hormonal changes in female donors may influence the cellular behavior of MenSCs, this study focused on the potential impact of premenstrual syndrome (PMS), an area that remains largely unexplored. The aim of this study was to compare the wound healing capacity of MenSCs derived from women with (n=5) and without PMS (n=5), using human dermal fibroblasts (HDFs) as a reference cell type. Wound healing dynamics and migratory behavior were assessed using a scratch assay at four defined time points (0, 6, 24, and 48 h). In addition, potential paracrine effects of conditioned media from MenSCs on HDFs were evaluated. MenSCs demonstrated significantly higher migratory activity than HDFs ($p < 0.01$). Only a non-significant trend was observed between MenSCs from PMS-positive and PMS-negative donors at 24 h, suggesting slightly enhanced wound closure in the PMS-negative group. HDFs treated with MenSC-derived conditioned medium also showed a time-dependent increase in migration, although this effect remained non-significant. Across all groups, wound closure was primarily driven by time ($p < 0.001$).
These findings highlight the regenerative potential of MenSCs and provide a basis for further investigation of their therapeutic applications, especially in the field of women's health. However, larger sample sizes are required to validate these preliminary results and to better understand the influence of hormonal status on MenSC function.

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P-11-b-38

一般演題 Others2 (Miscellaneous)

Antrodia cinnamomea Inhibits Liver Fibrosis

Modulating HIF-1/2-TWIST-BMI1 Signaling and EMT in TGF-beta1 Induced Fibrosis

©Tai An Chiang[1)]、Ya Fang Huang[2)]、 Zhao Ming Pan[1)]、Yi Shan Chiang[1)]、Pei Fen Wu[3)]、Shi Hao Dai[4)]
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Antrodia cinnamomea, an endemic medicinal fungus native to Taiwan, has been traditionally employed in folk medicine and as a complementary therapy for various ailments. Liver fibrosis, characterized by excessive extracellular matrix (ECM) deposition from an imbalance between fibrogenesis and fibrolysis, remains a progressive condition without approved drugs to reverse established fibrosis. To evaluate the anti-fibrotic potential of A. cinnamomea extracts, we developed an in vitro model of liver fibrosis by stimulating HepG2 hepatoma cells with transforming growth factor-β1 (TGF-β1). We examined modulation of the hypoxia-inducible factor (HIF)-1/2–TWIST–BMI1 signaling axis and epithelial-mesenchymal transition (EMT).TGF-β1 treatment markedly upregulated the fibrotic marker fibronectin, accompanied by significant elevations in HIF-1α, HIF-2α, TWIST, and BMI1 protein expression. A. cinnamomea extracts dose-dependently reduced HIF-1α and HIF-2α levels ($p<0.05$), with parallel downregulation of downstream TWIST and BMI1, effectively inhibiting EMT progression and promoting partial phenotypic reversion. Immunofluorescence confocal microscopy vividly demonstrated restoration of epithelial morphology, including E-cadherin upregulation and vimentin downregulation. Furthermore, ECM protein accumulation was substantially diminished in extract-treated groups ($p<0.05$), confirming robust suppression of fibrotic processes.Collectively, these findings reveal that A. cinnamomea extracts counteract liver fibrosis by targeting the HIF-1/2–TWIST–BMI1 axis to inhibit EMT and stemness traits, yielding improvements in both molecular markers and cellular phenotypes. This research provides mechanistic validation of its anti-fibrotic efficacy, supporting development of natural product-based therapeutics and innovative strategies. It underscores liver fibrosis as a dynamically controllable pathology, challenging its reputation as irreversible.

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P-11-b-39

一般演題 Others2 (Miscellaneous)

Antrodia cinnamomea Extract Regulates EMT in Liver Fibrosis

HIF-1/2-TWIST-BMI1 Axis in Liver Fibrosis Reversal Mechanisms

©Tai An Chiang[1)]、Ya Fang Huang[2)]、 Zhao Ming Pan[1)]、Yi Shan Chiang[3)]、Pei Fen Wu[4)]、Shi Hao Dai[5)]
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Liver fibrosis has traditionally been viewed as a progressive, irreversible pathology, driven by hepatocyte phenotypic changes and excessive extracellular matrix (ECM) deposition via epithelial-mesenchymal transition (EMT). To explore natural compounds' potential in reversing fibrosis, this study used a TGF-β1-induced HepG2 cell model to mimic fibrotic conditions and assessed Antrodia cinnamomea extracts' effects on EMT reversibility and fibrosis markers.TGF-β1 stimulation significantly downregulated epithelial marker E-cadherin ($p<0.05$) while upregulating mesenchymal markers N-cadherin and vimentin ($p<0.05$), confirming EMT induction with fibrotic traits. A. cinnamomea extract treatment markedly restored E-cadherin expression and suppressed N-cadherin and vimentin levels ($p<0.05$), effectively inhibiting and partially reversing EMT. Time-course analysis showed gradual normalization of EMT markers toward baseline with extended treatment, underscoring the process's dynamic, regulatable nature. Immunofluorescence staining via confocal microscopy further validated morphological reversion from mesenchymal- to epithelial-like phenotypes, including reinstated E-cadherin membrane localization, offering compelling cellular evidence. Additionally, fibrosis-related proteins were broadly reduced in extract-treated groups ($p<0.05$), indicating attenuated ECM accumulation and lessened fibrotic severity.

In conclusion, A. cinnamomea extracts ameliorate liver fibrosis features by reversing EMT, contesting its irreversibility. These results spotlight the extracts' promise as antifibrotic agents, furnishing mechanistic insights into natural compounds' roles and establishing a basis for innovative antifibrotic therapies.

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P-11-b-40

一般演題 Others2 (Miscellaneous)

Reusable Strap System Reducing Phlebotomy Waste and Enhancing Safety

A governed reusable strap loan model improving safety and reducing phlebotomy waste

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Phlebotomy stations are high-volume service points where small consumables accumulate into substantial environmental impact. In our hospital laboratory, staff historically used single-use self-adherent elastic wraps to support post-venipuncture compression for patients unable to maintain pressure independently because of reduced hand strength, mobility aids, caregiver constraints, or time-sensitive clinical needs. Seasonal behaviors such as hurried dressing further shortened recommended compression time and increased risks of bleeding, bruising, and swelling. Although clinically convenient, the wrap is a single-use item that contributes directly to medical waste and recurrent procurement costs.

To align patient safety with sustainable resource stewardship, we introduced a governed loan–use–return model using reusable, disinfectable buttoned compression straps to replace single-use wraps whenever appropriate. A donation of 1,000 straps enabled immediate implementation without requiring patient pre-purchase. Staff identified patients who required assisted compression after venipuncture, applied a reusable strap, and provided brief instructions. A simple governance mechanism—an instruction sticker affixed to the patient’s queue ticket—marked the loan and served as the return indicator. Returned straps were collected with the ticket, disinfected according to local procedures, and recirculated. Patients leaving urgently were allowed to purchase straps at cost, preventing stock loss while maintaining continuity of care.

Between 2022 and 2025, issuance of single-use wraps decreased from 936 to 432 rolls, representing a 53.8% reduction. Total expenditure during this period was NT$73,440, compared with an estimated NT$112,320 under constant 2022-level use, resulting in approximately NT$38,880 in avoided procurement costs. The intervention demonstrated operational feasibility, equitable access to hemostasis support, and measurable environmental benefit.This pragmatic model shows that sustainability and patient safety can be simultaneously advanced within routine laboratory operations. The governed reusable-strap system offers a scalable, low-cost approach for reducing waste in phlebotomy services and may be transferable to other outpatient procedures where single-use materials are applied for convenience.

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P-11-b-41

一般演題 Others2 (Miscellaneous)

Employer Branding in Generational Change

An Analysis of Expectations in Biomedical Analytics in Austria

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The shortage of skilled Biomedical Analysts (BMA) in Austria poses challenges for healthcare providers, particularly in recruiting Generation Z. This study identifies the specific employer branding expectations of Generation Z in the Austrian BMA sector, contrasting them with the preferences of older Generations X and Y.

A quantitative research approach was employed using a standardized online survey (CAWI). The final sample consisted of active BMA professionals (55.7%) and students (44.3%). Data analysis was conducted using inferential statistical methods, including t-tests, Mann-Whitney U-tests, and Chi-square tests, to evaluate the formulated hypotheses.

The analysis reveals a qualitative shift in values within the industry. While overall expectations of employer branding do not differ quantitatively across generations, significant differences exist in prioritization. Generation Z weights "soft factors"—such as corporate culture, appreciation, and perceived meaning of work—significantly higher than material factors. In contrast, older generations place a significantly higher value on job security and stable framework conditions. Furthermore, Generation Z shows a clear preference for digital channels, specifically career websites and social media, for information gathering. Employer branding in the BMA sector must adopt a culture-centered and digitally visible strategy to remain competitive. Future measures should prioritize societal meaningfulness and an appreciative, transparent feedback culture. To ensure long-term retention across all cohorts, organizations should combine digital recruitment for the youth with security-focused internal communication and mentoring programs for the experienced workforce.

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P-11-b-42

一般演題 Others2 (Miscellaneous)

Automation of the decantation step in density gradient PBMC isolation

Comparative evaluation of PBMCs isolated by automated and manual decanting

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Peripheral blood mononuclear cells (PBMCs) are widely used in basic research, clinical diagnostics, and cell-based therapies, and reliable separation of PBMCs from whole blood is a critical preparatory step. However, the conventional density gradient centrifugation method commonly used for PBMC isolation is labor-intensive and requires a certain level of technical expertise. In addition, operator-dependent variability in cell recovery has been recognized, posing challenges to procedural reproducibility in laboratory workflows.

This study aimed to introduce automated handling into density gradient PBMC separation using separation tubes, with the goals of lowering operator workload and achieving cell quality comparable to that obtained by skilled operators. The decantation step, which is considered an operator-dependent process in PBMC separation, was selected as the target for automation.

Based on the motion analysis of skilled operators, a decanting device was designed, and suitable decanting motions for PBMC separation were investigated through preliminary experiments using colored water evaluation. Subsequently, blood samples obtained from healthy donors were divided and processed in parallel by skilled operators or the decanting device for PBMC isolation, with all procedures other than the decanting step performed manually by the operators. Comparative analyses demonstrated that white and red blood cell counts and the distribution of T cell subsets were comparable between samples processed by the device and those processed manually by skilled operators. In addition, the isolated cells were cryopreserved, and post-thaw viability was approximately 80% for both automated and manual processing, showing comparable results. These results suggest that the developed decanting device achieves performance comparable to that of experienced operators and may serve as an alternative to manual decanting. Accordingly, it is expected to contribute to the automation and standardization of PBMC isolation workflows.

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P-11-b-43

一般演題 Others2 (Miscellaneous)

Basic Analytical Performance Evaluation of HISCL HIT IgG Assay Kit

Using Automated Blood Coagulation Analyzer CN-6500

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Background: Heparin-induced thrombocytopenia (HIT) is a potentially fatal, immune-mediated adverse reaction associated with unfractionated or low-molecular-weight heparin (UFH or LMWH) therapy, characterized by thrombocytopenia and thrombosis. HISCL HIT IgG Assay Kit quantitatively detects IgG antibodies against PF4/heparin complexes in human plasma and serum and may aid in the diagnosis of HIT when interpreted with other clinical findings.
Objective: This study evaluated the basic analytical performance of HISCL HIT IgG Assay Kit using Automated Blood Coagulation Analyzer CN-6500, including Precision, Linearity, Detection capability, Effects of anticoagulant drugs, On-Board-Stability, and correlation between plasma and serum samples.
Methods: Analytical evaluations were conducted in accordance with CLSI guidelines. Measurements were performed using CN-6500 and HISCL HIT IgG Assay Kit. Plasma and serum samples from healthy donors, donors containing anticoagulant drugs, and samples containing HIT IgG anti-body were analyzed.
Results: Precision study demonstrated maximum coefficients of variation (CVs) of 2.3% for repeatability, 2.4% for within-laboratory precision, and 2.5% for between-laboratory precision. Linearity was demonstrated across the entire measurement range of 0.10-128.00 U/mL, with a maximum deviation of 7.0% from theoretical values near the medical decision level. The limits of blank (LoB), detection (LoD), and quantitation (LoQ) were 0.01 U/mL, 0.014 U/mL, and 0.08 U/mL, respectively. On-Board stability was verified for up to 90 days. No significant interference was observed with UFH or LMWH up to 1.2 IU/mL or with Argatroban up to 1.5 μg/mL. A strong correlation was observed between plasma and serum samples (slope: 1.05; correlation coefficient: 1.00).
Conclusions: HISCL HIT IgG Assay Kit demonstrated favorable analytical performance across all evaluated parameters, supporting its basic clinical utility in routine laboratory practice.

P-11-b-44

一般演題 Others2 (Miscellaneous)

Patient Involvement in Research: From Strategy to Practice

Biomedical Laboratory Scientist Bridging Patients and Research Partnerships

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In 2021, Odense University Hospital (OUH) and University of Southern Denmark (SDU) implemented a new comprehensive research strategy in response to increasing demands from funding bodies and patient organizations for patient involvement in health research. The ambition was to involve patients in all phases of research. This led to an initiative engaging patients as Research Partners (RP) at the Department of Pathology, OUH.
A team of four researchers launched the project using a learning-by-doing approach, with one member, a Biomedical Laboratory Scientist (BLS), as Research Partner Coordinator (RPC). Initial challenges included recruiting patients in a Pathology Department without direct patient contact and identifying meaningful research activities for RP participation. Recruitment through social media had limited success, whereas collaboration with patient organizations proved effective. Sustaining RP engagement and ensuring their active involvement in research became the next key focus.
In the 2022 pilot phase, four patients joined as RP. By 2026, the group had expanded to eight active RP's, despite some member turnover. The RP's contribute by reviewing funding applications, participating in research meetings, commenting on strategies and future projects and discussing initiatives from a patient perspective. The RPC role has become central to the initiative, coordinating communication, meetings, and connections between researchers and RP. Equally important, the RPC supports RP by ensuring they feel acknowledged and valued while understanding their experiences as patients within the healthcare system.
The local initiative has been highly successful and will influence the upcoming 2026 OUH/SDU research strategy on patient involvement. A key element is appointing a dedicated coordinator for RP. The local initiative reveals that a BLS is highly qualified for this role, coordinating activities and communication as well as understanding and supporting RP needs and perspectives.

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P-11-b-45

一般演題 Others2 (Miscellaneous)

Barriers and Motivators for Research among Biomedical Laboratory Scientists

A Mixed-method Study in a Danish Pathology Department

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Evidence-based healthcare is essential. International ethical codes emphasize the role of biomedical laboratory scientists (BLS) in research and implementation of scientific advances. Despite this, literature reveals limited knowledge on BLS research, although barriers and motivators are explored in other healthcare professions. The aim of this study is to explore barriers and motivators for BLS research.

The study was conducted at the Department of Pathology, Odense University Hospital. Seventy-four BLS were invited to complete a questionnaire of forty-two items, and ten BLS participated in follow-up semi-structured interviews. Interviews were recorded and fully transcribed. Data was analyzed by descriptive statistics and thematic content analysis.

The survey response rate was 69%. All agree that BLS research is important in evidence-based practice, but fewer perceive it important for developing personal competencies. Awareness of the local research frameworks is limited, and insecurities about research skills are present. Three main themes emerged from interviews: limited awareness of research opportunities, motivators and barriers to conduct research, and self-perceived research competencies. Despite being motivated, barriers include work-life balance, impression of limited support from management and colleagues and a notion of inferiority to other professions. Most informants feel confident in laboratory tasks but are uncertain about initiating projects and academic writing, expressing a need for mentorship.

This study reveals that BLS recognizes the importance of research for evidence-based practice but fewer in relation to their own professional growth. Barriers include limited knowledge on research opportunities, support systems, and internal hierarchies. The informants emphasize the need for research culture, improved communication, mentorship, and interdisciplinary collaboration to enhance motivation.

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P-11-b-46

一般演題 Others2 (Miscellaneous)

Intelligent A-E Tier Laboratory Inventory Platform: In-House Development

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Abstract

Objectives Clinical reagent management faces vast item variety and strict expiration controls, where traditional manual methods risk stockouts or overstocking. Conventional software development often suffers from cross-domain communication barriers between IT engineers and clinicians. This study presents an intelligent inventory platform developed entirely in-house by medical technologists using Python Flask, bypassing requirement translation to achieve 100% precision in implementing clinical operational logic and optimizing supply chain resilience.

Methods

The platform features an adaptive, closed-loop A-E tier replenishment model that digitalizes clinical expertise. Materials are classified into five tiers based on turnover rates and traits, utilizing specialized replenishment models (e.g., fixed-volume periodic orders or expiry-triggered mechanisms) integrated with automated Email or order system dispatching. To counter consumption fluctuations, "low-stock replenishment" and "predicted expiration waste" defensive mechanisms were established. Furthermore, visualization curves assist in trend analysis, and a Large Language Model (LLM) was integrated via a Text-to-SQL framework to support adaptive data queries and synthesis.

Results

Post-deployment, the platform demonstrated exceptional stability, with over 90% of commonly used reagents successfully transitioning to automated precision replenishment. The automated workflow reduced administrative operational time by approximately 80%. Regarding risk mitigation, the platform achieved zero missed orders and zero stockouts, while dual-curve analysis effectively identified abnormal reagent depletion to minimize waste.

Conclusions This study demonstrates that medical technologists can effectively develop specialized digital tools. Transforming frontline experience into digital replenishment models and scheduled ordering mechanisms eliminates reliance on external IT departments, while significantly enhancing laboratory operational efficiency and supply chain resilience.Tz-Jain Ni / E-mail: 019587@tool.caaumed.org.tw

P-11-b-47

一般演題 Others2 (Miscellaneous)

The evolving role of Biomedical Laboratory Scientists in digital transformation

A new framework for competences and practice

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Introduction: Biomedical Laboratory Scientists (BLs) have traditionally focused on manual laboratory workflows and technical production and validation for diagnostics. The digital and computational era, driven by advances in technology, such as artificial intelligence (AI), globalization, and the employment of regulation and governance frameworks such as the European Health Data Space (EHDS), is transforming laboratories into data-driven ecosystems. Current BLs training often lacks emphasis on digital literacy and data governance, creating significant readiness gaps that jeopardize patient safety and institutional efficiency.

Aim: To propose a comprehensive competence framework that redefines BLs roles, skills, and competences for EHDS-compliant practice.

Methods: A literature review of EHDS regulation and laboratory competency standards was conducted. Findings were synthesized into a three-tiered framework: foundational (digital literacy and compliance), intermediate (data governance and quality), and advanced (innovation and leadership).

Results: The framework identifies 12 core domains representing key skills and competencies that can be grouped according to complexity. The foundational level focuses on adapting workflows for primary use for direct healthcare delivery by structuring data according to international standards like LOINC and SNOMED CT. The intermediate level emphasizes data "fitness for use" for secondary purposes, such as research and innovation, utilizing HL7 FHIR standards. Finally, the advanced level addresses strategic leadership, leveraging the EHDS for AI, bioinformatics, and large-scale research.

Conclusions: BLs must evolve urgently to digitally skilled health professionals, bridging the gap between laboratories, IT departments, and clinical teams. This framework provides a validated roadmap for training redesign and workforce planning, ensuring that BLSs remain central to delivering high-quality, interoperable diagnostic data in the computational era.

Keywords: Biomedical Laboratory Scientists, EHDS, digital roles, framework

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P-11-b-48

一般演題 Others2 (Miscellaneous)

Reusable Straps Reduce Phlebotomy Waste and Improve Safety

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Reusable Straps Reduce Phlebotomy Waste and Improve Safety

Background:
Phlebotomy services generate considerable medical waste due to routine use of single-use elastic wraps for post-venipuncture compression, particularly in patients unable to maintain pressure independently. While convenient, these materials increase environmental burden and cost.

Methods:
A governed loan–use–return model was implemented using reusable, disinfectable buttoned compression straps. Donated straps were provided to patients requiring assistance, with a simple tracking mechanism using labeled queue tickets. Returned straps were disinfected and recirculated, while patients unable to return them could purchase at cost.

Results:
From 2022 to 2025, single-use wrap consumption decreased from 936 to 432 rolls (−53.8%). Total expenditure was NT$73,440, compared to an estimated NT$112,320 without intervention, resulting in cost savings of approximately NT$38,880.

Conclusion:
This reusable strap system effectively reduces waste and cost while maintaining patient safety. The model is practical, scalable, and applicable to other outpatient procedures requiring temporary compression support.

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P-11-b-49

一般演題 Others2 (Miscellaneous)

DENND1A rs2479106 Variant and PCOS Phenotypes in Filipinos

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Polycystic Ovary Syndrome (PCOS) is a multifactorial endocrine disorder characterized by menstrual irregularities, hyperandrogenism, and polycystic ovarian morphology. Despite its increasing prevalence among Filipino women, limited local genetic studies have explored the association between genetic variants and the phenotypic manifestations of PCOS, highlighting the need for further investigation in the local setting. As a preliminary study, this research examined the demographic characteristics, phenotypic manifestations, and genotypic distribution of the *DENND1A* rs2479106 variant among women with and without PCOS and determined the association between identified genotypes and the clinical features of the disorder. A quantitative case-control research design was employed involving Filipino women recruited from two private clinics in Tarlac City. PCOS diagnosis was based on the Rotterdam criteria and ultrasound findings confirmed by a licensed obstetrician-gynecologist. Genomic DNA was extracted from collected blood samples, and genotyping of the *DENND1A* rs2479106 polymorphism was performed through qPCR-based analysis. Chi-square analysis revealed the association between genotypic distribution and phenotypic characteristics. Results showed a high frequency of the A allele, observed at 68.57% among PCOS cases and 66.67% among controls.The findings indicate that although the A allele was more prevalent in both groups, variations in the *DENND1A* rs2479106 genotypes showed minimal observable differences across the phenotypic features of PCOS. Further studies with a larger sample size and inclusion of additional genetic, hormonal, and environmental factors are recommended to provide a more comprehensive understanding of PCOS among Filipino women. Correspondence: Jason Dominic C. Rondina, Principal Investigator, Faculty of Pharmacy, Department of Medical Technology, University of Santo Tomas.Email: jasondominic.rondina.pharma@ust.edu.ph Phone: +63-929-396-8605

P-11-b-50

一般演題 Others2 (Miscellaneous)

Knowledge, Attitudes, and Perceptions of Medical Technologists Toward Laboratory AI

AI Adoption Among Medical Technologists in University-Affiliated Clinical Laboratories in Metro Manila

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BACKGROUND: Artificial Intelligence (AI) is transforming healthcare by improving diagnostic accuracy, streamlining workflows, and supporting data-driven decision-making. However, AI adoption in Philippine clinical laboratories remains limited, and the perspectives of Medical Technologists (MTs) toward its implementation remain underexplored. This study assessed the knowledge, attitudes, and perceptions (KAP) of registered MTs toward AI adoption in university-affiliated clinical laboratories in Metro Manila and identified influencing factors.
METHODS: A quantitative, descriptive-predictive, cross-sectional design was employed. A total of 147 responses were collected through purposive sampling, of which 121 were valid and included in the final analysis after data cleaning and screening. Data were gathered using a researcher-developed questionnaire adapted from existing instruments and analyzed using descriptive statistics and multiple linear regression.
RESULTS: Respondents were predominantly female, early-career professionals with limited AI exposure, including minimal training and institutional support. Despite this, respondents demonstrated generally high knowledge (M = 5.54/7) and favorable attitudes (M = 24.96/35), while perceptions remained moderate (M = 35.79/60). Higher knowledge was observed in data security, workflow efficiency, and AI integration through training, while gaps were noted in ethical considerations. Respondents expressed willingness to adopt AI but reported lower confidence in its reliability and integration into existing workflows. Regression analysis showed that only attitudes were significantly predicted ($R^2 = 0.161$, $p = 0.009$), with male sex, AI training, and AI tool exposure identified as significant predictors. AI training demonstrated the strongest positive association, while AI tool exposure was negatively associated with attitudes toward AI. Major barriers included lack of training, data privacy concerns, high costs, and limited institutional support, while training availability, clear guidelines, and management support were identified as facilitators.
CONCLUSION: The findings emphasize the need for AI training, institutional support, and clear implementation guidelines to facilitate safe and effective AI integration in clinical laboratories despite ongoing concerns regarding reliability, ethics, and workflow integration.

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P-11-b-51

一般演題 Others2 (Miscellaneous)

An Innovative POCT Integration Strategy for Institution-Level Management

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Background: Point-of-care testing (POCT) enables rapid laboratory testing near the patient and supports timely clinical decision-making. However, institution-wide implementation often faces challenges, including decentralized devices, numerous operators, inconsistent quality monitoring, manual data entry, delayed critical-value notification, and limited traceability. These issues may compromise patient safety and reduce management efficiency.
Methods: This quality-improvement study developed and implemented an institution-level POCT information management platform in a multi-campus healthcare system. The platform integrated POCT analyzers with hospital information systems, nursing information systems, middleware, and databases through wired and wireless connectivity. Core functions included physician-order reminders, barcode-based patient identification, automatic result upload, critical-value alerts, operator authorization, quality-control lockout, equipment monitoring, and dashboard visualization. Workflow, quality, operational, and user-related indicators were compared before and after implementation.
Results: After implementation, the billing omission rate dropped from 0.15% to 0%, while monthly incidents of expired reagent waste and paper use were reduced from 2 cases to 0 and by 15,000 sheets, respectively. Staff satisfaction also rose from 3.5 to 4.7 points.Automated result transmission and barcode verification enhanced result traceability and reduced manual workload.
Conclusions: The institution-level POCT platform improved workflow efficiency, quality monitoring, and patient safety while supporting digital transformation and sustainable smart-hospital development.
Keywords: POCT; quality management; patient safety; digital transformation

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P-11-b-52

一般演題 Others2 (Miscellaneous)

CAR-T Therapy Complication in lymphoma patients in Taiwan

Standardized Monitoring and Clinical Outcomes in 14 DLBCL Cases

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Background and Objectives: CAR-T cell therapy is recognized by NCCN Guidelines as a transformative treatment for relapsed/refractory (R/R) hematologic malignancies. The process involves isolating T cells via leukapheresis and genetically engineering them to target malignant B cells. Prior to infusion, lymphodepleting chemotherapy is administered to minimize tumor burden and mitigate the risk of severe complications, such as Cytokine Release Syndrome (CRS), Immune Effector Cell-Associated Neurotoxicity Syndrome (ICANS). As CRS and ICANS typically manifest within 7–14 days post-infusion, our clinical team implemented daily physical assessments and the Immune Effector Cell-Associated Encephalopathy (ICE) scoring system to ensure early detection and optimize patient outcomes.
Methods: This study analyzed 14 patients with Diffuse Large B-Cell Lymphoma (DLBCL) receiving CAR-T therapy as a second-line or later treatment. Inclusion criteria included a residual tumor count of ≤3 lesions and an ECOG performance status <2 prior to infusion. The clinical team monitored vital signs (temperature, SpO2, and blood pressure) daily to grade CRS severity. ICANS was assessed twice daily using the ICE score, evaluating five domains: Orientation (4 points), Naming (2 points), Following Commands (1 point), Writing (1 point), and Attention (2 points).
Results: Among the 14 patients, the clinical outcomes were as follows:

- **CRS:** 1 was asymptomatic, 9 experienced Grade 1, 3 experienced Grade 2, and 1 experienced Grade 4.
- **ICANS:** 12 were asymptomatic, 1 experienced Grade 1, and 1 experienced Grade 4. Retrospective analysis revealed that cases with severe (Grade 4) toxicities had an ECOG score of approximately 3 and a larger tumor volume despite having only 3 lesions. This suggests that higher baseline tumor burden and poorer performance status are **Conclusion: As evidenced by the data above, CAR-T cell therapy exhibits a favorable safety profile.**

P-11-b-53

一般演題 Others2 (Miscellaneous)

The Performance of Plasma Neurodegenerative Biomarkers in Taiwanese Screening population.

Using the ultrasensitive ImmunoMagnetic Reduction(IMR) method to provides real-world distribution data

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Background
Alzheimer's disease is the most common type of dementia and is associated with progressive cognitive decline. Immunomagnetic reduction (IMR) is a novel ultrasensitive assay capable of detecting plasma neurodegenerative biomarkers. Plasma Aβ42 × t-Tau (IMR AD) levels have been reported to correlate with Alzheimer's disease risk. This study aimed to evaluate the distribution of IMR AD-defined risk categories in a Taiwanese screening population.
Materials and Methods
A total of 1,844 de-identified IMR AD test records collected between September 2019 and February 2026 were retrospectively analyzed. Samples were obtained from 42 healthcare institutions in Taiwan, including medical centers, regional hospitals, district hospitals, and clinics. The age range of tested individuals was 16 to 93 years. These tests were all performed by the Precision Medicine Center at Chi Mei Hospital. IMR technology was used to quantify plasma biomarkers based on magnetic signal reduction caused by antigen-antibody binding.
Results
Among the 1,844 IMR AD test records, 1,378 cases were classified within the healthy range, accounting for 74.7% of all tests. A total of 376 cases, representing 20.4%, fell within the subclinical risk range, while 90 cases, representing 4.9%, were classified within the moderate-to-high risk range.
Conclusion
In this Taiwanese screening population, approximately 20.4% of IMR AD test records fell within the predefined subclinical risk range. This finding provides real-world distribution data for IMR AD testing in Taiwan and may support the identification of individuals who warrant further cognitive health monitoring.

P-11-b-54

一般演題 Others2 (Miscellaneous)

Exploration of Serum miRNA Associated with Early Fibrosis in MASH

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Metabolic Dysfunction Associated Steatohepatitis (MASH) is a progressive liver disease associated with an increased risk of liver fibrosis and cirrhosis. However, predicting which patients with fatty liver disease will develop fibrosis remains difficult. The present study aimed to identify candidate serum miRNA biomarkers predictive of future liver fibrosis by investigating changes in collagen-regulatory miRNAs in the liver and serum during the early stage of MASH development.
A MASH mouse model was established by feeding 6-week-old male C57BL/6NJcl mice a high-fat diet. Liver tissues were collected at 1, 2, and 6 weeks after the initiation of feeding, and pathological analyses were performed to confirm MASH progression. Total RNA was extracted from liver tissues and serum samples obtained from control and NASH mice at 2 weeks after feeding initiation, and miRNA expression profiles were analyzed using microarray analysis. miRNAs showing expression changes greater than 1.5-fold were further analyzed, and fibrosis-related miRNAs were predicted using pathway analysis with OmicsNet.
Histological analysis of liver tissues from MASH mice at 2 weeks revealed steatosis, ballooning degeneration, and inflammatory cell infiltration, confirming the establishment of MASH. At 6 weeks, α-SMA immunostaining demonstrated hepatic stellate cell activation, while Sirius Red staining revealed liver fibrosis. Microarray analysis identified 9 upregulated and 47 downregulated miRNAs in the livers of MASH mice. In serum samples, 21 miRNAs were upregulated and 7 were downregulated in the MASH group. Pathway analysis predicted that miR-29 targets collagen-related genes. miR-29 expression was decreased in the liver but increased in serum during MASH development. These findings suggest that reduced hepatic miR-29 expression may contribute to increased collagen expression and fibrosis progression in MASH. Because miR-29 has been associated with various fibrotic diseases, it may serve as a potential biomarker for fibrosis progression in MASH.
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P-11-b-55

一般演題 Others2 (Miscellaneous)

From the Blood to the Brain

Development of Novel Human Brain Organoid-on-Chips from PBMCs of Thai Children

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The human brain is a highly complex organ. Direct investigation is limited by ethical concerns and the inaccessibility of early-stage human brain tissue. Although in vitro systems such as induced pluripotent stem cell (iPSC)-derived brain organoids have facilitated studies of human neurodevelopment, these models still lack essential features of the native brain microenvironment. Organ-on-a-chip technology offers a better recapitulation of physiological conditions and dynamic cellular interactions. To develop a human brain-organoid on-a-chip model. Firstly, microfluidic chip molds were designed and simulated using COMSOL Multiphysics. The molds were printed using a high-resolution Formlabs Form 3B+ 3D printer, after which the chips were fabricated from polydimethylsiloxane (PDMS) and assembled via plasma bonding. In this study, iPSCs were generated from peripheral blood mononuclear cells from Thai children by introducing the Yamanaka factors to reprogram cells into a pluripotent state. Pluripotency of the iPSCs was validated using RT-qPCR, immunofluorescence staining, and trilineage differentiation assays. The iPSCs were subsequently aggregated into embryoid bodies, induced toward neuroepithelial tissue via neural induction, and cultured in both microfluidic chips and conventional methods to generate cerebral organoids. The cerebral organoids were then fixed, cryo-sectioned, and analyzed for neuronal marker expression. COMSOL Multiphysics simulations revealed that the designed microfluidic chips exhibited velocity and shear stress profiles suitable for brain organoid culture. In addition, we successfully generated and validated iPSCs from peripheral blood mononuclear cells of Thai children. The iPSCs expressed core pluripotency markers (OCT4, NANOG, and SOX2) and differentiated into all three germ layers. Cerebral organoids cultured in both methods exhibited high expression of neuronal markers (*FOXG1*, *MAP2*, *PAX6*, *TUBB3*, and *TBR1*) and developed organized neuronal structures consisting of layered neural progenitor cells and neurons. Finally, human brain organoids-on-a-chip derived from Thai children were successfully developed, providing a promising in vitro platform for studying neurodevelopmental disorders.

P-11-b-56

一般演題 Others2 (Miscellaneous)

Optimizing Outpatient Phlebotomy Through Precision Capacity Management

A data driven laboratory quality improvement project in a tertiary medical center

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Objective
Outpatient phlebotomy is a high-volume laboratory service affecting patient experience and workflow efficiency. From January to September 2025, our tertiary medical center handled 275,445 outpatient phlebotomy visits, with approximately 70% occurring between 07:30 and 09:00. Peak waiting time averaged 30.75 minutes, indicating the need for adaptive capacity management.

Methods
This quality improvement project analyzed laboratory information system data using Microsoft Power BI. Root cause analysis identified unstable phlebotomy staffing due to competing electrocardiography duties, insufficient morning appointment diversion, and limited service capacity. Using a Plan-Do-Check-Act framework, interventions included transfer of electrocardiography responsibilities, dynamic adjustment of appointment quotas based on weekday demand, extension of appointment availability until 16:00, and planned expansion through an additional temporary second-floor phlebotomy station.

Results
Following electrocardiography duty transfer, overall average waiting time decreased from 26.68 to 23.06 minutes, and from 36.8 to 32.0 minutes during peak electrocardiography workload hours. Monthly appointment utilization increased from 1,190 to 1,918 visits, while peak-period appointments (08:01–09:00) rose from 380 to 613. Historically lower-demand weekdays, particularly Thursdays and Fridays, also showed increased appointment uptake, demonstrating effective redistribution across peak hours and weekdays.

Conclusion
Precision capacity management improved outpatient phlebotomy efficiency and provides a scalable model for high-volume laboratory services.

P-11-b-57

一般演題 Others2 (Miscellaneous)

Post-Transcriptional Cyclin E Regulation by FIRdExon2 in ESCC

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Background: Far upstream element-binding protein-interacting repressor (FIR) is a transcriptional repressor of c-Myc. In tumor tissues, a splicing variant lacking exon 2 (FIRΔexon2) is highly expressed and has been reported to lose its transcriptional repressive function. Recent studies suggest that FIRΔexon2 inhibits FBXW7 function, thereby suppressing ubiquitination and proteasomal degradation of Cyclin E. However, the underlying mechanism in esophageal squamous cell carcinoma (ESCC) remains unclear.

Objective: To investigate the effects of FIRΔexon2 and BK697 on the FBXW7–Cyclin E axis and their possible involvement in post-translational regulation in ESCC.

Methods: The ESCC cell line TE1 was used. Cell viability after BK697 treatment was evaluated using a CCK-8 assay to determine the IC_{50} value. Cells were treated at the IC_{50} concentration for 24 and 48 hours. mRNA expression of FIR, FIRΔexon2, FBXW7, and Cyclin E was analyzed by qPCR, and protein expression was assessed by Western blotting. FIR and FIRΔexon2 were also knocked down using siRNAs.

Results: BK697 suppressed TE1 cell proliferation in a dose-dependent manner, with an IC_{50} of 47.39 μM. qPCR showed no significant changes in FBXW7 or Cyclin E mRNA expression, although FIR and FIRΔexon2 expression levels were altered. In contrast, Western blotting revealed decreased Cyclin E protein levels and increased FBXW7 protein levels after BK697 treatment. Similar discrepancies between mRNA and protein expression were observed in knockdown experiments.

Conclusion: These findings suggest that FIRΔexon2 regulates Cyclin E through post-translational mechanisms involving protein stability. FIRΔexon2 may influence Cyclin E degradation by modulating FBXW7 function rather than its expression level, potentially contributing to cell cycle dysregulation in ESCC.

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P-11-b-58

一般演題 Others2 (Miscellaneous)

Improvement of Laboratory Workflow Efficiency Using the Atellica Sealer

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Shiori HASEGAWA、Hisanobu KOBATA

Background and Objective: Reducing turnaround time (TAT) is an important goal in clinical laboratory testing. In April 2026, our hospital introduced the Atellica Solution, including the Atellica Decapper and Atellica Sealer. This study evaluated the usefulness of the Atellica Sealer in improving laboratory workflow and handling additional test requests.

Methods: Initially, specimens were automatically sealed 2 hours after result transmission. However, when additional testing was requested after sealing, specimens had to be removed from the sample handler (SH), unsealed, and reloaded onto the analyzer. To address this issue, system settings were modified to allow additional testing through retransmission of test orders from the laboratory information system (LIS) alone. Workflow efficiency and operation time before and after the modification were compared.

Results: After the system modification, specimens remained stored within the SH and could be used for additional testing without retrieval, unsealing, or reloading. Additional test requests from clinicians were handled rapidly through LIS retransmission alone. The elimination of manual handling procedures reduced operation time and improved workflow efficiency. Furthermore, automatic sealing and analyzer-based storage reduced direct specimen contact and minimized opportunities for contamination.

Conclusions: The modified Atellica Sealer workflow reduced the workload associated with additional testing and improved operational efficiency. Storage within the analyzer may also provide advantages in specimen preservation and contamination control compared with conventional room-temperature storage. These improvements are expected to contribute to further reductions in TAT and enhanced laboratory safety.

P-11-b-59

一般演題 Others2 (Miscellaneous)

Two Clocks, one laboratory: Rethinking turnaround time

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Background: Turnaround time (TAT) is widely used as quality indicator in laboratory medicine. It is commonly applied across different types of analyses, from rapid emergency testing to complex diagnostic workflows. However, it is unclear whether TAT reflects the same dimension of quality in all settings.

Aim: To explore how TAT reflect different aspects of quality within one laboratory, comparing TAT in rapid emergency analyses with an interpretation-intensive analysis in hemostasis diagnostics.

Methods: TAT was assessed for emergency analyses (hemoglobin, C-reactive protein, international normalized ratio (INR) and troponin T) and for coagulant activity of coagulation factor VIII (FVIII:C), measured by chromogenic assay, an analysis representing investigation of increased bleeding tendency. The proportion of analyses requiring interpretive comments was evaluated as a marker of post-analytical diagnostic work.

Results: All emergency analyses demonstrated consistently short turnaround times (<120 minutes) and did not include interpretive comments. FVIII:C demonstrated longer TAT (up to several days) and a high proportion of interpretive comments (65%). In emergency testing, TAT reflects efficiency in the analytic process, while in interpretive hemostasis diagnostics, TAT also includes clinical reasoning and commenting of test results.

Conclusion:

TAT is easy to measure and commonly used as a quality indicator. TAT represents efficient sample flow for emergency analyses, but our findings raise the question whether TAT is suitable to report for interpretation-intensive analyses without taking into consideration the percentage and quality of interpretive comments. A “two-clock” perspective may provide a more accurate understanding of TAT as a quality indicator.

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P-11-b-60

一般演題 Others2 (Miscellaneous)

AI-Assisted Automated Human Papillomavirus Report Generation System

Improving Laboratory Reporting Efficiency Through Automated Workflow Integration

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Purpose

Human papillomavirus (HPV) laboratory reports require individualized report preparation based on test results. Conventional workflows rely on medical technologists manually entering patient information and laboratory findings, increasing repetitive workload, processing time, and transcription error risk. This study aimed to develop an automated HPV report generation system to improve laboratory workflow efficiency.

Methods

An automated reporting system was developed using Python programming language with support from an artificial intelligence language model for workflow development and code optimization. A graphical user interface was implemented for user-friendly operation. The system utilized the Pandas library to process Excel data exported from the laboratory information system, including data cleaning, HPV test filtering, and result restructuring. Google Drive and Google Docs APIs were integrated to automatically apply report templates, populate patient information and HPV test results, and highlight positive (“Detected”) findings through predefined text formatting. The system enabled batch generation of individualized HPV laboratory reports.

Results

Manual preparation of one HPV report required approximately 3 minutes. After implementation, an average batch of 23 reports was completed within approximately 1 minute, corresponding to 2.6 seconds per report. Based on an average monthly workload of 90 HPV reports from January 2025 to April 2026, processing time was reduced by approximately 69-fold.

Conclusion

AI-assisted automation effectively reduced repetitive manual tasks, shortened report preparation time, improved laboratory workflow efficiency, and decreased transcription error risk.

Figure 1. User Interface

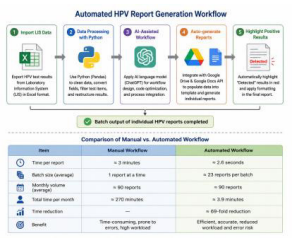

Figure 2. Automated HPV Report Generation Workflow

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一般演題 Others2 (Miscellaneous)

Management Analysis of Hyper-Critical Laboratory Values

A Patient-Centered Investigation into Clinical Timeliness and Safety Outcomes

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Background
Rapid notification of critical laboratory values is vital for patient safety. Our hospital monitors 29 critical items, including four "hyper-critical" analytes requiring automated SMS alerts and verified clinical intervention within one hour. This study evaluates the management efficiency of these high-risk interventions over three years.
Materials and Methods
Upon LIS release of a critical value, an automated SMS is sent to the physician, and technologists must verify transmission within 5 minutes. Management is considered complete if resolved within one hour. We analyzed 2023–2025 data to evaluate proportions, 5-minute notification rates, and 1-hour intervention completion rates for hyper-critical values (glucose, potassium [K], sodium [Na], calcium [Ca]).
Results
Hyper-critical findings stably comprised 3.46%, 3.40%, and 3.54% of all notifications from 2023 to 2025. Potassium was the most frequent analyte (53.1%, 58.0%, 52.3%), followed by sodium and glucose; calcium had zero cases. All hyper-critical items maintained a 100% 5-minute notification rate. The 1-hour intervention completion rates (100.0%, 99.6%, 99.8%) matched the overall 24-hour response rates (99.8%, 99.9%, 99.9%).
Conclusion
To ensure rigorous tracking, our laboratory combines communication software with active manual logging to prevent communication gaps. Hyper-critical values consistently represent 3–4% of notifications with a sustained 100% timely notification rate. Quarterly feedback of these trends to clinical departments especially regarding continuous potassium monitoring remains a vital CQI tool for prioritizing patient safety.
Keywords
patient safety, hyper-critical values, notification rate
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一般演題 Others2 (Miscellaneous)

Prevalence of Hookworm Infection in Fecal Samples of Stray Dogs

from a Public Pound and Selected Private Animal Welfare Organizations in Quezon City, Philippines

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Hookworms are significant gastrointestinal nematodes in dogs, linked to anemia, malnutrition, and zoonotic conditions like cutaneous larva migrans. Despite being endemic to tropical regions, urban epidemiological data remains scarce in the Philippines, particularly in densely populated areas like Quezon City. This study aimed to determine hookworm prevalence among stray dogs in a public pound and private animal welfare organizations within the city. Fecal samples were collected from 67 dogs across 23 barangays and processed using the Formalin–Ethyl Acetate Concentration Technique (FEACT) with the Mini Parasep system. Sediments were Lugol-stained and microscopically examined for eggs, with results validated by qualified professionals. The study revealed a prevalence rate of 38.81% (26 positive; 41 negative), indicating that approximately four in ten dogs were infected. Geographic distribution was uneven; Payatas recorded the highest number of positive cases, followed by Commonwealth and Fairview. These findings provide critical baseline data, confirming the persistence of zoonotic soil-transmitted helminths in urban shelter settings. The prevalence rate underscores a substantial public health risk to animal handlers, shelter staff, and local communities. The study highlights the urgent need for routine fecal screening, consistent deworming protocols, and enhanced sanitation practices to mitigate transmission risks in high-density urban environments.

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一般演題 Others2 (Miscellaneous)

Building High-Reliability Laboratories: ISO 15189 vs CAP Accreditation

Strategic Integration of Quality Governance in Multi-Tiered Healthcare Systems

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Purpose: To explore the commonalities and differences between ISO 15189:2022 and CAP accreditation standards, thereby facilitating the integration of organizational quality governance and frontline technical practice in healthcare systems. **Methods:** A comparative analysis was conducted between the ISO 15189:2022 framework and the CAP All Common and General Checklists to identify areas of alignment and divergence in quality governance, risk management, and technical practice. **Results:** ISO 15189 establishes a patient-centered, risk-based governance model emphasizing impartiality (Clause 4.1), patient rights (Clause 4.3), public complaint processes (Clause 7.7.1), measurement uncertainty (Clause 7.3.4), clinical consultation (Clause 5.3.3), and user and patient feedback (Clause 8.6.2). In contrast, CAP adopts a prescriptive, practice-oriented framework driven by peer inspections, featuring requirements for test orders, specimen identification and retention, amended report traceability, semiannual method comparisons (COM.04250), IQCP (COM.50300), method verification and LDT validation (COM.40300, COM.40640), competency assessments (GEN.55500), and Chemical Hygiene Plans (GEN.76000). Both require internal quality control (Clause 7.3.7.2; CAP IQCP), management reviews (Clause 8.9; GEN.20326), validated information systems with downtime procedures (Clauses 7.6.3–7.6.4; GEN.43066, GEN.43837), and facility and safety controls (Clause 6.3; GEN.76000). **Conclusion:** ISO 15189 and CAP provide complementary approaches to laboratory quality assurance. Integrating CAP's operational requirements with ISO 15189's risk-based, patient-centered governance principles may strengthen accreditation preparedness, quality management, and continual improvement, supporting the advancement of high-reliability laboratories.

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一般演題 Others2 (Miscellaneous)

Evaluation of walk-in cool room control measures for auditing:

compliance practicalities for the Australian Standard AS ISO 15189:2023 accredited medical laboratory

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The implementation of Australian Standard AS ISO 15189:2023 to support the conformity evaluation of medical laboratory walk-in cool rooms (WICs) has received limited attention within the pathology services industry.
The aim of this study was to develop a compliance tool to assist medical laboratories in achieving accreditation by determining the compliance status of WIC use. Relevant requirements for conformity evaluation were elicited from Australian Standards, Australian/New Zealand Standards, International Standards, and the Building Code of Australia. A total of 56 requirements were identified to support the conformity evaluation of the WIC and its refrigeration system located in a machinery room.
Of these, 13/56 (23%) requirements related directly to the WIC, 21/56 (37%) requirements to in-service inspection of the WIC and its refrigeration system, 11/56 (20%) requirements to maintainability of the WIC refrigeration system, and 11/56 (20%) requirements to marking maintainability.
This paper offers a practical tool for AS ISO 15189:2023 medical laboratories seeking to determine the conformity status of their WICs.

P-11-b-65

一般演題 Others2 (Miscellaneous)

Repurposing Furosemide for Acute Myeloid Leukemia Treatment

Evidence from Clinical Observations and In Vitro Molecular Mechanisms

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Objective
Acute myeloid leukemia (AML) progression is closely linked to TNF-α-driven inflammation. Following a clinical observation where a leukemia patient's peripheral blast cells decreased significantly after receiving only the diuretic Furosemide, this study aimed to verify Furosemide's "drug repurposing" anti-leukemic potential and its underlying molecular mechanisms.
Materials and Methods
We retrospectively analyzed the patient's bone marrow via immunohistochemistry (IHC) to detect TNF-α, TNFR1, and TNFR2 expression. In vitro, human AML HL-60 cells and normal PBMCs were evaluated using CCK-8 assays, Liu's stain, and Western blotting to assess cell viability, morphological differentiation, and apoptotic markers (Caspase-3/7 and PARP).
Results
Clinically, Furosemide monotherapy significantly reduced bone marrow TNF-α, TNFR1, and TNFR2 expression ($p < 0.05$), correlating with decreased peripheral blasts. In vitro, Furosemide exhibited dose- and time-dependent growth inhibition on HL-60 cells (IC50: 1660–2170 μM) without harming normal PBMCs, indicating a highly favorable safety window. Furthermore, Furosemide induced mature morphological differentiation and triggered caspase-dependent apoptosis, evidenced by elevated cleaved caspase-3, cleaved caspase-7, and cleaved PARP expressions at 2000 μM.
Conclusion
Furosemide possesses significant anti-AML activity by inhibiting TNF-α-related inflammation, inducing cell differentiation, and promoting apoptosis. Its selective cytotoxicity toward cancer cells highlights its strong translational potential as a safe, low-toxicity adjuvant therapy for AML.

Keywords
Acute Myeloid Leukemia, Furosemide, Drug Repurposing

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P-11-b-66

一般演題 Others2 (Miscellaneous)

Misidentification in Leukocyte Differential Counts

-Analysis Using Logistic Mixed-Effects Modeling-

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Background Peripheral blood morphology examination is an essential competency in medical laboratory science education. However, the difficulty of identifying blood cell types varies according to morphological similarity and observer experience. Previous analyses using the Difficult Index (DI) suggested that monocytes were the most difficult leukocyte subtype to classify. This study applied a logistic mixed-effects model for a more comprehensive evaluation of blood cell identification difficulty.
Objective This study aimed to compare the difficulty of identifying different blood cell types, including six leukocyte differentials, reticulocytes, and platelets, while accounting for inter-student variability.
Methods The study included students who completed hematology laboratory training at Toin University of Yokohama between 2021 and 2023. Peripheral blood morphology examinations were administered using Google Forms. Each response was treated as binary data (correct = 1, incorrect = 0). A logistic mixed-effects model was constructed with response accuracy as the dependent variable, blood cell type as a fixed effect, and student and slide item as random effects. The overall effect of blood cell type was evaluated using the Wald χ^2 test, and pairwise comparisons were adjusted using the Holm method.
Results A total of 107 valid responses and 1,391 analyzable answers were included. Previous DI analysis showed the highest DI for segmented neutrophils (0.953) and the lowest for monocytes (0.463). Blood cell type significantly affected response accuracy (Wald $\chi^2(7) = 597.58$, $p < 0.001$). Monocytes showed the highest misclassification rate, followed by eosinophils and band neutrophils. The order of difficulty was: monocyte > eosinophil > band neutrophil > basophil > lymphocyte > platelet > segmented neutrophil > reticulocyte.
Discussion These findings confirm that monocytes are the most difficult blood cell type for students to identify accurately. Educational programs should therefore emphasize monocyte identification and reinforce training for eosinophils and band neutrophils. (+81-45-974-5109)

P-11-b-67

一般演題 Others2 (Miscellaneous)

Effects of Dietary NaCl Levels on Experimental Ulcerative Colitis Severity

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Background
Ulcerative colitis (UC) is an inflammatory bowel disease characterized by chronic inflammation of the colonic mucosa. Excessive sodium chloride (NaCl) intake has been reported to enhance intestinal inflammation; however, the effects of different NaCl intake levels on UC severity remain unclear. This study investigated the effects of dietary NaCl concentration using a dextran sulfate sodium (DSS)-induced colitis model.
Methods
Male Wistar rats were divided into three groups (n = 6/group): a low-salt diet group (LSD, 0.03% NaCl), a control diet group (0.3% NaCl), and a high-salt diet group (HSD, 4.0% NaCl). Experimental colitis was induced with 3% DSS for 10 days. Disease activity index (DAI), histological changes, inducible nitric oxide synthase (iNOS) expression, and inflammatory cytokines were evaluated.
Results
DSS administration induced body weight loss in all groups; however, the reduction was more severe in the LSD and HSD groups than in the control group. The HSD group exhibited marked body weight loss and the highest DAI scores throughout the experimental period. Histological analysis demonstrated enhanced epithelial damage and inflammatory cell infiltration in both the LSD and HSD groups compared with controls, with the most severe tissue injury observed in the HSD group. In addition, increased iNOS-positive areas were observed in both groups, particularly in the HSD group. Serum TNF-α levels were also elevated in the LSD and HSD groups compared with the control group.
Conclusions
These findings suggest that both excessive and insufficient NaCl intake exacerbate DSS-induced colitis and promote intestinal inflammatory responses. Dietary NaCl balance may therefore play an important role in regulating intestinal inflammation and UC severity.
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P-11-b-68

一般演題 Others2 (Miscellaneous)

Evaluating a Machine Learning Model for Patient Specimen Mix-ups

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Objective: This study aimed to develop a machine learning model using the KNIME platform to detect patient specimen mix-ups based on longitudinal biochemical data and to evaluate its performance across various decision thresholds.
Methods: The study included 89,754 test records from 15,025 patients who underwent testing at least twice during a one-year period beginning January 1, 2024. Machine learning was performed on 12 biochemical parameters using KNIME (Tree Ensemble Learner) to analyze longitudinal variations within individual patients. After data filtering, 52,638 records were excluded, leaving 25,981 records for training and 11,135 records (9,637 non-mix-up cases and 1,498 mix-up cases) for validation. Performance was assessed using recall, precision, and accuracy.
Results: Decision thresholds ranging from 0.005 to 0.9 were evaluated. At a threshold of 0.05, recall and precision for the "non-mix-up" class were 0.953 and 0.999, respectively, whereas those for the "mix-up" class were 0.996 and 0.766. Six mix-up cases were missed, corresponding to a false-negative rate of 0.40% (6/1,498). When the threshold was lowered to 0.006, recall and precision for the "non-mix-up" class were 0.845 and 1.000, respectively, while those for the "mix-up" class reached 1.000 and 0.501. Although no mix-up cases were missed, 1,492 out of 9,637 non-mix-up cases were incorrectly classified as mix-ups. While the highest overall accuracy of 0.993 was observed at thresholds of 0.4 and 0.5, 50 and 66 mix-up cases were missed, respectively. Therefore, clinical threshold selection requires careful consideration to minimize clinically significant false negatives.
Conclusion: This study showed that a specimen mix-up detection model can be successfully developed in a secure, standalone environment using KNIME, minimizing data leakage risks. Although the system has not yet been introduced into routine clinical practice, further refinement and validation are planned to support future clinical deployment.
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P-11-b-70

一般演題 Others2 (Miscellaneous)

Characterization of a novel factor X variant, c.163dup

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Introduction: Congenital coagulation factor X (FX) deficiency is a rare bleeding disorder that may cause epistaxis or bleeding complications following dental extractions or surgical procedures in heterozygous individuals. More severe bleeding is often experienced in compound heterozygous and homozygous individuals.
Aim: To investigate a new FX variant found in a Norwegian family (mother and two of her children).
Methods: FX activity, FX antigen, Prothrombin time (PT) Quick, APTT, DNA sequencing and thrombin generation were performed in samples from three family members.
Results: The mother was compound heterozygous with a novel F10 variant (c.163dup) in combination with a previously known variant (c.424G>A). One child was heterozygous for c.163dup and the other child heterozygous for c.424G>A. The novel variant leads to a premature STOP codon and was predicted to cause mRNA degradation through nonsense mediated decay. Both the mother and child with the c.163dup variant had prolonged PT Quick (14,1 and 13,5 s, respectively), but the APTTs (35 and 38 s) were within reference range or borderline values. Both individuals had reduced FX activity (28 and 43 IU/dL) and reduced FX antigen levels (24 and 29 %), indicating a type 1 deficiency. The mother had much lower thrombin generation than pooled normal plasma (PNP), and the child heterozygous for c.163duphad thrombin generation intermediate to PNP and the mother. The child heterozygous for c.424G>A had normal values for all coagulation analyses.
Conclusion: We identified and characterized a novel *F10*variant that causes a type I deficiency and is associated with increased mucosal bleedings in compound heterozygous form. Bleeding symptoms may vary, and it is important to report clinical and laboratory characteristics in newly discovered variants.

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P-11-b-71

一般演題 Others2 (Miscellaneous)

Operational Evaluation of Blood Gas Analyzers Using Analytics

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Purpose: Blood gas analyzers are frequently used outside of laboratories as point-of-care testing (POCT) devices, making centralized management challenging. At our hospital, the Clinical Laboratory manages six analyzers across five clinical departments using Analytics (Siemens Healthineers), a data solution system that visualizes operational data. This study evaluates operational performance using Analytics and explores workflow improvement opportunities.
Methods: Six RAPIDPoint500e blood gas analyzers at Hamamatsu University Hospital were installed in the Department of Emergency Medicine, the Clinical Laboratory, the Angiography and Catheterization Laboratory, the High Care Unit (HCU), and the general ward. We analyzed measurement counts, reagent cartridge consumption, QC measurement frequency, and instrument utilization rate.
Results: In the Angiography and Catheterization Laboratory, HCU, and general ward, 400-test reagent cartridges could not be fully consumed before their expiration dates. Switching to 250-test cartridges resulted in an estimated annual cost reduction of approximately 8%. Reviewing QC frequency eliminated approximately 650 excess tests per year. Furthermore, approximately 35% of specimens from general ward were processed in the Clinical Laboratory, indicating insufficient awareness of device utilization across departments.
Discussion: These findings demonstrated that cost reductions were achievable through optimizing QC frequency and selecting appropriate cartridge sizes. This system is expected to improve centralized POCT management, optimize device allocation, and enhance laboratory testing quality. Moving forward, we are exploring further opportunities to advance operational efficiency throughout the hospital, including identifying device users, providing training to staff outside the testing department, and improving workflows.
Conclusion: The Analytics system enables centralized visualization of blood gas analyzer operations.
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P-11-b-72

一般演題 Others2 (Miscellaneous)

Identification of ISO 35001:2019 requirements for medical laboratory internal auditing

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The implementation of ISO 35001:2019 by medical laboratories to support accreditation of ISO 15189:2012 remains a challenging task for the pathology services industry. The main aim of this study was to quantify the requirements and recommendations that are connected to internal auditing in ISO 35001:2019. The contributing objectives included identifying requirements in ISO 35001:2019 for quantification and determinating the relative effort required for each subclause to be considered by internal auditors in the Plan-Do-Check-Act (PDCA) cycle. The requirements and recommendations were identified in Clause 4 (Context of the organization) to Clause 10 (Improvement) of ISO 35001:2019 by conducting a comprehensive content analysis. A total of 1007 requirements and 17 recommendations were identified in Clause 4 to Clause 10 of ISO 35001:2019. Then the distribution of requirements across the PDCA cycle was determined. The 'plan' phase has one clause, Clause 6 (Planning), containing two subclauses and 78/527 (14.8 %) requirements. The 'Do' phase has one clause, Clause 8 (Operation), containing ten subclauses and 279/527 (52.9 %) requirements. The 'Check' phase has one clause, Clause 9 (Performance evaluation), containing three subclauses and 109/527 (20.7 %) requirements. The 'Act' phase has one clause, Clause 10 (Improvement), containing three subclauses and 61/527 (11.6 %) requirements. The information has the potential to enhance the applicability and auditability of ISO 35001:2019 by using change and project management activities to support implementation and internal audit processes.

P-11-b-73

一般演題 Others2 (Miscellaneous)

Evaluation of the Effects of Pin1 Inhibition in ESCC

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Background: Anti-PD-1 (αPD-1) antibody monotherapy has limited efficacy in esophageal squamous cell carcinoma (ESCC), underscoring the need for combination strategies. The proline isomerase Pin1 is overexpressed in ESCC and regulates malignant phenotypes and the tumor microenvironment (TME). In other cancers, Pin1 inhibition enhances PD-L1 expression and potentiates the efficacy of αPD-1 antibody. We investigated the effects of Pin1 inhibition in ESCC and its relationship with immune-related factors in clinical specimens.

Methods: ESCC cell line KYSE410 was treated with the Pin1 inhibitor ATRA + ATO, and cell viability, migration, and protein expression were evaluated after 72 hours. Proteins (Pin1, E-cadherin, NF-κB, PD-L1, HIF-1α, and PKM2) were assessed by Western blotting. β-actin was used as a control. Biopsy specimens from ESCC patients treated with αPD-1 antibody treatment after chemoradiotherapy at our hospital were analyzed. We performed immunohistochemical staining (IHC) for Pin1 and CD8 and analyzed the correlation with αPD-1 antibody treatment response.

Results: ATRA + ATO reduced proliferation and migration in a concentration-dependent manner. Pin1, NF-κB, HIF-1α, and PKM2 were downregulated, whereas E-cadherin and PD-L1 were upregulated. The IHC results showed that high Pin1 expression was associated with poor response to αPD-1 antibody treatment and fewer CD8+ lymphocytes.

Conclusion: Pin1 inhibition by ATRA + ATO was suggested to suppress malignant phenotypes by reducing NF-κB and increasing E-cadherin. Furthermore, based on reductions in HIF-1α and PKM2, the increase in PD-L1, and IHC results, Pin1 inhibition was suggested to improve the immunosuppressive state of the TME while increasing PD-L1 expression alone. Based on these findings, the combination of Pin1 inhibition and αPD-1 antibody may be useful in ESCC. In the future, we will investigate the effects of Pin1 under low-glucose and hypoxic conditions, which more closely mimic the TME, and conduct in vivo studies.

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P-11-b-74

一般演題 Others2 (Miscellaneous)

Identification of ISO 15189:2022 requirements for medical laboratory internal auditing

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The implementation of ISO 15189 requirements by medical laboratories to support accreditation requires and relentless determination. The transition from ISO 15189:2012 to ISO 15189:2022 requires planned synchronisation to ensure that managerial and technical actions are aligned with achieving strategic objectives. The aim of this study was to quantify the requirements in ISO 15189:2022. The contributing objectives included the identifying requirements for quantification in a process-based quality management system (QMS) model and performance of crosswalk analysis between ISO 15189:2012 and ISO 15189:2022 to identify differences. The requirements were identified in ISO 15189:2022 by conducting a content analysis. A total of 1506 requirements and 10 recommendations were identified in Clause 4 to Clause 8 of ISO 15189:2022 and it was found that 877/1506 (58%) requirements were new requirements requiring further considerations by medical laboratories. The overall percentage ranged from 1/1506 (0.1%) requirements in Subclauses 5.1, 7.2.4.3, 7.2.7.2, 7.4.1.3, and 7.6.5, to 88/1506 (6%) requirements in Subclause 8.8.3.2 of ISO 15189:2022. The distribution of requirements was then arranged according to the four major stages, and it was found that 570/1929 (29%) requirements were associated with 'strategic management' including 381/570 (67%) new requirements, 445/1929 (23%) requirements were associated with 'process control, design and planning' including 239/445 (54%) new requirements, 473/1929 (25%) requirements were associated with 'analytical processes' including 207/473 (44%) new requirements, and 445/1929 (23%) requirements were associated with 'process evaluation and improvement' including 278/445 (62%) new requirements. The present study has offered a model for the exploration of ISO 15189 application by providing some insight into how ISO 15189:2022 requires the medical laboratory to provide guidance relating to compliance as operations management.

P-11-b-75

一般演題 Others2 (Miscellaneous)

Automated LOINC Mapping System Combining LLM and Official API

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Objective
Mapping local clinical data to LOINC (Logical Observation Identifiers Names and Codes) is vital for global medical data standardization and cross-system interoperability. However, traditional manual mapping is highly time-consuming and often yields scattered or null results due to varied test names across different facilities. This study aims to construct a closed-loop laboratory query system integrating a Large Language Model (LLM) with intelligent retrieval logic to provide rapid, accurate coding recommendations.

Methods
Developed with the Vite and Vue frameworks, the system provides an intuitive interface for laboratory personnel. The core engine utilizes an LLM to accurately comprehend test names and derive LOINC core classifications and synonyms. During the retrieval phase, the system adaptively manages API responses: if results are excessive, a "multi-path intersection counting mechanism" performs cross-referencing and calculates weights for precise filtering; if null, a "semantic expansion mechanism" broadens conditions to re-query. Finally, the LLM cross-references selected codes with original names, offering clear applicability explanations to assist personnel in rapid verification and decision-making.

Results
Tested across biochemistry, immunology, hematology, and coagulation domains in our department, the system achieved an automated mapping accuracy exceeding 95% compared to conventional manual queries. Operational efficiency improved drastically, reducing the average query time per item from 60 seconds to just 10 seconds. This workflow successfully builds a smooth, efficient automated coding process, effectively resolving verification dilemmas stemming from inconsistent clinical test names while significantly boosting data standardization efficiency.

Conclusions
By successfully combining LLM semantic reasoning with official API retrieval, this study establishes a highly practical coding assistant. This intelligent workflow significantly enhances LOINC mapping efficiency, minimizes manual workloads on laboratory staff, and provides a reliable, systematic solution for cross-institutional healthcare data interoperability.

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P-11-b-76

一般演題 Others2 (Miscellaneous)

Diagnostic Support System for Pre-Chemotherapy Hematologic Toxicities

Automated Detection and Multidisciplinary Notification of Severe Cytopenia

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Background: Chemotherapy-induced hematologic toxicities, including anemia, neutropenia, and thrombocytopenia, may lead to serious adverse events if not recognized before treatment. Our institution uses a Diagnostic Support System (DSS) for automated laboratory data analysis to enhance patient safety and support clinical decision-making. We evaluated the utility of the DSS for early detection and notification of severe hematologic toxicities prior to chemotherapy administration.

Methods: Following validation of laboratory results in the Laboratory Information System, the DSS automatically analyzes data using predefined algorithms. Cases meeting Grade 3 or higher criteria for hemoglobin level, neutrophil count, or platelet count according to CTCAE version 5.0 were identified. Medical technologists reviewed patient information in the electronic medical record and documented comments. Physicians and pharmacists subsequently reviewed the notifications and determined appropriate treatment strategies when necessary.

Results: Between September 2025 and March 2026, the DSS generated 136 notifications among 6,749 chemotherapy administrations. The mean turnaround time from specimen reception to DSS analysis was 71 minutes, and 80% of notifications were issued within 1 hour. The DSS enabled timely detection of severe hematologic toxicities and promoted information sharing among multidisciplinary healthcare professionals. Cases requiring more than 1 hour for analysis frequently involved labor-intensive tests, such as manual peripheral blood smear review, resulting in some notifications being issued after scheduled patient visits.

Conclusion: The DSS enabled medical technologists to detect severe hematologic toxicities before chemotherapy administration and rapidly communicate findings to physicians and pharmacists. This approach contributed to safer chemotherapy management. However, delays associated with specific laboratory tests reduced notification timeliness, highlighting the need for further optimization of both system design and operational workflow.

P-11-b-77

一般演題 Others2 (Miscellaneous)

Effect of Water Intake on Venous Dilation with Tourniquet Application

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Background: Successful venipuncture depends on adequate venous dilation. Although water intake before venipuncture has been reported to reduce vasovagal reactions (VVRs), previous studies have suggested that water intake decreases venous diameter. However, the measurements were limited to non-tourniquet conditions at 1 hour after ingestion of water. Therefore, little is known about the effect of water intake on veins during blood sampling.

Objective: In this study, we aimed to evaluate the effects of oral hydration on venous cross-sectional area (VCS) and dilation ratio in veins selected for venipuncture with and without tourniquet application.

Methods: Ultrasonography was performed to measure VCS under five conditions defined by water temperature and intake volume: no water intake, 250 mL of room-temperature (RT) water, and 500 mL of RT, 4°C, or 55°C water. VCS was measured with tourniquet application after 15, 30, 60, and 120 minutes of water drinking. The dilation ratio was calculated as post-tourniquet VCS divided by pre-tourniquet VCS. The dilation ratio before ingestion of water was used as the baseline value.

Results: The dilation ratio significantly decreased 15 minutes after ingestion of 500 mL of RT or 4°C water compared with baseline values before ingestion.

Discussion : These results suggest that the osmopressor response induced by water intake may contribute to the decrease in VCS observed 15 minutes later. Peripheral veins exhibit high contractile sensitivity to sympathetic activation and norepinephrine. In addition, it has been reported that the osmopressor response induced by water intake increases muscle sympathetic nerve activity and plasma norepinephrine concentrations, leading to vasoconstriction and increased peripheral vascular resistance. These findings suggest that water intake may be associated with decreased VCS even under tourniquet conditions through sympathetic activation.

Conclusion: In conclusion, water intake before venipuncture may not always be beneficial for venous dilation.

P-11-b-78

一般演題 Others2 (Miscellaneous)

CRP and Leukocyte Correlations After COVID-19 Infection

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Background: In late 2019, Covid-19 infections ravaged the world. Since Covid-19 infections are concentrated in the respiratory tract, patients often suffer from respiratory symptoms, making the virus more easily transmitted through respiratory droplets. This article explores the correlation between C-reactive protein (CRP), eosinophils, lymphocytes, and neutrophils after Covid-19 infection to predict the impact on symptom recovery and allergic diseases (especially asthma or allergic rhinitis).

Materials and Methods: Data on C-reactive protein, eosinophils, lymphocytes, and neutrophils were obtained from a medical center in Taiwan between April 1, 2022, and April 30, 2023. The de-identified data, used for retrospective analysis, included 80 male and 80 female patients. Spearman Rank Correlation Analysis was performed using IBM SPSS Statistics 31.0 to analyze the correlations among these biomarkers after contracting Covid-19.

Results: Statistical analysis revealed a negative correlation between C-reactive protein and eosinophils (Spearman's rho = -0.266, $p < 0.001$); a negative correlation between C-reactive protein and lymphocytes (Spearman's rho = -0.422, $p < 0.001$); a positive correlation between C-reactive protein and neutrophils (Spearman's rho = 0.395, $p < 0.001$); and a positive correlation between eosinophils and lymphocytes (Spearman's rho = 0.381, $p < 0.001$).

Conclusion: Lymphocytes increase to mediate cellular and humoral immunity and to clear Covid-19. Therefore, the concentration of C-reactive protein decreases in patients as the disease enters the recovery phase. However, the positive correlation between eosinophils and lymphocytes may lead to an increased incidence of asthma or allergic rhinitis.

P-11-b-79

一般演題 Others2 (Miscellaneous)

Optimizing Ward Non-Urgent Testing Time via PDCA and ESG

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1. Objective:Prolonged turn-around time (TAT) for non-emergency ward specimens delays patient treatment and diagnostics. This study applies the PDCA cycle to optimize the laboratory testing workflow for approximately 450 non-emergency specimens monthly, aiming to shorten TAT, improve process efficiency, and align with ESG governance responsibilities. The primary goal was to reduce the average TAT from 4.0 hours to under 2.5 hours.
2. Methods:The study implemented the four-stage PDCA cycle. In the Plan phase, baseline analysis showed an average TAT of 4 hours, delayed by manual pre-analytical sorting and lengthy batch intervals. In the Do phase, three strategies were executed: (1) differentiating emergency and non-emergency specimens, (2) implementing an automated track system to accelerate processing, and (3) establishing a real-time computer-alert system for overdue tests. The Check phase monitored TAT and overdue rates for 3 months post-implementation, and the Act phase standardized successful workflows into SOPs.
3. Results:The average TAT decreased by 40%, from 4.0 to 2.5 hours, and the overdue rate (>4 hours) dropped from 28% to 6%. Staff reported higher workflow clarity, allowing focus on higher-level tasks. Highly standardized processing improved data reproducibility and patient satisfaction while achieving ESG goals: reducing resource waste (Environmental), lessening patient waiting times (Social), and protecting patient rights via streamlined processes (Governance).
4. Conclusion:Integrating ESG sustainability into systematic PDCA analysis effectively eliminates testing bottlenecks. Specimen categorization and automated pre-analytical workflow optimization serve as key drivers for efficiency. Given current healthcare labor shortages, expanding this model to other specimen types or night shifts will further enhance institutional efficiency and support medical service quality.

P-11-b-80

一般演題 Others2 (Miscellaneous)

The Spatiotemporal and Geospatial Evolution of Cholera in the Philippines

A 12-Year Visual Analysis of Endemic Footprints (2014 - 2025)

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Cholera in the Philippines is traditionally viewed as a transient, climate-driven event. This study aims to characterize the long-term spatiotemporal dynamics, prevalence, and endemic reservoirs of cholera. This retrospective longitudinal study (n = 54,885) analyzed 12-year spatiotemporal dynamics (2014–2025), calculating annual prevalence across national, regional, and provincial levels; visualized temporal trends; and mapped spatial density using Dot Density, Hotspot, and Choropleth techniques across four distinct 3-year epochs. Analysis revealed a peak national prevalence in 2016 (13.57 per 100,000) and a historical low in 2020 (1.74). While rainfall serves as an environmental catalyst, peaking in 2022, it is not the primary driver of outbreaks. The COVID-19 "Anthropause" demonstrated a non-linear relationship: despite moderate rainfall, prevalence reached record lows as restricted mobility limited human aggregation. This confirms that human migration and population density override natural climatic factors in driving transmission.

Geospatial mapping identified a significant geographic migration of the disease burden. The epidemiological landscape shifted from traditional hotspots in Region XIII toward Region VIII and emerging clusters in the Zamboanga Peninsula and BARMM. This identifies cholera as a "nomadic threat" that capitalizes on population shifts rather than stationary risks. Furthermore, the "Infrastructure-Density Paradox" shows that high-density urban zones remain vulnerable due to systemic failures, such as a 22.0% non-revenue water leakage rate. These structural deficits create permanent reservoirs that behavioral hygiene alone cannot eliminate.

P-11-b-81

一般演題 Others2 (Miscellaneous)

ISO/IEC 17024 Accreditation for Medical Lab Specialists

Taiwan's Experience in Competence Certification for Medical Technologists

©YU YA-YEN[1)]、Lee Ming-Shih[2)]、Tsao Kuo-Chein[3)]、Sung Yu-Ling [4)]
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Implementing the Medical Technology Specialist Competence Certification Program in Taiwan: Achieving ISO/IEC 17024 Accreditation

Background: Non-automated laboratory procedures, such as microscopic morphology and tuberculosis (TB) testing, rely heavily on individual competence. To objectively validate these skills, the Taiwan Society of Laboratory Medicine (TSLM) established an ISO/IEC 17024 personnel certification system.

Methods: TSLM launched the Clinical Microscopic Specialist Certification (written exam only) in 2021 and the TB Testing Specialist Certification in 2024. The TB program requires passing a written exam before a practical assessment (pre-treatment, identification, drug susceptibility). Both programs underwent Taiwan Accreditation Foundation (TAF) on-site evaluations.

Results: In May 2023, TSLM became the second organization globally—after ASCP BOC—to achieve ISO/IEC 17024 accreditation. By 2025, the microscopic program certified 34/174 candidates (19.5% pass rate), and the TB program (accredited 2025) certified 51/56. Both credentials carry a six-year validity requiring recertification.

Conclusion: Taiwan's CDC now mandates that accredited TB laboratories employ at least one certified specialist. Major medical centers also utilize these certifications for competency grading and recruitment. TSLM's experience demonstrates that ISO/IEC 17024 accreditation successfully elevates professional standards and diagnostic quality.

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P-11-b-82

一般演題 Others2 (Miscellaneous)

Improving TSH Turnaround Time

Implementation of an In-House CMIA System in Critical Care

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Purpose: Timely laboratory results are essential for clinical decision-making in emergency and critical care settings. Previously, thyroid-stimulating hormone (TSH) testing at our institution was outsourced, resulting in a turnaround time (TAT) of approximately 72 hours. To improve laboratory efficiency and result availability, an in-house chemiluminescent microparticle immunoassay (CMIA) system was implemented.
Methods: TSH testing was transitioned from an outsourced immunoradiometric assay to an in-house automated CMIA platform. A critical obstetric emergency case was reviewed to illustrate the clinical value of rapid reporting. A 35-week pregnant woman developed acute respiratory failure, massive hemorrhage, and cardiac arrest shortly after admission. Thyroid function testing revealed elevated TSH and decreased free T4, with results available within one hour using the new platform.
Results: Following CMIA implementation, TSH TAT decreased from approximately 72 hours to 1 hour, representing a 98.6% reduction. The new workflow eliminated delays associated with specimen transportation and external testing while improving result accessibility for emergency and intensive care clinicians.
Conclusion: Implementation of in-house CMIA testing substantially improved laboratory efficiency and reporting timeliness. Rapid availability of thyroid function results enhanced diagnostic support during a time-critical clinical event. This experience demonstrates the value of laboratory workflow optimization in strengthening clinical decision-making and supporting high-quality patient care.
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P-11-b-83

一般演題 Others2 (Miscellaneous)

Expanding the Role of an Independent Clinical Laboratory

Linking Clinical Practice, Research, and Social Implementation

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Background : Independent clinical laboratories have traditionally focused on outsourced diagnostic testing. However, growing healthcare demands require laboratories to contribute not only to testing services but also to innovative healthcare solutions. Our laboratory is operated through an industry–academia collaboration between the University of Tsukuba Hospital and LSI Medience, one of Japan's largest clinical laboratory service providers. Since 2010, Tsukuba i-Laboratory has expanded its role beyond conventional diagnostic testing.
Objective : To present an expanded role of an independent clinical laboratory and demonstrate its contributions beyond traditional testing services.
Implementation : Activities were categorized into four domains: (1) routine laboratory operations, (2) advanced diagnostics, (3) social implementation projects, and (4) industry–academia collaboration. We provide 24/7 laboratory services for 33 medical institutions. Advanced diagnostics include in-house multicolor flow cytometry with disease-specific panels. Social implementation initiatives include a mobile PCR testing system using a hydrogen fuel cell bus and drone-based specimen transportation under a smart city project. We also support diagnostic manufacturers through spot testing services using designated analytical platforms.
Outcomes : In 2025, our laboratory performed 5,226,135 tests while maintaining a turnaround time of within 1 hour for all client institutions. In-house flow cytometry improved reporting speed and diagnostic capability. Mobile PCR testing and drone-based specimen transport demonstrated innovative models for disaster response and regional healthcare. Collaboration with manufacturers accelerated the development and implementation of new diagnostic technologies.
Conclusion : Independent clinical laboratories can serve as platforms linking clinical practice, research, and social implementation. Our experience demonstrates a sustainable model contributing to regional healthcare and medical innovation.
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P-11-b-84

一般演題 Others2 (Miscellaneous)

Seasonal Variation in Clinical Laboratory Tests

A Comprehensive Evaluation Using 25 Million Measurements

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Background: Seasonal variation has been reported for several clinical parameters, including HbA1c and blood pressure. However, comprehensive evaluations covering a broad range of laboratory tests remain limited, and the magnitude of seasonal variation across different analytes has not been fully characterized.

Objective: To comprehensively evaluate seasonal variation in routine clinical laboratory tests using large-scale, real-world data.

Methods: We retrospectively analyzed laboratory data obtained between January 2022 and December 2025 at a community hospital. A total of 850,145 test orders, encompassing 25,243,531 individual measurements across 105 laboratory parameters, were included. Monthly median values were calculated for each analyte. A Seasonal Variation Index (SVI) was defined as the difference between the maximum and minimum monthly medians, divided by the interquartile range (IQR). Laboratory parameters were then ranked according to this index.

Results: The magnitude of seasonal variation differed substantially among analytes. Urine osmolality exhibited the highest SVI (0.523), followed by HbA1c (0.200) and urinary creatinine (0.170). A total of 47 parameters demonstrated an SVI greater than 0.10. Among glucose metabolism-related parameters, blood glucose and HbA1c demonstrated a consistent pattern of higher values during winter and lower values during summer. Several urine-related parameters also exhibited seasonal variation, suggesting potential influences of hydration status and urinary concentration.

Conclusions: This comprehensive analysis of over 25 million laboratory measurements revealed seasonal variation across numerous laboratory parameters. The magnitude and pattern of variation differed among analytes, particularly for parameters related to glucose metabolism and fluid balance. These findings suggest that seasonal factors should be considered when interpreting laboratory results, and further studies in diverse climates and populations are warranted.

Contact: amano223@gmail.com / +81-564-21-8111

P-11-b-85

一般演題 Others2 (Miscellaneous)

Identification of GEN Checklist requirements for medical laboratory internal auditing

©Dennis Mok[1)]、Rana Nabulsi[2)]、Naira Eloyan[3)]、Sharfuddin Chowdhury[4)]、Karlah Norkunas[1)]、Mohd Nazil Salleh[5)]
Faculty of Health, Southern Cross Univ., Australia[1)]、Dubai Health, United Arab Emirates[2)]、Armenian Medicinal Products Regulatory Authority, Armenia[3)]、Mater Misericordiae Univ. Hospital, Ireland[4)]、Univ. College of MAIWP International Malaysia[5)]

The implementation of the College of American Pathologists' Laboratory Accreditation Program to support medical laboratories not subject to United States regulations remains a popular choice for the human pathology services industry. Currently, the challenge of implementation is to ensure all requirements are met. The main aim of this study was to quantify the requirements that are connected to internal auditing in Laboratory General Checklist prepared by the College of American Pathologists. The contributing objectives included the identifying requirements for quantification and determining the relative effort required for each Laboratory General Checklist requirement from GEN.13806 [Quality management system (QMS)] to GEN.78010 (Disposal of patient materials) to be considered by internal auditors. The requirements were identified by conducting a comprehensive content analysis. A total of 663 requirements were identified in GEN.13806 to GEN.78010. The distribution of requirements ranged from 1/663 (0.2%) requirements in many General Checklist requirements (n = 47) to 25/663 (3.8%) requirements in GEN.60100 (Adequate space). The findings are particularly relevant to internal auditors who ensure the relevant processes are implemented according to specifications of the medical laboratory.

P-11-b-86

一般演題 Others2 (Miscellaneous)

Comparison of the Laboratory Results from Four Missions of JDR

Experience from Water Floods in the Pakistan, Earthquake in Nepal, Turkey , and Myanmar

©Chitoshi SATO、Noriko WATANABE、Maiko OOTA、Tomokazu NAJIMA

The authors are a member of the Japan International Disaster Relief Team of the Government of Japan. The authors have served as a clinical laboratory technologist in Pakistan, Nepal, Turkey, and Myanmar.

Each deployment differed in terms of the type of disaster, timing, location, and Emergency medical team type. In this report, we present the results of clinical laboratory conducted during the various missions and discuss the role of clinical laboratory in international disaster medical assistance.

Pakistan: The mission took place two months after the floods, and examining focused primarily on infectious diseases, particularly malaria.

Nepal: The area was a mountainous region active, located far from the capital. Because there were many trauma patients, unlike the previous deployment, the focus shifted primarily to ultrasound, biochemistry, complete blood counts, and water quality testing.

Turkey: Although this team was an EMT Type 2, its primary mission was to provide medical support to the region's main hospital. The greatest demand was for biochemical and complete blood count tests, followed by infectious disease screening and prenatal care.

Myanmar: This was an unprecedented mission in which the first team did not conduct clinical Laboratory; testing began with the second team. Due to international considerations, the result from this mission will not be made public.

—Membership of Japan Disaster Relief Team is based on a pre-registration system for volunteers. While they normally work at their respective facilities, when a deployment is ordered, they gather from all over Japan. Currently, laboratory equipment of JDR has been "standardized" so that it can be operated by clinical laboratory technologist s with varying levels of expertise. Consequently, preparations and planning are conducted in advance to ensure consistent "Quality of Clinical Laboratory" even when clinical laboratory technologists, the type of disaster, the timing and location of operations, and the type of EMTs.

P-11-b-87

一般演題 Others2 (Miscellaneous)

Evaluation of Serum IgG Responses to *Cutibacterium acnes* Phylotypes

©Kaoru Furukawa[1)]、Daisuke Sakonishi[2)]、Ibuki Tamura[1)]、Yuriko Kurihara[1)]
Graduate School of Clinical Technology ,Tokyo University of Technology[1)]、School of Health Sciences, Tokyo University of Technology[2)]

Background: Host immune responses against the skin commensal *Cutibacterium acnes* (*C. acnes*) are involved in acne vulgaris pathogenesis. Patients exhibit high serum *C. acnes* IgG levels. *C. acnes* antigen profiles differ by phylotype. Phylotype IA1, predominant in patients, secretes abundant extracellular proteins such as CAMP factor, inducing severe inflammation. Whether serum IgG levels depend on phylotype-specific antigenic differences or other bacterial factors, such as intracellular invasion, remains unclear.

Objective: This study analyzed associations of IgG levels against four phylotypes with intracellular invasion and disease severity.

Methods: We measured IgG levels against four phylotypes (IA1, IA2, IB, II) in serum samples from 96 subjects by ELISA. We quantified intracellular invasion into human HEK293T cells using facial isolates, collected severity data, and analyzed associations.

Results: Serum IgG levels differed significantly among the four phylotypes ($p < 0.0105$), being prominently highest in Phylotype IA1. However, these levels correlated significantly with neither intracellular invasion nor disease severity.

Discussion: The lack of correlation with invasion and severity suggests antibody production does not result from physical bacterial invasion or exacerbation-induced epidermal disruption. Results align with a reported antigen recognition pathway without tissue destruction. In this mechanism, antigen-presenting cells constitutively take up antigens across the epidermal barrier to induce adaptive immunity. The prominent IA1 levels in this steady state likely result from skin predominance and high exposure, alongside abundant secretion of highly immunogenic extracellular proteins such as CAMP factor. These findings suggest IgG production may be directly determined by extracellular antigen quality and quantity during constitutive uptake, rather than invasion dynamics or inflammation severity.

Conclusion: Host humoral immunity against *C. acnes* may be directly determined by extracellular antigen quality and quantity, rather than bacterial invasion or inflammation severity.

P-11-b-88

一般演題 Others2 (Miscellaneous)

Test this si I dont have to test you

A visibility camgaign for biomedical laboratory scientist

©Heidi Andersen[1)]、Mari Tjernsmo Melby[1)]、Heidi Andersen[1)]
The norwegian institute of biomedical science[1)]

Introduction
Biomedical laboratory scientists (BLSs) are essential to diagnostics and public health, but remain largely invisible to the public and decision-makers.
NITO BFI developed a national campaign to increase awareness by linking sexual transmitted disesaes (STIs) prevention to laboratory diagnostics.
The message was: “Test this – so I don’t have to test you.”
Methods
The campaign was developed with a communications agency and used condom packages featuring BLS models as the main communication tool.
A total of 6,000 condoms were distributed through targeted activities including Arendalsuka, student recruitment events, social media, and International Condom Day.Supporting materials included posters, photographs, and short-form digital content.
A baseline survey measured public awareness prior to launch, with follow-up evaluation planned.
Media coverage and stakeholder engagement were used as early indicators of impact.
Results
The campaign functioned as a low-threshold conversation starter on diagnostics, prevention, and the role of BLSs.
At Arendalsuka, it enabled direct dialogue with politicians, health stakeholders, and students.
The initiative gained attention in professional and national media and increased political visibility for NITO BFI, including participation in a national health reform reference group.
Conclusion
A creative campaign can make an invisible profession visible. By linking prevention, diagnostics, and professional identity, NITO BFI achieved increased public engagement, media attention, and stronger visibility in policy contexts.

P-11-b-89

一般演題 Others2 (Miscellaneous)

Simplifying On-Call and Standby Rosters with Commercial AI Tools

An operational workflow analysis of automated scheduling and its impact on staff management.

©Rika SUZUKI[1)]、Saori ABE[1)]
South Miyagi Medical Center[1)]

【Background】In our clinical laboratory, which employs 26 biomedical laboratory scientists, shift scheduling had become increasingly complex due to multiple duty patterns—including night duty, day duty, and on-call standby—and numerous constraints such as individual weekday restrictions, minimum rest intervals, and balancing weekday and holiday workloads. Recent increases in requests for days off, the addition of four new technologists to night-duty rotations, and the integration of the pathology and microbiology laboratories further increased scheduling difficulty. As manual scheduling by supervisors reached its operational limits, we introduced a commercially available AI-based shift-creation tool to improve efficiency and sustainability.
【Methods】Before implementation, we compared AI-generated scheduling with a fully rotation-based system and selected the AI-based approach. The AI system was configured through iterative adjustments to complex duty patterns and constraints, enabling automatic generation of schedules up to one year in advance and early release of schedules three months ahead. After initial generation, staff were allowed to negotiate shift exchanges under supervisory oversight, while supervisors performed only minor final adjustments. A shared annual leave-request sheet was also used to support coordination of days off and identify candidates for duty substitutions.
【Results】Post-implementation surveys showed highly positive feedback, with staff reporting improved ability to plan personal activities and greater ease in obtaining requested leave. Negotiation of shift exchanges also facilitated communication among staff from different sections, enhancing overall workplace interaction.
【Conclusion】This initiative reduced supervisory workload, improved work–life balance, and fostered closer interdepartmental relationships, demonstrating its effectiveness as a labor-management strategy in the clinical laboratory.
E-mail suzuki.rika@gws.southmiyagi-mc.jp

P-11-b-90

一般演題 Others2 (Miscellaneous)

Evaluation of the OC-SENSOR R70

©Yumiko SUZUKI[1)]、Kouta OGINASA[1)]、Junko NAGAI[1)]、Kiyoshi KAMIYAMA[1)]
Department of Clinical Laboratory, Medical Diagnostic Center of URAWA Medical Association[1)]

[Introduction]
Our clinical laboratory performs approximately 60,000 tests annually, including colorectal cancer screening for Saitama City. This study aimed to evaluate the analytical performance of the OC SENSOR R70, a newly developed analyzer by Eiken Chemical Co., Ltd., designed as the successor to the OC SENSOR PLEDIA.
[Methods/Results]
Within-run precision was assessed using three-level controls in 20 replicate measurements, yielding coefficients of variation (CVs) from 1.06% to 1.98%. Between-day precision over one month showed CVs of 1.11%–1.49%. Linearity was confirmed up to 1,000 ng/mL using a 10-point dilution series with triplicate measurements. The hook effect was evaluated using a high-concentration sample (~600,000 ng/mL), with the “OR” (over range) indication correctly observed. Carryover testing with alternating high and blank samples demonstrated a rate of 0.0006%. The limit of detection, determined by the 2.6 SD method, was 8.9 ng/mL. Automatic dilution accuracy was confirmed using high-concentration samples and a urinary glucose standard measured with the Hitachi Automatic Analyzer 3100. Comparison of 1,208 stool samples between the OC SENSOR PLEDIA and R70 showed no significant differences, with a regression slope of 0.9676 and correlation coefficient (r) of 0.997. On-board reagent stability was evaluated over 35 days using R1 and R2 reagents in the cooling chamber, with CVs of 1.41%–1.92% and changes within 5%.
[Conclusion]
The OC SENSOR R70 demonstrated excellent analytical performance. It is integrated reagent cooling chamber ensures improved reagent stability, and in-cell automated dilution retesting eliminates the need for separate sample cups, reducing operational costs. These features make the OC SENSOR R70 a valuable analyzer for colorectal cancer screening programs.
Contact:(048)824-1629

Social Events

Welcome Ceremony

Free of charge | Dress Code: Smart Casual

Venue 1 (2nd floor, Convention Hall) September 23 (Wed.) 16:30-17:30

Following the welcome addresses by the IFBLS President and the President of the Host Country, representatives from each nation will enter the venue carrying their national flags. Please enjoy the presentation of the IFBLS awards and a special Japanese cultural performance featuring shodō (calligraphy) artistry.

Welcome Reception

Free of charge | Dress Code: Casual

Venue 2 (2nd floor, International Conference Room) September 23 (Wed.) 18:00-20:00

Meal Style: Buffet (Standing)

At the Welcome Reception held on the evening of the first day of the congress, we invite you to enjoy networking with fellow participants. Interviews with attendees and delicious food will also be provided, so we hope you will join us.

Beer Party

Free of charge | Dress Code: Casual

Venue 1 (2nd floor, Convention Hall) September 24 (Thu.) 18:00-20:00

Meal Style: Japanese festival booths and food stands (alcoholic drinks available)

Join us for the Beer Party on the second evening of the congress, where you can experience the lively atmosphere of a Japanese festival with traditional casual music, festival booths, and festival food-stalls. A special live band performance is also scheduled—don't miss it!

Opening Ceremony

Security Screening in place | Dress Code: Business Attire

Venue 1 (2nd floor, Convention Hall) September 25 (Fri.) 14:00-15:00

This is an official event to celebrate the opening of the Congress.

The Congress Organizer will deliver an address, followed by messages from guests.

The Japanese national anthem will be sung.

Please be aware of the following points concerning the opening ceremony:

* For the safety of all attendees, a security screening will be conducted, so please arrive with sufficient time to spare.

* A government-issued photo ID (such as a passport or driver's license) is required for entry into the venue.

* Please be seated no later than 15 minutes before the ceremony begins. From 13:50 onward, entry and exit will not be permitted until the ceremony concludes.

* Photography and audio recording are strictly prohibited. Please set your mobile phones and smartphones to silent mode or turn them off.

Gala Dinner

Paid / Registration required | Dress Code: Casual

Venue 1 (2nd floor, Convention Hall) September 25 (Fri.) 19:00-21:00

Meal Style: Buffet (Standing)

At the Gala Dinner held on the evening of Day 3 of the conference, we will be serving a delicious buffet in a seated format. You can also enjoy performances by a brass band and a disco-time with a DJ. We warmly invite you to join us and enjoy a wonderful opportunity to connect with fellow participants.

GAD & Closing Ceremony

Venue 2 (2nd floor, International Conference Room) September 27 (Sun.) 9:00-12:00

Outstanding posters will be awarded a poster prize at the closing ceremony.

Lab. Visiting / Sight Tour

Pre-Registered only

September 26 (Sat.) September 25 (Fri.) 19:00-21:00

【Course A】Visiting Laboratory (Kazusa DNA Research Institute, Nokogiri Mt, etc.)

【Course B】Sightseeing (Naritasan Shinshoji Temple, sake brewery tour,etc.)

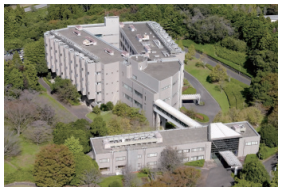
Please note that bus departure time varies according to the courses

If you arrive late at Bus Terminal and miss the bus, you cannot join the program and the fee is not refundable.

Personal Insurance is necessary in this program, too

The Organizing Committee is not responsible for any unexpected accidents that cause any forms of damages, property losses, or cancellation expenses to participants.

All participants are recommended to arrange their own insurance for coverage.



Kazusa DNA Research Institute

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International Exhibition Hall 8

• September 24 (Thu.)

Origami Workshop	10:00-12:00 / 13:00-16:30
Matcha Tea Service	10:00-12:00 / 13:00-16:30
Japanese Cypress Shaving Workshop	10:30-12:00 / 13:00-16:30
Japanese Fan Workshop	10:00-12:00 *the first 20 to arrive
Miso Workshop	13:00-15:30

• September 25 (Fri.)

Origami Workshop	9:00-12:00 / 15:30-17:00
Matcha Tea Service	9:00-12:00 / 15:30-17:00
Tatami Keychain Workshop	9:00-11:00 *the first 20 to arrive
Leather Bookmark Workshop	12:00-14:00 *the first 20 to arrive

*Fan, keychain, Leather workshop programs are monitoring from Chiba Convention Bureau. Please take a few minutes to fill out the survey.

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