# The International Congress of Pathology & Laboratory Medicine (ICPALM) 2025: Pathology & Artificial Intelligence: Transforming Diagnostic & Patient Care held on 21st – 23rd July 2025 at Shangri-La Hotel, Kuala Lumpur, Malaysia

**ICPALM 2025: International Speakers**

**1. Anatomical Pathology**

**Cancer reversion: A new therapeutic approach from systems biology**

Kwang-Hyun Cho
*Department of Bio and Brain Engineering at Korea Advanced Institute of Science and Technology (KAIST) & Director of the Laboratory for Systems Biology and Bio-inspired Engineering*

Current cancer treatments predominantly rely on inducing cancer cell death. However, from an evolutionary perspective, this approach inherently leads to limitations such as drug resistance, recurrence, and adverse side effects. What if cancer cells could be reprogrammed to revert to a state resembling normal cells instead of being destroyed? In this talk, I will introduce the concept of 'cancer reversion', a novel therapeutic strategy that aims to reverse cancer cells to a non-malignant state from a systems biology perspective. Furthermore, our recent research findings will be discussed, highlighting how this approach has the potential to overcome the fundamental limitations of current anticancer therapies and provide an eventual cure of cancer while maintaining the quality of life of patients.

**The Challenges and Pitfalls in the Diagnosis of Extranodal Extension in Head and Neck Squamous Cell Cancers**

Jane Dahlstrom OAM
*ACT Pathology, Canberra Health Services, School of Medicine and Psychology, Australian National University, Australia.*

Extranodal extension (ENE) in p16-negative head and neck squamous cell cancers (HNSCC) is a critical prognostic factor, influencing staging, treatment decisions, and patient outcomes. However, its diagnosis presents significant challenges and pitfalls, stemming from both clinical and pathological complexities. A multidisciplinary approach, involving oncologists, radiologists, surgeons and pathologists, is essential to mitigate diagnostic pitfalls and ensure accurate staging. Clinically, ENE often manifests subtly, complicating its detection through physical examination alone. Imaging modalities such as computed tomography (CT) and magnetic resonance imaging (MRI) are important for identifying radiologic ENE (rENE), yet their sensitivity and specificity remain limited, particularly in distinguishing subtle cases. Radiological findings may be confounded by inflammation, fibrosis, or adjacent anatomical structures, leading to potential misdiagnoses. Pathologically, the assessment of ENE relies on histological examination of lymph nodes (LN)s. Currently, histopathologically detected major (>2mm) ENE (pENE) in surgical neck dissection specimens from patients with HNSCC leads to treatment escalation with addition of adjuvant radiotherapy or chemoradiation given its significantly poorer prognosis. There is marked variation in the prevalence reported of pENE ranging from 20% to 80%. The reasons include variability in macroscopic examination, definitions and interobserver interpretations posing challenges in achieving diagnostic consistency. Practical guidelines have been recently published by the pENE Working Group, a body established to refine and harmonize diagnoses in head and neck pathology with the goal of improving the care provided to patients with diseases of the head and neck. pENE should be diagnosed only when viable carcinoma extends through the primary LN capsule and directly interacts with the extranodal host environment with or without desmoplastic stromal response. Identifying the original LN capsule and reconstruction of its contour can assist in the detection and assessment of pENE. Principles that can be used for assessment of pENE in challenging histologic situations such as the nodal hilum, post fine needle aspiration or adherent lymph nodes are provided.

**Diagnostic Approach to Non-Neoplastic Salivary Gland Lesions**

Jane Dahlstrom OAM
*ACT Pathology, Canberra Health Services, School of Medicine and Psychology, Australian National University, Australia.*

Non-neoplastic salivary gland lesions encompass a diverse range of conditions and can broadly be divided into developmental or non-developmental. The non-developmental lesions include inflammatory, infectious, autoimmune, deposits, and obstructive pathologies. Accurate diagnosis is essential for effective management, as these lesions often mimic neoplastic processes both clinically and radiologically. A systematic diagnostic approach to these conditions, integrating clinical, radiological, and pathological findings is required. Age, gender and features such as pain, swelling, xerostomia, systemic symptoms and whether single or multiple glands are involved guide the differential diagnosis. Imaging modalities, including ultrasound, CT and MRI, play a pivotal role in characterising many lesions and identifying ductal obstructions or sialolithiasis. Fine-needle aspiration cytology (FNAC) serves as a minimally invasive tool to distinguish between inflammatory and neoplastic processes, while serological tests aid in diagnosing autoimmune conditions like Sjögren's syndrome and IgG4-related disease. Histopathological examination remains the gold standard for definitive diagnosis, particularly in cases of chronic sialadenitis or granulomatous inflammation. Non-neoplastic lesions are more frequent in major salivary glands with non-specific chronic sialadenitis constituted the most common diagnosis in surgically excised specimens. A multidisciplinary approach, involving general practice, radiologists, surgeons and pathologists,

ensures comprehensive evaluation. The diagnostic framework outlined underscores the importance of integrating clinical acumen with diagnostic tools to differentiate non-neoplastic salivary gland lesions from their neoplastic counterparts.

**WHO classification of tumours 6th edition: Challenges and the strategy**

Dilani Lokuhetty
*Head of WHO Classification of Tumours Programme, WHO International Agency for Research on Cancer*

WHO Classification of Tumours (WCT) has embarked on the 6th edition of (WCT-6) following completion of the 5th edition (WCT-5). WCT-6 is being built on the strong foundation of the WCT-5, with several new innovations implemented to overcome the challenges faced. One main challenge would be to extend the evidence based pathology nature of the classification. This is planned to be achieved through the Evidence Mapping project funded by the European Union. Another would be to maintain the global relevance of the WCT in the current era of rapid advances in the fields of molecular and computational pathology. WCT/low-middle income setting subcommittee (SC) which has been initiated will bring forward plans to balance the effects of molecular/technical advances on WCT on a global setting. Several other SC's planned will give guidance on inclusion of relevant molecular genetic information to the WCT in a meaningful way, help to build up the whole slide image library of the WCT supporting future technological advances, provide guidance on utilising artificial intelligence in pathology, ensure harmonisation of tumours occurring at multiple organ sites, provide information to fine tune Grey zone tumours and help to clarify and refine certain tumours. Close liaison with radiologists through the Radiology SC is also planned to build up a Rad-Path image library. WCT-6 classification frameworks will be updated together with the content based on new research evidence and will be rewritten where necessary. Several surveys have been conducted to obtain end-user and editor feedback to improve the content and the process of WCT-6. The past has been a success story with WCT as the gold standard for tumour diagnosis, and we look forward to the future on a stronger footing.

**Our journey along the digital and AI path for the WHO classification of tumours**

Dilani Lokuhetty
*Head of WHO Classification of Tumours Programme, WHO International Agency for Research on Cancer*

The WHO Classification of Tumours (WCT) programme considers advances in the digital and AI path as being important for its future editions, as we move along this WCT journey. Having identified this need, WCT has initiated a computational and digital pathology subcommittee with experts in the field to move forward with the strategy of 'incorporating digital and AI technology into the WCT'. Blow process is designed to attain this objective in a stepwise manner.

***Step 1*** **Data Collection** by collecting pathology slides, clinical data, molecular data, etc.
**Data Digitisation** by converting analogue data into digital formats such as whole slide images (WSIs) and structured databases. We are looking at collecting at lease one WSI for each tumour type/subtype to be available on our WCT website.

***Step 2*** **Data Curation** by involving quality control, labelling, and annotation thus ensuring standardised and reliable datasets for further processing.

***Step 3*** **Developing patch testing capabilities** allowing image comparison to narrow down the differential diagnosis

***Step 4*** **AI Model Development** by training models for tasks like tumour typing based on the classification, grading, and subtype prediction using machine learning techniques (especially deep learning)
Validation by rigorous validation of models against ground-truth datasets using metrics such as accuracy, sensitivity, specificity, and reproducibility.
Integration by AI tools integration into diagnostic workflows, supporting pathologists with decision-making.

The outputs of this process is expected to inform the WCT, enhancing its precision, reproducibility, and global consensus. In the real-world context, these endeavors will further enhance already existing global standardisation and diagnostic precision, especially in regions with fewer pathology experts. WCT is also exploring the possibility of the development of an AI tool through its Evidence Map (EVI MAP) project funded through an EU grant. This aims to produce AI guided Evidence maps based on the latest research evidence supporting the editors and authors to update the WCT by bringing in information based on the latest research evidence to the volumes. Digital and AI solutions WCT has explored are yet at their early stages and will hopefully fully materialise to contribute to the future WCT volumes. This technological pipeline will help to modernise pathology and will help to update the WCT with data-driven insights. It will also support equity in diagnostics, particularly by enabling scalable tools for low-resource settings. Finally, the combination of AI and expert consensus is expected to increase the diagnostic reproducibility and accuracy of tumours included in the WCT across the globe.

**A Multiple Instance Learning Convoluted Neural Network for the Pathological Classification of Lymphoid Proliferations from Whole Slide Images**

Tan Soo Yong
*Department of Pathology at the National University of Singapore, Singapore*

We developed an AI algorithm for distinguishing reactive lymphoid hyperplasia from various types of B- and T-cell lymphomas using just unannotated H/E-stained slides at 50×, 100× and 200× magnification. Using a tile-based multiple instance learning framework, we obtained an initial 139 whole-slide images, with an average file size of 1.91GB. Preprocessing of the dataset

was performed by generating 192×192 pixel tiles at 50×, 100× and 200× magnifications. Stride lengths of 50% was set at the 5× and 10× magnification levels to augment the sample set. These tiles were then sorted into one of 10 classes: anaplastic large cell lymphoma (ALCL), classical Hodgkin's lymphoma (CHL), follicular lymphoma (FL) including high-grade and low-grade, large B-cell lymphoma (large BCL), mantle cell lymphoma (MCL), marginal zone lymphoma (MZL), small lymphocytic lymphoma (SLL), T-cell lymphoma (TCL), reactive lymphoid tissue (reactive LN) such as follicular hyperplasia and Kikuchi's disease, and 'uninformative' tiles. We achieved a per-tile accuracy of between 67% to 97%, and a per-WSI accuracy of between 80.8% to 100%.

**Cellular Origins and Pathogenesis of Intestinal T-cell Lymphomas**

Tan Soo Yong
*Department of Pathology at the National University of Singapore, Singapore*

Monomorphic epitheliotropic intestinal T-cell lymphoma (MEITL) is a form of primary intestinal T-cell lymphoma that shares with enteropathy-associated T-cell lymphoma (EATL) an association with increased intra-epithelial lymphocytes (IELs). For this reason, it used to be classified as Type 2 EATL but there is no association with celiac disease and there are clinical, pathological and molecular differences between these two diseases. Whilst mutations of the JAK/STAT pathway are present in both MEITL and EATL, frequent mutations of SETD2 and defective H3K36 trimethylation of H3 K36 are distinctive in MEITL. MEITL and EATL are both considered to be T-cell lymphomas but it has now been suggested that at least a subset of EATL that arises from Refractory Celiac Disease II (RCDII) may be of Group 1 Innate Lymphoid Cell (ILC1) origin, given its common CD4- CD8- double negative phenotype and absent or unproductive TCR gene rearrangements. The discovery that a majority of MEITL cases express CD8aa rather than CD8ab has raised the possibility that this neoplasm arises from unconventional T-cells that may be of TCRαβ or TCRγδ lineages that express CD8α homodimers.

**What we need to know about the pathology of gestational trophoblastic disease**

Annie NY Cheung
*CAP Laboratory Accreditation Program, Queen Mary Hospital, University of Hong Kong, Hong Kong*

Gestational trophoblastic disease (GTD) represents a family of trophoblast disorders with heterogeneous phenotype and clinical behaviour. The most common member is the potentially malignant hydatidiform mole which can be distinguished into complete and partial moles based on distinct genetic and morphological features. Invasive mole is defined as hydatidiform mole with myometrial or vascular infiltration. The family also includes overtly malignant choriocarcinoma, placental site trophoblastic tumour and epithelioid trophoblastic tumour as well as abnormal (nonmolar) villous lesions and non-neoplastic extravillous trophoblastic lesions such as exaggerated placental site and (atypical) placental site nodule. Advances in diagnostic radiology and extensive use of radiological examination in early pregnancy lead to more diagnostic challenges to pathologists, particularly the differential diagnosis of early complete mole, partial mole and abnormal nonmolar villous lesions. Majority of complete moles are diploid and purely androgenic while most partial moles are triploid having excessive paternal genome with maternal contribution. Molecular cytogenetic studies, besides enhancing our understanding of pathogenesis, also facilitate diagnosis and management. Various laboratory techniques including microsatellite analysis and in situ hybridization and imprinting gene $p57^{kip2}$ immunohistochemistry have been increasingly applied for differential diagnosis. Molecular cytogenetic studies are also useful in distinguishing gestational and non-gestational trophoblastic choriocarcinoma, which are treated with different chemotherapy regime. The basic prerequisite of processing adequate or all evacuated material for histopathological evaluation as well as correlation with clinical, radiological and biochemical findings remains the most important diagnostic approach. We should also understand clearly the diagnostic expression pattern and limitation of various tests to avoid misinterpretation.

**The challenge of HPV negative cervical cancers**

Annie NY Cheung
*CAP Laboratory Accreditation Program, Queen Mary Hospital, University of Hong Kong, Hong Kong*

Cervical cancer remains a common cancer among women globally, particularly prevalent in Asia. High-risk Human Papillomavirus (hr-HPV) is a recognised carcinogen for nearly all, but not all of cervical cancers. One of the important developments in the 5$^{th}$ Edition of WHO classification of female genital tumours is the distinction between HPV associated and HPV independent cervical cancers. The recognition of HPV independent cervical cancers is essential in this era when HPV vaccine and HPV molecular test based cervical cancer screening is widely applied. It has also been reported HPV negative cervical cancers are associated poorer prognosis than HPV associated cancers. The reasons underlying HPV negative cervical cancers include: (1) Incorrect classification of a non-cervical cancer; (2) False HPV-negative cases and (3) Real HPV-negative cervical cancer. Incorrect classification of a non-cervical cancer is often related to involvement of the uterine cervix by endometrial carcinoma while extrauterine origin is also a possibility. False HPV-negative cases may be due to HPV genotypes not covered by the HPV tests, low virus copy numbers or presence of PCR inhibitors, samples with abundant blood or glacial acetic acid treatment. Quality control of HPV tests is important. There are genuine HPV negative cervical cancers, mainly adenocarcinomas. Gastric type adenocarcinoma is the most common HPV negative adenocarcinoma, is associated with poorer prognosis and sometimes the first presentation of Peutz-Jegher syndrome.

**2. Chemical Pathology**

**The Clinical Value of Artificial Intelligence in Laboratory Medicine: Current Applications and Emerging Frontiers**

Damien Gruson
*Department of Laboratory Medicine, Cliniques Universitaires Saint Luc, Brussels*

In the dynamic landscape of modern healthcare, artificial intelligence (AI) is no longer a distant promise but an active driver of innovation. Laboratory medicine, at the intersection of data, diagnostics, and clinical decision-making, has become a key field where AI demonstrates transformative potential. Today, AI supports laboratory workflows by enhancing diagnostic precision, automating pre-analytical and analytical phases, improving quality control, and optimising resource allocation. Beyond operational benefits, AI-powered models increasingly contribute to clinical decision support systems, guiding risk stratification, differential diagnoses, and treatment strategies, particularly in complex conditions such as heart failure and diabetes-related complications. However, the integration of AI into laboratory medicine is not without challenges. High-quality, unbiased data remain critical, as do robust validation frameworks to ensure safety, fairness, and reproducibility. Ethical concerns, including algorithmic transparency, inclusivity, patient privacy, and environmental sustainability, are now central to responsible AI adoption. Laboratories have a vital role in addressing these challenges: they act as stewards of quality, as co-developers alongside data scientists, and as ethical gatekeepers ensuring AI applications enhance — rather than erode — patient care. Looking forward, hyperautomation, exposome analytics, and the integration of multi-omics platforms will further redefine the scope of laboratory medicine. Personalised proficiency testing, real-time monitoring through AI-based sensors, and advanced phenomics are pushing the boundaries of what's possible. As we navigate this era of accelerated technological evolution, interdisciplinary Collaboration between laboratory professionals, clinicians, policymakers, and technologists will be critical to shape an AI-driven future that is safe, effective, equitable, and sustainable

**From Deep Medicine to Network Medicine: Redefining Cardiovascular Prevention and Patient-Centreed Care with AI**

Damien Gruson
*Department of Laboratory Medicine, Cliniques Universitaires Saint Luc, Brussels*

Artificial intelligence (AI) is ushering in a new era in cardiovascular medicine — one that moves beyond traditional risk factor models to embrace deep, dynamic, and personalised insights. Recent advances in multimodal AI integrate data from wearables, imaging, genomics, and environmental exposures, enabling proactive cardiovascular prevention strategies. For patients with diabetes, where heart failure often develops in the absence of conventional risk markers, AI can detect subtle signals of early deterioration, improving outcomes through timely intervention. Generative AI, large language models, and predictive analytics are reshaping the patient experience. Personalised communication, culturally adapted health education, and virtual care assistants enhance engagement, health literacy, and adherence. Meanwhile, on the provider side, AI supports clinical documentation, suggests differential diagnoses, and delivers smart triage solutions — critical tools in increasingly strained healthcare environments. Importantly, the promise of AI must be balanced against its risks. Hallucinations in AI decision-making, data privacy breaches, biased algorithms, and unsustainable energy consumption threaten the responsible deployment of these tools. Laboratory professionals, alongside clinicians and policymakers, must advocate for energy-efficient AI models, transparent environmental reporting, and fair, patient-centreed regulatory frameworks. As we step into this AI-driven future, we enter a world of deep and networked medicine — where laboratory data, environmental analytics, and patient-generated data converge to deliver hyper-personalised care. This convergence offers the unprecedented opportunity to not only improve cardiovascular outcomes but also redefine healthcare itself. To succeed, we must act now, fostering multidisciplinary Collaboration, ethical innovation, and sustainable practice to build a smarter, more inclusive, and patient-focused tomorrow.

**AI in Clinical Biochemistry**

Bernard Lewis Croal
*President of the Royal College of Pathologists (RCPath), United Kingdom*

Interest in applications of AI across diagnostics has grown substantially in recent years. The increasing use of diagnostic tests along with more complex scope and imaging has challenged the worldwide laboratory workforce crisis. While much focus has been on diagnostic imaging AI within anatomical pathology and radiology, focus is now turning on the more numeric based laboratory disciplines such as Clinical Biochemistry. Traditional AI approaches, including its subsets of machine learning and deep learning, are well primed for application to clinical biochemistry data. However, when combined with other laboratory, diagnostic and clinical data, then much more can be promised in the future. The United Kingdom alone delivers more than 1.5 billion numeric lab test results every year. This increasing volume and complexity means that test selection, interpretation and clinical action could be optimised by using AI tools to bring efficiency, improved finances and better outcomes for patients. AI tools could be developed that apply to test ordering, stewardship, laboratory processes, analytical turnaround, interpretation, and therapy selection – notably for personalised cancer treatments. There are of course many barriers that will inhibit AI progress and implementation. These include lack of data standardisation and interoperability, insufficient technologists and programmers, medicolegal implications and concerns, and overall cost. The future of AI in Clinical Biochemistry nevertheless remains bright, with better, faster and more efficient systems that will have the potential to optimise patient outcomes.

**The Diagnostic Labs of Future-The impact of HAI, Robotics and Automation**

Andrew Coleman
*Technical Product Manager Automation, Informatics and Workflow at Siemens Healthineers*

The challenges faced by labs are well-known and include staffing shortages, financial pressures, sustainability, and increasingly complex care pathways. Alongside these challenges are local and globally disruptive trends, with aging populations, demand for precision medicine and access to care colliding with the desire to integrate lab data with AI, robotics and automation. Diagnostic labs have the opportunity to pioneer not just AI but importantly its responsible application, elevating user and patient experience with safer and faster product development, enhanced operational efficiencies and improved clinical insights. Collaboration with research partners allows development of novel testing approaches based on AI algorithms while in-house development provides for accelerated product development and support. Robotics too is increasingly entering the diagnostic laboratory, with systems once seen building cars or transporting sushi no being deployed to relieve the burden from overburdened laboratory staff by taking on dirty, time-consuming, error-prone or repetitive tasks, particularly in pre- and post-analytical phases. These robots are even starting to provide coverage during times of acute staffing shortages, 'running' full shifts and limiting the need for staff intervention to only those most critical samples and results. Automation has traditionally suffered from the perception that it is oversized, or limited to laboratories with higher sample demands. Modern laboratory automation however may even be integrated into analytical systems, saving both space and resources in a single solution. Innovations in each of these areas will continue to come at laboratories at a pace, and partnering with experienced vendors will be critical to enable future laboratories to meet current and novel challenges.

**Green Laboratory in Medical Laboratory Settings: Concept, Approach and Implementation**

Lia G Partakusuma
*Indonesia Health Care Corporation (IHC), Indonesia*

Healthcare facilities, particularly medical laboratories, contribute significantly to environmental impacts through high energy consumption, chemical usage, and biomedical waste generation. As sustainability becomes a global priority, implementing green practices within clinical laboratories is essential to align healthcare operations with environmental stewardship. A "Green Laboratory" refers to a laboratory that integrates environmentally sustainable strategies into its daily operations without compromising diagnostic quality or safety. This presentation explores the concept of a Green Laboratory specifically in medical laboratory settings. It outlines key sustainability pillars such as energy and water efficiency, sustainable procurement, waste minimisation, and behaviour-based culture change among healthcare workers. It also addresses common barriers—including operational demands, limited resources, and regulatory constraints—and proposes feasible solutions tailored to hospital environments. Case studies and implementation frameworks will be presented to demonstrate practical steps such as baseline audits, staff engagement, green lab certifications, and Collaboration with waste vendors. Emphasis is placed on how small but strategic interventions can lead to cost savings, improved compliance with health and environmental regulations, and enhanced institutional image. By adopting green laboratory principles, medical laboratory not only reduce their environmental footprint but also support patient-centreed care in a more holistic and responsible way. This presentation aims to inspire healthcare leaders, lab managers, and policymakers to initiate or accelerate the greening of their laboratory services.

**New Psychoactive Substance Challenges and Australia Experience**

Dimitry Gerostamoulos
*Victorian Institute of Forensic Medicine in Melbourne, Australia.*

The prevalence of novel psychoactive substances (NPS) continues to be a significant issue for laboratories seeking to identify, detect and quantify new synthetic drugs. While the overall number of new NPS identified has decreased, there is cause for concern regarding the number of new potent opioids (fentanyl and nitzene derivatives) circulating in North America and possibly being an issue in Australia and New Zealand. Thousands of deaths have occurred across Canada and the United States relating to the use of fentanyl and fentanyl derivatives (commonly being referred to as fentalogs). While many forensic toxicology laboratories have the capacity to measure some of these compounds, incorporating standardised and validated methods is an uphill task. Once these opioids are detected in medico-legal cases, whether postmortem or clinical, the varying potencies and the lack of pharmacological studies make interpretation difficult. This presentation will focus on the current dangers associated with fentalogs/nitazenes and more broadly NPS as well as the demands placed on forensic toxicologists to identify, detect, report and then interpret their findings in medico-legal cases.

**Therapeutic Drug Monitoring (TDM) and Pharmacogenomic Testing Practices in Thailand**

Chonlapat Susaken
*Department of Pathology, Faculty of Medicine Ramathibodi Hospital, Mahidol University, Bangkok, Thailand.*

This talk provides an overview of the current pharmacogenomics (PGx) practices and research in Thailand, and address the challenges and lessons learned from delivering clinical pharmacogenomic services in Thailand. The PGx research began in 2004,

biomarkers to identify a high-risk patient with severe cutaneous adverse drug reactions (SCARs) have been identified in the Thai population, such as HLA-B*15:02 (carbamazepine) and HLA-B*58:01 (allopurinol), etc. Furthermore, the pharmacogenomics studies investigating the relationships of genetic polymorphisms in drug-metabolising enzymes (DMEs) with pharmacokinetics and drug responses have been studied in the Thai population, such as TPMT and NUDT15 with 6-MP, CYP2C19 with clopidogrel and UGT1A1 with irinotecan, etc. The PGx biomarkers on HLA and DME genes in the Thai population will be summarised and discussed. The future of pharmacogenomics guided therapy in clinical settings across Thailand appears promising because of the availability of evidence of clinical validity of the pharmacogenomics testing and support for reimbursement of pharmacogenomics testing.

**3. Forensic Pathology**

**Digital Pathology: A Personal Perspective**

Suzy Lishman
*Senior Advisor on Medical Examiners, The Royal College of Pathologists & President of The Association of Clinical Pathologists*

Digital pathology is transforming the way in which cellular pathology is practised. After many years of being used for research and training, digital pathology is increasingly being used in routine diagnostic practice. This talk shares the personal experience of a consultant in the UK with the introduction and routine use of digital pathology and artificial intelligence. It will explore the benefits and challenges of digital pathology and the future opportunities that this new technology might bring.

**The Role of the Medical Examiner in United Kingdom**

Suzy Lishman
*Senior Advisor on Medical Examiners, The Royal College of Pathologists & President of The Association of Clinical Pathologists*

Medical examiners in the UK have a different background and role from those in the US and elsewhere. They are not pathologists and do not perform post-mortem examinations. In the UK, medical examiners are senior doctors from any specialty who review the patient record and speak to the attending doctor and bereaved family to ensure that the cause of death is recorded correctly, deaths are referred to the Coroner appropriately, and any concerns about care are escalated to help improve care for future patients. Medical examiners work part-time in the role, alongside their main clinical post. After several years of a voluntary scheme, the medical examiner system became statutory in England and Wales in September 2024, making it a legal requirement that all deaths must be reviewed by either a Coroner or a Medical Examiner. This talk will explain the role of the medical examiner and the impact that the service has had on death certification, bereaved families and patient safety.

**Imaging Modalities in Forensic Neuropathology Practice**

Linda Elizabeth Iles
*Forensic Pathologist, Head of Forensic Pathology Services, Victorian Institute of Forensic Medicine, Adjunct Associate Professor, Department of Forensic Medicine, Monash University*

The integration of postmortem computed tomography (PMCT) into forensic pathology practice has been the discipline's most important advance over the past 25 years. Likewise, it has enhanced forensic neuropathology practice, offering non-invasive visualisation of intracranial and spinal pathology prior to autopsy. This presentation will focus on the utility, strengths, and limitations of PMCT and PMCT angiography, and touch on the emerging use of magnetic resonance imaging (PMMRI).

**Neuropathology of non-accidental head injury in infants and children: Current Insights, Diagnostic Challenges and Controversies**

Linda Elizabeth Iles
*Forensic Pathologist, Head of Forensic Pathology Services, Victorian Institute of Forensic Medicine, Adjunct Associate Professor, Department of Forensic Medicine, Monash University*

Abusive head trauma (AHT) remains a leading cause of morbidity and mortality in infants subjected to physical abuse. This presentation will provide an overview of the forensic and neuropathological findings in AHT, as well as differential diagnoses such as accidental trauma and medical mimics. The presentation will highlight the importance of multidisciplinary Collaboration in the interpretation of findings and the implications for diagnosis, legal proceedings, and child protection, with an aim to promote an understanding of the pathological processes underlying AHT and the complexities involved in its identification and differentiation.

**Neuropathological Findings in the Spinal Cord in Infant Abusive Head Trauma: Emerging Evidence and Diagnostic Relevance**

Linda Elizabeth Iles
*Victorian Institute of Forensic Medicine and Department of Forensic Medicine, Monash University*

Infant abusive head trauma (AHT) is increasingly recognised as involving not only intracranial injury but also significant pathology within the spinal cord and its associated structures. This presentation will explore the emerging neuropathological findings in the spinal cord in cases of AHT, highlighting their relevance to both diagnosis and understanding of injury mechanisms. It will also address the challenges in identifying and interpreting spinal pathology postmortem, the current limitations of spinal cord examination in routine forensic practice, and the potential value of targeted spinal evaluation in suspected AHT.

**Death investigation: The Procurator Fiscal Service**

Ralph BouHaidar
*Chair of Forensic Pathology, University of Edinburgh Consultant Forensic Pathologist, NHS Lothian Associate Postgraduate Dean for Diagnostics*

Unlike the rest of the UK, the Crown Office and Procurator Fiscal Service (COPFS) is Scotland's public prosecution service and death investigating authority. All sudden, suspicious, accidental and unexplained deaths are conducted by COPFS on behalf of the Lord Advocate with the help of dedicated staff in specialist teams including the Scottish Fatalities Investigation Units and the National Homicide Team. This presentation will run through the role of the Procurator Fiscal in the investigation of death and their interaction with the Forensic Pathologist across the various centres in Scotland. There will be a number of illustrations and examples of how the system functions on a day-to-daybasis through a number of cases and reports.

**Digitalisation and Simulation in forensic practice: Sharing experience**

Ralph BouHaidar
*Chair of Forensic Pathology, University of Edinburgh Consultant Forensic Pathologist, NHS Lothian Associate Postgraduate Dean for Diagnostics*

Forensic Pathology like many other medical specialities is slowly catching up with the current trend of digitalisation and simulation. These offer novel and versatile approaches to the teaching of medical students, pathology trainees, police and other allied forensic practitioners and is currently applied in a number of scenarios including local and national training events. This presentation will summarise the past, current and potential future uses of these modalities in forensic pathology through examples of what is in use in Edinburgh and the rest of the UK including a run through the world's first forensic pathology real life manikin and its applications in training.

**4. Haematology**

**Haemoglobinopathies, molecular disease mechanisms and diagnostics**

Cornelis L Harteveld
*Department of Clinical Genetics, Leiden University Medical Centre, Netherlands*

Haemoglobinopathies are the most common monogenic disorders in the world population with an ever-increasing global disease burden. As most haemoglobinopathies show recessive inheritance, carriers are usually clinically silent. Laboratory haematology and biochemical analysis are standardised methods able to reveal carriers of sickle cell-, alpha- and beta-thalassemia. Large data sets and machine learning are subject of investigation to detect carriers more efficiently in automated settings in some Clinical Chemistry Laboratories. To prevent severe forms of haemoglobinopathy, carriers should be informed about the genetic consequences of being a carrier, with the option of partner analysis offering counselling and prenatal diagnostic testing to couples at risk. The development of genetic tools such as Array analysis and Next Generation Sequencing in addition to state-of-the-art screening at the haematologic, biochemic, and genetic level, have contributed to the discovery of an increasing number of rare rearrangements and novel factors influencing the disease severity over the recent years. During the presentation, an overview will be given of the basic requirements for adequate carrier diagnostics, the importance of genotype-phenotype correlation and how this may lead to the discovery of exceptional interactions causing a clinically more severe phenotype in carriers. Examples will be given of β-thalassemia carriers presenting with features of β-thalassemia intermedia of various clinical severity which involve duplicated α-globin genes, mosaic partial Uniparental Isodisomy or haplo-insufficiency of a non-linked gene SUPT5H on chromosome 19q, first described in two Dutch families with β-thalassemia trait without variants in the HBB gene.

**Haemoglobinopathies Carrier Diagnostic: The Leiden Experience**

Cornelis L Harteveld
*Department of Clinical Genetics, Leiden University Medical Centre, Netherlands*

The laboratory diagnosis of patients and carriers for haemoglobinopathies has undergone many technological improvements in haematologic and molecular diagnostic techniques since the first prenatal diagnoses by Southern blot analysis in the 1970s. In the following decades, the application of a wide variety of PCR-based molecular diagnostic techniques allows for the detection of the complete range of haemoglobinopathy mutations. This has led to the establishment of comprehensive national prevention programmes in many endemic countries and in non-endemic countries such as those in Northern Europe, in which the prevalence and heterogeneity of the haemoglobinopathies have been significantly increased by population immigration. Despite the great technological advances in mutation detection, the screening of haemoglobinopathies still requires the combined use of haematological and molecular techniques to arrive at an accurate diagnosis and requires specialist knowledge of genotype/phenotype relationships because of the multitude of complex phenotypes which result from interactions between genotypes and co-inherited globin gene disorders. The latest technological advances in variant analysis techniques involving Next Generation Sequencing (NGS) are progressively replacing Sanger sequencing as the 'gold standard' in the molecular genetic lab. NGS has led to new insights into disease mechanisms, for instance, the discovery of a novel disease gene SUPT5H causing beta-thalassemia trait and will continuously unravel modifying factors through massive parallel sequencing.

**Haemoglobin Variant Curation**

Cornelis L Harteveld
*Department of Clinical Genetics, Leiden University Medical Centre, Netherlands*

Consistent and accurate interpretation of sequence variants is a prerequisite for offering safe and reliable diagnostic genetic services. In an attempt to standardise sequence variant calling in relation to disease, the American College of Medical Genetics and Genomics (ACMG) and the Association for Molecular Pathology (AMP) published a joint guideline based on a set of shared standards for the classification of variants in Mendelian diseases. The generality of these standards and their subjective interpretation between laboratories has prompted efforts to reduce discordance of variant classifications, with focus on the expert specification of the ACMG/AMP guidelines for individual genes or diseases. Recently, this was also done for variants involved in the haemoglobinopathies. The ClinGen Variant Curation Expert Panel (VCEP) adapted the ACMG/AMP criteria for the classification of variants in three globin genes (HBB, HBA2, HBA1) related to recessively inherited haemoglobinopathies, including five evidence categories, and published a pilot of cases demonstrating the process of specification and the underlying rationale. During the presentation, an impression will be given of this pilot study by the ClinGen Haemoglobinopathy Variant Curation Expert Panel. This demonstrates the necessity of disease-specific adaptation of the ACMG/AMP variant classification for variants involved in haemoglobinopathy.

**Regulatory Oversight and Educational Issues of Pathology AI tools**

Donald S. Karcher
*President, College of American Pathologists & Professor and Immediate Past Chair of Pathology, George Washington University Medical Centre, Washinton, United States*

Artificial Intelligence (AI) tools are increasingly being used in all areas of medical practice, including in pathology and laboratory medicine. From image-based analysis to clinical decision support to computational analysis in genomic studies, these tools are bringing powerful new capabilities to diagnosis, individual patient management, and public health maintenance. With the rapid development and deployment of these tools, ensuring their safety, reliability, and applicability has become a major challenge. In this context, regulatory oversight of AI in medicine is currently being developed in many countries. To benefit from the potential of AI, it's important that this regulatory oversight protects patients and public health without stifling the continued development of pathology and other medical AI tools. With the rapid increase in the use of AI in pathology, there is also a compelling need to train pathologists and other clinical laboratory personnel to properly select, verify/validate, monitor, and incorporate these tools into daily practice. This presentation will focus on the regulatory and educational issues in the era of AI in pathology and laboratory medicine.

**AI-Driven Morphological Assessment of Blood Cells**

Donald S. Karcher
*President, College of American Pathologists & Professor and Immediate Past Chair of Pathology, George Washington University Medical Centre, Washington, United States*

Haematologic diagnosis and patient management have traditionally relied on effective manual morphologic evaluation of peripheral blood, bone marrow, and other relevant specimens. With the rapid development of image-based artificial intelligence (AI) tools in pathology and laboratory medicine, an increasing number of such tools are being developed to automate and improve the morphologic assessment of peripheral blood cells and other haematologic specimens. This presentation will focus on the development and use of AI tools in haematologic diagnosis and patient management.

**Leukaemic Stem Cell in AML MRD Monitoring**

David Westerman
*Peter MacCallum Cancer Centre, Australia*

Multiparameter flow cytometry is pivotal in the diagnosis and monitoring of AML patients, functioning alongside ancillary tests including morphology, cytogenetics and molecular characterisation. A key role for flow cytometry is in the assessment and quantification of measurable residual disease (MRD), which has gained increasing importance in recent years in AML, given a significant expansion of targeted agents available or being trialled, and its known importance as a prognostic factor. Leukaemic stem cells (LSC's) have the ability to initiate leukaemia in vivo and are represented by a small subset of cells with a CD34+CD38- immunophenotype. They are thought to be the most resistant to therapy. There is now a sizeable body of literature describing validated flow cytometry assays for LSC detection, leveraging technical and analytical methods used for AML MRD analysis. Normal HSCs are defined by the lineage (Lin)− CD34++ CD38− immunophenotype and can be distinguished from abnormal LSCs, which display leukaemia-associated immunophenotypes including aberrant lineage marker expression and/or asynchronous or increased/decreased antigen expression. This presentation will summarise the scientific data where LSC's have demonstrated their clinical significance and will also demonstrate the flow cytometric approach with examples.

**Lymphoma Diagnosis From Bone Marrow Trephine Biopsies: Opportunities and Challenges**

Kenneth Lee
*Douglass Hanly Moir Pathology, Sonic Healthcare, New South Wales, Australia*

The diagnosis of lymphoma in trephine biopsy is often part of an overall diagnostic or progress assessment of the disease. Although bone marrow trephine assessment serves as an important part of the diagnostic and progress assessment pathway, the assessment of bone marrow trephine alone is not optimal in the overall diagnosis. Careful correlation with the radiological, peripheral blood, flow cytometry and bone marrow aspirate is essential in establishing the correct diagnosis. In addition, integration of molecular results is now part of the complete diagnostic workup of some lymphomas. Careful assessment of the architectural pattern of the lymphoma involving the trephine, and the identification of the immunophenotype of the lymphoma serve as the primary triage in terms of establishing the differential diagnosis and classification. However, the immunophenotype of certain lymphomas may overlap with each other and may pose a diagnostic dilemma. It is with careful integration of the other diagnostic modalities and molecular findings that the final diagnosis may be established. In addition, the presence of marrow involvement by a certain lymphoma may not necessarily be reflective or concordant with the nodal disease. This session focuses on the challenges and opportunities in lymphoma diagnosis in trephine biopsy. The challenges will include the morphologic and immunophenotypic assessment of the common lymphomas in terms of differential diagnoses, and the opportunities will include integrating the other diagnostic modalities in order to establish the final diagnosis.

**5. Genetic Pathology**

**Curative clinical gene therapy works! Hou$ton...We have a problem!**

John Rasko
*Sydney Medical School, University of Sydney, Australia*

Gene therapies offer transformative potential for treating and curing diseases. Building on the work of German pathologist Rudolph Virchow, who noted that "omnis cellula e cellula" ("every cell arises from another cell"), we understand that genetic material in each cell contains the information propagated from one generation to the next. The concept behind using genes as medicine involves overcoming the technical and safety hurdles required to introduce new genetic material into cells to add back functionality or reprogram them to cure diseases. Gene modification can be achieved through two primary methods: in vivo and ex vivo. In vivo gene therapy involves injecting genes directly into the body, potentially targeting organs or tumours. Ex vivo gene therapy involves removing a patient's cells, modifying them outside the body, and then reintroducing them to the patient. Both methods have been successfully employed in various clinical settings. Examples of these potential cures from my own clinical experience will be shown. Gene therapy has made significant strides in treating haemophilia. By providing a one-time treatment that allows patients to produce necessary clotting factors themselves, gene therapy reduces reliance on ongoing treatments and avoids risks associated with blood product transfusions. Over the past 20 years, advancements in this field have led to approved therapies for both haemophilia A and B in major markets. Additionally, transfusion dependent beta thalassaemia and sickle cell disease can also now be treated using approved ex vivo gene therapies. And yet, despite sustained evidence of technical and clinical success, there is still so much we need to achieve to provide for people suffering with unmet medical needs, especially in thousands of rare diseases. A major problem that is yet to be overcome is how these advanced medicinal products can be introduced in an equitable manner, given their current staggering costs, regulatory and logistical challenges. Access to proven, well-regulated and safe gene therapies remains the main hurdle to widespread implementation. International regulation of unproven therapies should be strengthened to curtail this predatory multi-billion-dollar trade. We should seek to offer compassionate and equitable therapies to those who do not benefit from existing advanced therapeutics because they don't live in a wealthy country, or they cannot afford adequate health care. And in economically advantaged countries our goals should be to accelerate approvals of treatments that are proven in rigorously-designed clinical trials by adopting novel approaches to funding and reimbursement. The future of gene and cell therapy remains

promising. The ability to modify genetic material and reprogram cells offers the potential to address a wide range of diseases. While ethical, regulatory, and economic considerations are critical, progress in this burgeoning field suggests that gene and cell technologies could one day provide cures for many currently incurable conditions, offering hope for a brighter future in medicine.

**Detection of Ultra-Rare Circulating Tumour Cells For Precision Oncology**

John Rasko
*Sydney Medical School, University of Sydney, Australia*

Circulating tumour cells (CTCs) are cancer cells in the blood that are shed from the primary tumour as they travel to colonise a metastatic site. The detection of CTCs is increasingly important in precision oncology for several reasons, including: 1. CTCs may facilitate early detection and monitoring of cancer, allowing for early diagnosis, recurrence monitoring, and real-time tracking of tumour dynamics without invasive biopsies; 2. CTCs offer a real-time non-invasive snapshot "liquid biopsy" of the tumour's molecular characteristics, including mutational status, gene expression, and expression of epithelial–mesenchymal transition markers, thereby supporting personalised treatment choices and adjustments to therapy as the cancer evolves; 3. CTC analysis may guide targeted therapies, by identifying actionable mutations or resistance markers, and avoiding ineffective therapies; 4. CTC isolation and behaviour in vitro using cell and organoid culture may shed light on metastatic mechanisms and tumour evolution. Over many years we have characterised and validated the first-in-Australia platform detection technology (AccuCyte® CyteFinder®, from Rarecyte) to enumerate and isolate CTCs from cancers such as pancreatic cancer, head and neck cancers, lung cancer, appendiceal cancers, mesothelioma and glioblastoma to be outlined in this talk.

**Point-of-Care Diagnosis for Epithelial Ovarian Cancer using Haptoglobin from Ovarian Cyst Fluid**

Mahesh Choolani
*National University of Singapore, Singapore*

Ovarian cancer remains the most lethal malignancy of the female reproductive tract. While early detection and timely intervention can significantly reduce mortality, there is currently no effective, clinically validated screening strategy for asymptomatic women. As such, routine screening is not recommended. Diagnosis still relies heavily on paraffin histopathology, the gold standard, though it often takes up to two weeks and may necessitate a second operation. The two most critical determinants of improved survival are early diagnosis and optimal initial debulking surgery.

Frozen section analysis provides timely intraoperative assessment of malignancy; however, access to this service remains inconsistent and uneven across healthcare systems. To address this gap, we identified haptoglobin as a robust biomarker in ovarian cyst fluid. It is significantly elevated in both early- and late-stage malignancies compared to benign tumours. Haptoglobin (AUROC 0.999 [95% CI 0.997–1.000]) markedly outperforms CA125 (AUROC 0.895 [95% CI 0.814–0.977]) and other conventional approaches. This discovery led to the development of OvaCis, a CE-marked and HSA-registered intraoperative diagnostic kit. By providing surgeons with a rapid and reliable intraoperative test, OvaCis enables more accurate decision-making, minimises the need for repeat surgeries, and ultimately enhances outcomes for women with ovarian cancer.

**AI in Obstetrics and Gynaecology**

Mahesh Choolani
*National University of Singapore, Singapore*

The integration of artificial intelligence is transforming Obstetrics & Gynaecology (O&G), not by replacing clinicians, but by amplifying our capacity to care for patients. The American Medical Association aptly describes this shift as Augmented Intelligence - AI designed not to displace but to enhance clinical expertise. Tools such as ChatGPT-4, Bing, Gemini, and Bard do not diminish the role of doctors, nurses, or allied health professionals; instead, they elevate our ability to deliver precise, timely, and patient-centred care, while accelerating learning for trainees and seasoned clinicians alike. In O&G, machine learning algorithms support the early detection of complications, enabling pre-emptive and safer interventions. AI-driven decision support systems personalise treatment pathways by analysing individual patient profiles, while human-AI Collaboration fosters clinical judgement that is both data-informed and context-sensitive. Freed from the administrative burden of routine tasks, care teams can focus on what matters most—complex cases, nuanced conversations, and compassionate care. The result is better outcomes, fewer complications, and more efficient use of limited healthcare resources.

Augmented Intelligence also provides a vital response to workforce shortages and rising healthcare costs, strengthening our systems without compromising the quality of care. But with this power comes responsibility. We must embed safeguards against bias, ensure data privacy, and confront the risks of hallucinations in Large Language Models. Equity of access remains paramount. Ultimately, AI is not a replacement for human touch, it is a catalyst for better care, smarter education, and a more sustainable future in women's health.

**Next Generation Sequencing Solutions for Clinical Oncology (Platinum Symposium II)**

Aarti Gokhale
*Integrated DNA Technologies, Singapore*

Description: Next Generation Sequencing has revolutionised genomics and clinical research applications by enabling rapid and cost-effective sequencing of DNA and RNA, providing unprecedented insights into genetic variation, disease mechanisms, and personalised medicine. Integrated DNA technologies have been a key contributor to this genomic revolution. Building from a strong foundation of innovation, expertise, and reliability, we have evolved from an oligo manufacturer to a leading genomics solutions provider. We will share comprehensive solutions that enable researchers to efficiently detect single nucleotide variants, copy number variations, indels, and key genomic signatures like MSI, TMB, and HRD via a streamlined workflow, powered by patented Anchored Multiplex PCR (AMP™) chemistry, and Archer Analysis's user-friendly bioinformatics platform. Additionally, we will introduce the flexibility, scalability and high performance of the xGen Next Generation Sequencing solutions.

**Clinical Impact of Rapid NGS Molecular Profiling**

Daphne Goh
*Thermo Fisher Scientific, Singapore*

Molecular profiling has become a cornerstone of precision oncology, enabling personalised treatment decisions based on tumour genomics. As the list of actionable biomarkers continue to grow, next generation sequencing has emerged as a critical tool in precision oncology, enabling the identification of actionable genetic alterations that can guide targeted therapies. Ultra-fast molecular profiling with NGS delivers comprehensive genomic profiling in a single day, represents a transformative advancement with the potential to significantly improve clinical outcomes, particularly in time-sensitive cases such as advanced or rapidly progressing cancers.

**Preimplantation genetic testing in Melbourne, Australia – The First 23 Years**

David Amor
*Developmental Medicine, University of Melbourne, Australia*

Melbourne, Australia, was a pioneer centre for IVF, and the location of birth for the world's
second IVF baby. Preimplantation genetic testing (PGT) commenced at Melbourne IVF in 2002, with the first PGT baby born in 2004. In this talk, I will provide an overview of the practices and processes of PGT at Melbourne IVF, where I have been a consultant geneticist since 2004, including the use of PGT for monogenic disorders, chromosome rearrangements, and aneuploidy screening. I will (1) The history of PGT at Melbourne IVF, and current clinical, laboratory and counselling processes; (2) regulatory, legal and funding aspects of PGT in Australia;(3) ethical issues and consent in PGT, including the fate of embryos found to be affected by a genetic condition; (4) selection and approval of the specific genetic conditions that are appropriate for PGT; (5) PGT in specific circumstances, including: sex selection, exclusion testing in the setting of hereditary neurodegenerative diseases; HLA matching to create a 'saviour sibling'; PGT for mitochondrial gene variants; PGT in the setting of de novo and mosaic gene variants; genes and conditions that are challenging to test by PGT.

**From Cytogenetics to Genomics: The Evolution of Genetic Testing in Clinical Practice**

David Amor
*Developmental Medicine, University of Melbourne, Australia.*

It is now more than 60 years since the birth of human cytogenetics and more than 20 years since the completion of the human genome project. Whilst translation of genomics into health care was initially slow, this is now accelerating, and it is estimated that over the next 20 years, most people in developed countries will have had their genome sequenced. In this talk I will discuss recent successes in genomics, including the identification of causes of intellectual disability and rapid diagnosis of critically ill infants. As the cost of sequencing falls, we expect to see increased use of genome sequencing in healthy individuals, including for newborn screening, with the aim of diagnosing rare diseases early and using genomic information to predict and prevent common diseases. The ultimate goal will be the integration of genomic data and clinical data within the electronic medical record, with aggregated datasets promising new insights into disease risk and mechanisms. In reproductive medicine, we expect to see increased use of preconception carrier screening, along with the use of genomic sequencing on prenatal diagnosis samples. In the next 20 years, genomics will herald a new era of precision medicine, but its success will require extensive education of doctors, scientists and the general public, as well as addressing bioethical and psychosocial aspects.

**Advancing Molecular Pathology through Next Generation Sequencing Innovation**

Chonglei Bi
*Singapore Precision Medicine Centre, Singapore*

Advances in the next-generation sequencing (NGS) are transforming molecular pathology, enabling more precise, comprehensive, and timely oncology diagnostics. This presentation introduces Illumina's latest innovations, led by the MiSeq i100 Series—a fast, reliable platform with streamlined workflows tailored for routine clinical use. With Illumina's broader oncology portfolio and its strategic Collaboration with Pillar Biosciences, the assay flexibility has been extending from targeted DNA panels to emerging multi-omics applications. Central to Illumina's strategy is a commitment to make genomics universally accessible and affordable. At Illumina, there are ongoing initiatives to reduce per-sample costs, shorten turnaround times, and simplify bioinformatics. These advances are already improving cancer care through earlier detection, personalised therapy selection, and longitudinal monitoring. By accelerating access to high-quality sequencing, Illumina aims to empower clinicians and researchers worldwide, driving the next wave of precision oncology and ultimately improving patient outcomes.

**From Pixels to Precision: How Multimodal AI is Redefining Pathology Diagnostics & Drug Discovery**

Wang Xiaomei
*Global AI Inclusive Networks, Singapore*

The integration of multimodal artificial intelligence (AI) into pathology is revolutionising both diagnostics and pharmaceutical research. At PathoAI, we have developed China's first NMPA-approved multimodal pathology foundation model capable of recognising 57 tumour subtypes across 9 organs. This breakthrough exemplifies how AI can transform static pathology images into dynamic, clinically actionable insights.
Our approach combines three pioneering innovations:
1) Organ-Specific Feature Pyramid Networks, enabling hierarchical analysis from cellular to whole-slide features
2) Pathology Chain-of-Thought framework, which replicates and visualises diagnostic reasoning paths with human-interpretable logic
3) Lightweight deployment architecture, making precision pathology accessible even in resource-limited settings
Beyond diagnostics, our multimodal AI serves as the intelligent engine for our digital pathology CRO platform, where it accelerates drug and medical device development through automated, quantitative analysis of therapeutic effects across species. By integrating pathology images with clinical, genomic, and imaging data, we are creating a new paradigm where AI bridges traditional diagnostic boundaries.
This presentation will demonstrate:
• Real-world cases where our model achieved 98.7% concordance with expert pathologists in tumour subtyping
• How pharmaceutical partners reduced preclinical pathology analysis time by 70%
• The roadmap toward multimodal precision oncology, where AI synthesizes pathology, EHRs, and multi-omics data for MDT decision support
The future of pathology lies not in replacing human expertise, but in amplifying it through AI that understands both pixels and clinical context. Join us to explore how this convergence is reshaping global healthcare standards.

**6. Medical Microbiology**

Automation of the microbiology laboratory: beyond the Yellow Brick Road? (Plenary 4)

Deborah Marriot
*Clinical Microbiology and Infectious Diseases, St Vincent's Hospital, Sydney; Professor, Faculty of Medicine, University of New South Wales and Adjunct Professor, University of Technology, Sydney.*

**The past.** Microbiology began with the first documentation of microscopic organisms by Anthony Van Leven Hook in the 1670s. Subsequently, Louis Pasteur and Robert Koch established the germ theory, demonstrating that specific microbes cause specific illnesses with 1857 marking the inception of Microbiology as a distinct science. **The present.** Culture-based Microbiology has, unlike haematology and clinical chemistry, relied on manual methods. However, it must be recognised that even in the realm of 'traditional microbiology' there is a significant disparity in the scope of practice and capabilities of laboratories particularly in low- and middle-income countries. The late 20th and early 21st centuries have seen a significant growth in the role of molecular biology and the commencement of automation of some aspects of microbiology practice such as processing of midstream urine. **The future.** Automation at multiple stages of sample processing including sample handling, inoculation and incubation, Gram stain, plate reading and organism identification, and antimicrobial susceptibility testing. **The reality.** In a time with the number of microbiologists is decreasing, automation has been demonstrated in several publications to increase efficiency and productivity, improve reliability and accuracy, reduce turnaround time and in the longer-term result in cost savings. The future automation of the laboratory at St. Vincent's Hospital Sydney will provide an illustration of the process. **The challenges.** The initial cost of purchase of automation systems is significant with ongoing maintenance cost an issue. Laboratory staff require retraining to operate automated systems. In hospitals with a complex patient mix such as transplantation or haematologic malignancies the complexity and variability of specimens maybe challenging for an automated system.

**Antifungal therapeutic drug monitoring: challenges and opportunities**

Deborah Marriot
*Clinical Microbiology and Infectious Diseases, St Vincent's Hospital, Sydney; Professor, Faculty of Medicine, University of New South Wales and Adjunct Professor, University of Technology, Sydney.*

The role of antifungal therapeutic drug monitoring (TDM) is increasingly recognised in precision medicine, involving optimising efficacy and minimising toxicity of antifungal agents. While TDM for 5-fluorocytosine and azoles is well established, its use for echinocandins is growing, especially in complex clinical cases. However, there remain several barriers to widespread acceptance, most notably the lack of a dedicated clinical lead to advocate for and sustain the service. Without a senior clinician consistently highlighting the role of TDM the services are doomed to failure. Resistance to change is real
Turnaround time is frequently cited as a challenge, particularly when testing is centralised, hindering the timely adjustment of therapy. The cost of running an assay remains a major issue as many laboratories rely on mass spectroscopy or HPLC to determine antifungal concentrations, requiring expensive equipment and highly trained staff. However, newer commercial immunoassays offer faster, more cost-effective options on standard chemistry platforms. Funding remains inconsistent where some healthcare systems cover TDM costs, while others pass them to patients or insurers.
Proper sample timing is another hurdle but can be addressed through Bayesian modelling tools that aid dose prediction which are increasingly available. Interpretation and implementation of TDM results take skill and time, particularly in complex and changing patient pharmacokinetic settings. Pharmacists and physicians have competing priorities unless dedicated time is set aside.
Opportunities to streamline TDM process, provision of clear TDM standards of practice, enhance resource allocation for all aspects of TDM services and educate healthcare professionals on the benefits of precision medicine will improve the uptake of TDM, therefore optimise patient management.

**Artificial Intelligence: An Emerging Diagnostic Tools and Way Forward For The Clinical Microbiologist**

Pattarachai Kiratisin
*Faculty of Medicine Siriraj Hospital, Mahidol University, Thailand*

Artificial intelligence (AI) is poised to revolutionise clinical microbiology by enabling faster, more accurate infectious disease diagnostics. Traditional laboratory workflows often involve time-intensive methods that delay diagnosis and contribute to antimicrobial resistance (AMR). AI—particularly through machine learning and deep learning—offers scalable solutions across the diagnostic pipeline, including automated image analysis for direct pathogen identification and antimicrobial susceptibility testing (AST), as well as prediction of AMR profiles from genomic data. Integration of AI with molecular tools such as next-generation sequencing (NGS) enhances the detection of novel pathogens and resistance mechanisms, addressing diagnostic challenges where conventional methods fall short. In parallel, AI-driven analytics enable the synthesis of large-scale clinical, laboratory, and epidemiological data to support outbreak detection, real-time surveillance, and individualised antimicrobial therapy—core priorities for modern microbiology laboratories. For clinical microbiologists, AI represents an opportunity for augmentation rather than replacement. As AI automates routine diagnostics, microbiologists can redirect expertise toward complex interpretation, stewardship, and strategic public health roles. This shift calls for cross-disciplinary training in data interpretation, algorithmic reasoning, and digital integration. To ensure effective adoption, critical challenges must be addressed, including data standardisation, algorithm validation, regulatory oversight, and ethical implementation. As this technology matures, embracing AI will enhance diagnostic precision, improve turnaround times, and reinforce the role of microbiologists in global infectious disease management.

**Application of Artificial Intelligence in Managing High Rates of Antimicrobial Resistance**

Pattarachai Kiratisin
*Faculty of Medicine Siriraj Hospital, Mahidol University, Thailand*

Antimicrobial resistance (AMR) is an escalating global threat, undermining treatment efficacy and straining healthcare systems. Addressing this crisis requires innovative, data-driven approaches—an area where artificial intelligence (AI) is emerging as a transformative force. AI excels at processing complex, large-scale datasets and is revolutionising AMR surveillance by enabling real-time trend detection, hotspot prediction, and early identification of novel resistance mechanisms. In diagnostics, machine learning models facilitate rapid antimicrobial susceptibility predictions from genomic or clinical data, allowing faster, more targeted therapy than conventional methods. Clinical decision support systems powered by AI integrate patient data, microbiological profiles, and resistance patterns to guide personalised antimicrobial therapy. This precision reduces unnecessary use of broad-spectrum agents, reinforces antimicrobial stewardship, and limits resistance selection pressure. Beyond clinical application, AI is accelerating drug discovery by predicting compound efficacy, optimising lead selection, and identifying novel drug targets—revitalising a stagnating antibiotic pipeline. AI is not just a complementary tool but a critical component in AMR management. Its integration across diagnostics, therapy, surveillance, and drug development promises to improve patient outcomes and contain resistance spread. As a path forward, realising AI's full potential demands robust data infrastructures, validated algorithms, and interdisciplinary Collaboration between health practitioners, microbiologists, data scientists, policymakers, and public understanding.

**ICPALM 2025: Local Speakers**

**1. Anatomical Pathology**

**Diagnosing Peripheral T Cell Lymphoma and the Importance of CD30 Expression**

Noraidah Masir
*Prince Court Medical Centre, Kuala Lumpur, Malaysia*

Diagnosing Peripheral T Cell Lymphoma: Peripheral T cell Lymphoma (PTCL) is a heterogeneous group of lymphomas with more than 30 distinct entities recognised. The tumour is found in a variety of anatomic locations, including nodal and extranodal sites. Accurate diagnosis of each entity is important for successful management. This can only be achieved by integrating the clinical features, tumour cell morphology, its immunophenotype and the molecular genetic abnormalities in the assessment of the lesion. Recognising specific morphological features is critical but can be challenging because the tumour cells are polymorphic and are mixed with inflammatory cells. The heterogeneity of cells may hamper diagnosis. Immunophenotyping which is an essential criterion for diagnosis requires a good panel of T cell antibodies as well some markers specific for subtyping. Molecular testing maybe necessary in difficult cases to prove clonality.
Importance of CD30 in PTCL: CD30 expression is an important predictive factor for targeted therapy. Anti-CD30 monoclonal therapy brentuximab vedotin effectively targets CD30+ PTCL. Thus, CD30 testing should be incorporated into standard IHC panels for PTCL. Better understanding of CD30 expression and its interpretation enable greater access to optimal care for patients with PTCL

**Role of Immunohistochemistry and Molecular Studies In Lymphoma**

Noraidah Masir
*Prince Court Medical Centre, Kuala Lumpur, Malaysia*

Immunohistochemistry (IHC) and molecular studies are invaluable tools in lymphoma pathology for classifying tumours, identifying their cell of origin, and guiding therapy strategies. IHC helps differentiate lymphoma subtypes which is essential for prognosis and treatment planning. It complements morphological assessment and molecular studies. In general, B and T cell markers determine cell lineage. In addition, a large panel of antibodies are available to detect specific subtypes each with distinct prognoses. Accurate classification therefore is pertinent in guiding treatment. Molecular studies complement immunophenotyping to provide a comprehensive understanding of lymphoma. It allows detection of clonal populations and identification of prognostic genetic abnormalities. Understanding the molecular pathways has guided us in the development of targeted therapies.

**XAI: The New Bridge for Morphological Diagnostics**

Afzan Adam
*Centre for Artificial Intelligence and Technology, Faculty of Information Science and Technology, Universiti Kebangsaan Malaysia, Bangi, Malaysia.*

Artificial intelligence (AI) is increasingly integrated into digital pathology, offering rapid and accurate analysis of tissue morphology. However, the deployment of complex machine learning (ML) models—particularly deep learning—has raised concerns among pathologists due to their opaque, "black-box" nature. Explainable AI (XAI) emerges as a critical solution, providing transparency and interpretability to AI-generated results, thereby fostering trust and clinical adoption.
This talk introduces the fundamentals of XAI and its application in morphological diagnostics. It highlights how XAI techniques—such as saliency maps, SHAP values, and attention mechanisms—can reveal the features or regions within whole slide images that drive model predictions. By aligning machine-derived explanations with established histopathological knowledge, XAI not only validates model outputs but also facilitates collabourative discovery between clinicians and algorithms.
Through case examples involving tumour detection and perhaps segmentation as well, the presentation illustrates how XAI helps pathologists understand and verify AI decisions, identify potential biases, and explore new diagnostic features. It also addresses challenges such as interpretability trade-offs, model generalization, and the integration of XAI into existing pathology workflows. Ultimately, the talk emphasises that the path forward in digital diagnostics is not about replacing human expertise but augmenting it with interpretable machine insights. As we move toward precision pathology, XAI stands as a bridge—connecting artificial intelligence with human intuition, and enabling a new era where diagnostics are not only automated but also explainable.

**Recent Updates of Bethesda Reporting System for Thyroid Cytology with Molecular Applications**

Norizal Mohd Noor
*Hospital Al-Sultan Abdullah, Universiti Teknologi MARA, Puncak Alam, Selangor, Malaysia*

Thyroid cytology is one of the most common aspiration cytology requests in patients with neck swelling, predominantly in pre-operative diagnosis. Due to the value of the interpretation of the sample towards the patient's care, laboratories strive to give the most in the cytology results. This is supported by an international reporting system of thyroid cytology, the Bethesda system. This

is a product of a collabourative global initiative that involves pathologists, radiologists, endocrinologists, and oncologists. Success stories of the utilisation of this system are abundant in the publication. The recent update of the system has included molecular applications to alleviate the diagnosis of Atypia of Unknown Significance. This further helps the clinician manage patients. This talk will discuss the current updates, especially looking into the utilisation of the molecular application.

**A Hidden Challenge: Insights from a Rare Parapharyngeal Tumour Case**

Noraida Khalid
*Pathology Department, Hospital Sultanah Aminah, Johor Bahru, Johor, Malaysia*

Parapharyngeal space neoplasms are rare tumours, accounting only for approximately 0.5–1% of all head and neck neoplasms. They often present with subtle symptoms, leading to delayed diagnosis. Tissue diagnosis for parapharyngeal space tumours is challenging, given the difficult surgical access for tissue sampling /deep location and the broad differentials to consider in view of complex anatomy / structures contained within this region. The purpose of this lecture is to share a very rare case of a parapharyngeal follicular dendritic cell sarcoma with the objective to create awareness of the existence in this location as it has peculiar histopathology features, which can lead to delayed diagnosis and misdiagnosis. Challenges encountered during diagnosis and lessons learned from the case will be highlighted.

**Psoriasis, dermatitis or psoriasiform dermatitis?**

Adawiyah Jamil
*Department of Medicine, Faculty of Medicine, University Kebangsaan Malaysia*

Psoriasis (PsO) and atopic dermatitis (AD) have distinct clinical and histological features. Rarely, both diseases co-exist in the same patient. Biological therapy for PsO maybe complicated by new onset dermatitis or worsening of pre-existing dermatitis. However, lesions with both AD and PsO characteristics have been described and labelled as psoriasis dermatitis, or psoriasiform dermatitis. Diseases grouped as psoriasiform dermatoses include lichen simplex chronicus, prurigo nodularis, pityriasis rubra pilaris, secondary syphilis and Reiter syndrome. How are these diseases differentiated? The immunopathogenesis and phenotypes of PsO with AD features, AD with PsO features, coexisting AD and PsO, development of AD-like dermatitis during PsO or AD treatment and development of PSO during AD treatment will be discussed.

**The Importance of Clinicopathological Correlation (CPC) in Dermatopathology**

Ikmal Hisyam Bakrin
*Premier Integrated Labs, Kuala Lumpur, Malaysia*

Getting an accurate diagnosis in dermatopathology requires a combination of clinical and pathological information. Optimal patient care through clinicopathological correlation is the result of a long and complex process. This journey involves comprehensive dermatology and dermatopathology training, solid foundational knowledge, effective communication between clinicians and pathologists/dermatopathologists, and keen observational skills on both sides. It is important to understand that histopathological examination is typically complementary and confirmatory. For an accurate diagnosis, appropriate timing, selection of the correct lesion, and the use of the proper biopsy technique are essential. The most characteristic microscopic features are often found in well-developed lesions, highlighting the importance of understanding the natural course of lesions. In some cases, repeated biopsies may be required to reach a definitive diagnosis. When biopsies are repeated, they should be evaluated in comparison with the previous ones. Without a doubt, biopsy results must be interpreted in the context of clinical findings, laboratory investigations, medical history, and disease progression. It is worth emphasising that certain dermatopathological diagnoses are site-specific. For example, endocrine mucin-producing sweat gland carcinoma and signet ring cell/histiocytoid carcinoma have predilection for specific anatomical locations. Similarly, cutaneous T-cell lymphoma tends to follow a distinct clinical psrogression and may localise to particular areas of skin distribution. In conclusion, strong Collaboration between dermatologists and pathologists/ dermatopathologists is crucial to increase the accuracy of histopathological diagnoses and ensure optimal patient care.

**Basic Approach to Skin Adnexal Tumours**

Shahawiah Abdul Wahab
*Pathology Department, Hospital Tengku Ampuan Rahimah, Klang Selangor*.

Skin adnexal tumours are often a source of confusion amongst even experienced pathologist. Many of these tumours have overlapping features, tumours are often only partially sampled and many cases do not fit neatly into well-established classification scheme. Categorisation the tumour into simple 3 groups; sebaceous glands, sweat gland- derived and follicular groups is very helpful in understanding the tumour. Review of the clinical and histopathological features will assist the pathologist in diagnosing these challenging lesions. Basic approach to morphology of tumour based on haematoxylin-eosin (H&E) section before using IHC is very important step and recommended. Immunohistochemical (IHC) staining however plays a crucial role in the diagnosis and

characterisation of skin adnexal neoplasms, especially when histological findings are inconclusive or overlapping. By using a panel of appropriate markers, pathologists can improve diagnostic accuracy and provide more precise information

**Lymphoma Pathology from a Clinician's Perspective: What Information Is Essential?**

Nor Rafeah Tumian
*Department of Medicine, Faculty of Medicine, Universiti Kebangsaan Malaysia, Cheras, Kuala Lumpur, Malaysia.*

Accurate lymphoma diagnosis and management heavily depend on pathology information, which clinicians must understand to effectively guide patient care. Pathology reports provide essential details on lymph node architecture, cellular morphology, and immunophenotyping, which help distinguish malignant lymphomas from reactive lymphoid conditions. Immunohistochemistry (IHC) is necessary for identifying lymphoma subtype-specific markers such as CD20 for B cells and CD3 for T cells, alongside proliferation indices like Ki-67. Genetic markers, including Bcl-2 and cyclin D1, further inform prognosis and therapeutic choices. Clinicians must interpret pathology within the broader clinical context because of lymphoma's heterogeneity, from indolent to aggressive forms and potential extranodal involvement. In the era of targeted therapies and novel agents, which are available in the treatment landscape of lymphoma, this information is essential to enable clinicians to make informed decisions, formulate and deliver appropriate treatment plans, with the aim of improving patient outcomes in lymphoma care.

**Practical approach to T-cell lymphoma**

Asmawiza Awang
*Pathology Department, Hospital Kuala Lumpur, Kuala Lumpur, Malaysia.*

T/NK-cell lymphomas are a less common subtype of lymphomas, comprising about 12% of all non-Hodgkin lymphomas. T/NK-cell lymphomas often have a poor prognosis compared to their B-cell counterpart, and making these diagnoses can be challenging. There is a broad spectrum of T-cell and NK-cell lymphoid proliferation and lymphomas, ranging from non-neoplastic proliferation to highly aggressive T/NK-cell lymphomas. The most crucial step in arriving at a lymphoma diagnosis is to ensure that a reactive lymphoproliferation is not mistaken for a neoplastic process. The latest 2022 WHO 5$^{th}$ edition of Haematolymphoid tumour classifications lists approximately 34 types of T/NK-cell lymphomas, which can be broadly categorised into precursor T-cell neoplasms and mature T-cell and NK-cell neoplasms. This edition also includes the tumour-like lesions with T-cell predominance, namely Kikuchi-Fujimoto disease, autoimmune lymphoproliferative syndrome, and indolent T-lymphoblastic proliferation.
Accurate diagnosis of T/NK-cell lymphoma is essential for appropriate clinical management and often relies on tissue biopsies. The heterogeneity of the clinical presentation and anatomical locations may contribute to the challenges in diagnosing these entities. The anatomical locations include lymph nodes, blood and bone marrow, and organ sites such as the intestines, liver, spleen and skin. Each disease entity could have a spectrum of histopathologic features and slight variations in the immunophenotype findings. Other modalities, such as flow cytometry and molecular studies, including clonality studies, may contribute to the diagnosis although these may not always be available.

**2. Chemical Pathology**

**Sustainable Diagnostic: Between making sense and being sensible**

Hareef Mohamad
*Premier Integrated Labs, Kuala Lumpur, Malaysia*

In the era of escalating healthcare demands and growing environmental concerns, the concept of sustainability in diagnostics is more relevant than ever. It refers to the implementation of laboratory practices that are environmentally responsible, economically viable and clinically effective, striking the right balance between making sense and being sensible. "Making sense" refers to the scientific validity and accuracy of diagnostic methods. This involves ensuring that diagnostic tools, technologies, and practices are based on sound research and are capable of delivering reliable results that can guide clinical decision-making. Accuracy and precision are paramount, as they directly influence patient outcomes, treatment strategies, and overall healthcare effectiveness. At the same time, in diagnostics making sense revolves around the principal of clinical appropriateness, selecting the right test for the right patients at the right time. Evidence-based medicine and clinical guidelines play a vital role in promoting meaningful test utilisation. These include reflex testing, risk stratification algorithms and decision support digital tools that can promote meaningful diagnostic yield. On the other hand, "being sensible" speaks to the practical application of diagnostics in real-world settings. This encompasses the accessibility, cost-effectiveness, and resource efficiency of diagnostic practices. It stresses the importance of developing tools that are not only accurate but also affordable and adaptable to diverse healthcare systems, particularly in low-resource or remote settings. Sustainable diagnostics, therefore, must consider the social, economic, and environmental contexts in which they are deployed. The core of sustainable diagnostics is to ensure long-term health benefits without compromising the integrity of the environment or the economy. By integrating technologies like AI, telemedicine, and mobile diagnostics, sustainability can be achieved through solutions that are scalable, easy to deploy, and that reduce the burden on healthcare infrastructure. For example, using less invasive tests or diagnostic devices that consume fewer resources can significantly reduce the environmental impact of medical practices. The shift towards green labs, use of LEAN methodologies to reduce waste and environmental management systems that focus

on operational sensibility. Sustainable diagnostics emphasise inclusivity, ensuring that underserved populations, often excluded from high-tech diagnostic innovations, have equal access to the latest medical tools. It fosters equitable healthcare systems where diagnostic advances are available to everyone, regardless of geographical or financial barriers. In sum, sustainable diagnostics are about making informed, responsible choices that ensure both scientific credibility and social responsibility in healthcare. It is not a compromise but a synergy between accuracy and eco-consciousness.

**Digital Transformation in Sustainable Management**

Mohd Jamsani Mat Salleh
*Seberang Jaya Hospital, Penang, Malaysia*

Digital transformation is a dynamic process that harnesses information and connectivity technologies to optimise operations, enhance efficiency, and foster innovation. In medical laboratories, where inefficiencies are prevalent, integrating digital workflows is crucial to improving quality and cost-effectiveness, leading to unprecedented advancements in diagnostics and patient care. This transformation involves not only modernizing IT infrastructure but also shifting the perception of value creation and delivery to enhance laboratory services. However, successful implementation relies on user-centered design and balanced technology adoption. Addressing security and privacy concerns through robust regulation is essential. Furthermore, digital transformation plays a pivotal role in sustainable management by optimising resource utilisation and reducing environmental impact, thereby enhancing the long-term viability of healthcare services. Careful planning is essential to ensure seamless implementation without adverse effects.

**Pharmacogenomics Testing in Malaysia**

Rebecca Tay Sook Hui
*Global Precision Diagnostics and Beacon Precision Diagnostics, Beacon Hospital, Petaling Jaya, Selangor, Malaysia.*

Pharmacogenomics (PGx) is revolutionising patient care by enabling safer, more effective prescribing through genetic-guided therapy. In Malaysia, the burden of adverse drug reactions (ADRs), variable drug responses, and escalating healthcare costs underscores the urgent need for pharmacogenomic implementation. This presentation outlines Malaysia's evolving PGx landscape, highlighting progress, challenges, and future directions. Recent public-private partnerships have accelerated awareness and adoption, with notable initiatives including 1st Malaysia Pharmacogenomics Summit and Malaysia's first clinically recommended genome-wide PGx test reporting from medical database accredited by UKAS, NQA and HAS and recognised by the Malaysia Book of Records. These genome-wide platforms support the interpretation of hundreds of drug-gene interactions in line with CPIC, DPWG, and FDA guidelines. Key implementation milestones include Collaborations with the Ministry of Health, academic institutions and hospital networks for PGx research and implementation strategy into oncology, cardiology, and primary care. Real-world clinical cases demonstrate its value in reducing ADRs, optimising dosing, and avoiding therapeutic failure. Despite advances, challenges remain such as limited clinician training, lack of reimbursement structures, and need for national guidelines. This presentation will share current implementation strategies aimed at enabling scalable and equitable access to PGx. As Malaysia advances toward personalised healthcare, PGx offers a powerful tool to transform trial-and-error prescribing into evidence-based precision therapy. Through strategic alignment, Malaysia is well-positioned to lead regional efforts in implementing pharmacogenomics for population health impact

**Digitalisation In Diabetic Healthcare**

Chew Boon How
*Department of Family Medicine, Faculty of Medicine and Health Sciences, Universiti Putra Malaysia, Serdang, Selangor, Malaysia*.

Artificial intelligence (AI) has already entered clinical practice, quietly yet decisively transforming diabetic healthcare worldwide. Tools like AI-based diabetic retinopathy screening and closed-loop insulin delivery are no longer experimental, they are here, now. However, in Malaysia, AI adoption in healthcare remains largely fragmented, largely 'general' uses rather than personalised uses, isolated pilot projects, evolving regulatory frameworks, and significant gaps in infrastructure, local validation, and clinician readiness. This talk equips clinicians with a clear understanding of AI fundamentals, the full development cycle of AI tools, and pragmatic strategies to responsibly engage with emerging technologies. Sharing some real-world examples and successes, and persistent challenges in diabetic healthcare. The presentation highlights both opportunities and hidden pitfalls. Critical issues such as data bias, transparency gaps, ethical risks, and integration barriers will be discussed frankly. Clinicians are urged to move from spectators to stewards, upskilling in AI literacy, leading multidisciplinary Collaborations, and advocating for ethical, evidence-based AI deployment. Malaysia's healthcare digital future demands clinical leadership that is informed, courageous, and proactive. The future of AI in healthcare, whether empowering or problematic will be shaped by the vigilance, wisdom, and action of today's healthcare professionals.

**Intraoperative PTH Monitoring: Exploring in Silico Aptamer Based Technology Diagnostic Tool**

Tuan Salwani Tuan Ismail
*Department of Chemical Pathology, School of Medical Sciences, Universiti Sains Malaysia, Kota Bharu, Kelantan*

Real-time monitoring of intraoperative parathyroid hormone (IoPTH) levels is critical for assessing the success of parathyroidectomy, especially in primary hyperparathyroidism cases. Traditional point-of-care testing (POCT) and immunoassay-based laboratory methods are reliable, but they face challenges, including long incubation periods and variability between batch lots, leading to inconsistent results. Moreover, cross-reactivity between targeted epitopes and a lack of standardisation among diagnostic manufacturers complicate the accuracy of these methods. Aptamers, with their high specificity and affinity for target molecules, present a promising alternative to traditional immunoassays. An aptamer-based POCT biosensor could provide real-time results without the long incubation periods required by conventional assays, improving IoPTH monitoring and ensuring complete surgical resection. The computational modelling and bioinformatics tools were employed to design and screen candidate aptamers for optimal structural conformation, binding affinity, and stability of intact PTH (1-84). This study explores the development of in silico-designed aptamers for IoPTH monitoring and assesses their potential as a diagnostic tool. Aptamer candidates specific to intact PTH (1-84) were generated through molecular docking and dynamic simulations, which confirmed strong theoretical and experimental binding affinity. Preliminary in vitro assays validated the aptamers' stability and specificity under physiological conditions. This in silico approach significantly reduced the time and resources needed for aptamer selection and optimisation. In conclusion, in silico aptamer-based technology offers a rapid, cost-effective, and practical alternative to conventional assays for IoPTH monitoring. With further validation, this approach could improve surgical outcomes and also can be applied in peripheral clinic setting for the measurement of PTH level.

**Diabetes associated autoantibodies: connecting the dots**

Saraswathy A/P Apparow
*Chemical Pathology Unit, Institute for Medical Research, National Institute for Health, Setia Alam, Selangor, Malaysia*

Diabetic autoantibodies are crucial key markers for the diagnosis of type 1 diabetes. Since their discovery, they have also been recognised for their potential to identify at-risk individuals prior to symptoms. To date, risk prediction using autoantibodies has been based on autoantibody number; it has been robustly shown that nearly all multiple-autoantibody-positive individuals will progress to clinical disease. However, studies have demonstrated that the rate of progression among multiple-autoantibody-positive individuals is highly heterogeneous. Accurate prediction of the most rapidly progressing individuals is crucial for efficient identification of candidates most likely to benefit from disease modification. This is increasingly relevant with the recent success in identifying late-onset autoimmune diabetes (LADA) candidates as the field moves toward population-based screening. There have been many studies investigating islet autoantibody characteristics for their predictive potential, beyond a simple categorical count, including longitudinal patterns such as changes in titer and autoantibody reversion and risk profiles specific to the autoantibody. These insights are the outworking of decades of prospective studies and might contribute to the granularity needed for earlier disease detection. Advances in assay technologies in the field of autoantibodies detection not only improve the accuracy of detection but also improve reproducibility in terms of multiplex platform analysis and are easily automated.

**Methodological Innovations and Strategic Advantages of Multi-omics in Precision Medicine**

Amirul Ridzuan Abu Bakar
*Industrial Biotechnology, Universiti Malaysia Perlis, Perlis, Malaysia*

Multi-omics integrates diverse biological data streams, including genomics, transcriptomics, proteomics, metabolomics, and microbiomics, to offer a comprehensive understanding of molecular interactions. This systems-level approach is reshaping modern medicine by enabling earlier diagnoses, more accurate risk assessments, and highly personalised therapies. Implementation begins with high-resolution data acquisition through advanced technologies such as single-cell sequencing, spatial molecular profiling, and mass spectrometry. These tools capture dynamic molecular changes at cellular and tissue levels, generating detailed and multidimensional datasets. Machine learning and artificial intelligence techniques, including deep learning and probabilistic modelling, are then employed to integrate and interpret this complex sea of data. These methods facilitate the identification of disease-associated patterns, inference of causal pathways, and prediction of clinical outcomes. Practical applications are emerging across various medical disciplines, demonstrating how multi-omics bridges the gap between molecular complexity and actionable clinical insights. Advances in computational infrastructure are further accelerating the feasibility of clinical adoption. By providing a foundational framework for understanding and applying multi-omics, this approach supports the transition toward more precise, proactive, and patient-centred care.

**From Untargeted to Targeted Lipidomics: A Novel Approach For Assessing First Myocardial Infarction Risk**

Sophia Rasheeqa Ismail
*Cardiovascular Unit, Institute for Medical Research, National Institutes of Health, Setia Alam, Selangor, Malaysia*

Lipidomics, the large-scale profiling of lipid species in biological systems, is emerging as a transformative approach in cardiovascular research and precision medicine. By capturing the complexity of lipid metabolism, it oQers deeper mechanistic insights, improves disease risk stratification, and identifies novel therapeutic targets. Untargeted lipidomics allows for broad, exploratory profiling of measurable lipids, supporting the discovery of new biomarkers and metabolic pathways. However, its use in clinical settings is limited by challenges in quantification and reproducibility. Whereas, targeted lipidomics addresses this by enabling precise, high-sensitivity measurement of predefined lipid species, making it more suitable for validation, clinical diagnostics, and therapeutic monitoring. In the context of the first myocardial infarction (MI), lipidomics provides a more nuanced understanding of dyslipidaemia than conventional lipid panels. Traditional biomarkers such as LDL and triglycerides often fail to identify individuals at risk, with up to 25% of first MI cases occurring in those without established risk factors. Lipidomic profiling has uncovered specific lipid species (such as ceramides, and triacylglycerols with low carbon number and double bonds) that show stronger associations with cardiovascular events and atherosclerotic plaque instability. These molecular markers reflect early and residual risk, oQering opportunities for earlier detection and more personalised intervention strategies. The integration of untargeted and targeted lipidomics represents a novel and promising approach to advancing cardiovascular risk prediction, enabling a shift toward more precise, mechanism-based prevention and care for myocardial infarction.

**Metabolomic Approach in Clinical Diagnostics of Chronic Diseases**

Chin Siok Fong
*UKM Medical Molecular Biology Institute, Universiti Kebangsaan Malaysia, Cheras, Kuala Lumpur, Malaysia.*

Metabolomics provides a powerful lens for understanding the biochemical disruptions underlying chronic diseases and offers novel opportunities for early diagnosis and personalised intervention. As a systems-level approach, it is increasingly recognised for its capacity to detect disease-specific metabolic alterations, inform risk stratification, and guide clinical decision-making before overt symptoms arise. When coupled with machine learning, metabolomic data can be transformed into predictive models with high clinical relevance. Through our investigations, metabolomic applications were explored across multiple chronic disease contexts. In obesity, untargeted LC-MS profiling identified lipid-related metabolic signatures that were integrated into predictive models and functionally validated, revealing their modulatory role in adipogenesis and insulin regulation. In type 2 diabetes mellitus, we utilised targeted cardiometabolic biomarkers in combination with machine learning algorithms to refine cardiovascular disease risk prediction. Additionally, in lung and colorectal cancers, targeted profiling of vitamers and trace elements enabled the development of stratification models that successfully classified patients into low, moderate, and high-risk categories with strong predictive performance. Collectively, these findings reflect the translational value of metabolomics in bridging molecular insights with clinical application. By capturing early biochemical perturbations and enabling precise patient classification, metabolomics stands as a critical enabler of predictive diagnostics and personalised therapeutic strategies in chronic disease management.

**3. Forensic Pathology**

**Challenges in Testimony of Head Trauma Cases**

Jessie Hiu
*Department of Forensic Medicine, Queen Elizabeth Hospital, Sabah, Malaysia.*

The Malaysian justice system operates on an adversarial model, where both the prosecution and defense present their cases, with the burden of proof resting on the prosecution to establish guilt beyond a reasonable doubt. In cases involving head injuries, the pathologist plays a crucial role in determining whether the injury was caused by inflicted trauma and in assessing whether the cause of death was influenced by factors such as substance abuse, medications, or natural diseases.
A particular challenge arises in cases where the victim initially survives the head trauma. While the primary brain injuries may be survivable, secondary brain injuries can occur, sometimes exacerbated by insufficient medical resources or delays in treatment due to logistical issues. These complications may ultimately lead to death, raising the legal question of whether such secondary factors justify a charge of murder. The central issue is whether these indirect causes of death, resulting from a lack of timely medical intervention or adequate infrastructure, should be considered a direct consequence of the initial trauma. This complexity underscores the challenge of determining whether the circumstances surrounding the death meet the legal criteria for murder under Malaysian law.

**Challenges and Opportunities of Digitalisation in Forensic Histopathology**

Mohd Suhani Mohd Noor
*Department of Forensic Medicine, Hospital Sultanah Bahiyah, Alor Setar, Kedah, Malaysia*

The digital revolution is transforming the traditional microscopy slide-based analysis. Digitisation is the conversion of analogue data into a digital format, and in histopathology practice, it ranges from simple digital photomicrographs to slide scanners producing high-resolution digital slides. Digitalisation in histopathology or digital pathology involves creating digital slides that are subsequently viewed and analysed by the pathologist using workstations. Slide viewing can be done remotely, thus obviating physical slides and microscopes. Digital pathology can improve slide management and reporting efficiency, enhance case discussion and facilitate peer review, enable advanced image analysis using artificial intelligence, and serve as an invaluable platform for histopathology training. Digital slides can last a long time, and digital slide archiving can overcome the perennial need for more space to store physical slides. The foremost challenge when implementing digital pathology is the high initial investment in acquiring the hardware and software and the necessity for a robust data storage and retrieval system to manage large volumes of digital images. The challenges and opportunities for implementing digital pathology will be discussed in the context of forensic histopathology, which tends to have a lower histology workload than surgical histopathology. A crucial element that forensic pathology centres can overlook in the quest for digital pathology is whether histopathology is practised as a routine or only selectively with low slide output. Given budgetary constraints and competing priorities, these centres should be pragmatic when assessing the suitability for adopting digital pathology.

**Between Negligent, Misconduct and Unreasonable Opinion: Are We Legally Answerable?**

Chandroth Navin Pankajakshan
*Department of Forensic Medicine, Hospital Pulau Pinang, Malaysia*

The modern practice of medicine places doctors in a position akin to working beneath the ever-present Sword of Damocles, where the threat of legal, ethical, or professional repercussions is never far.

Where do we draw the line between a clinical error, professional misconduct, and simply holding an unreasonable opinion? In the practice of medicine, where decisions are often made under pressure and with incomplete information the boundaries between acceptable judgment, negligent acts, and misconduct are not always clear-cut. This session explores the legal and ethical tensions that arise when medical professionals face scrutiny not just for what they do, but for what they believe or conclude in complex clinical situations.

Are we legally answerable for decisions that fall short of best practice, even when made in good faith? Can an unreasonable medical opinion, absent malice or recklessness, attract liability or disciplinary action? This session will examine how accountability is determined in a landscape where mistakes, disagreements, and professional uncertainty are inevitable. Ultimately, the talk aims to provoke critical reflection on the threshold of legal responsibility and what it means for the practice and protection of modern medical professionals.

**Difficult Forensic Case - Pathologist's View**

Siew Sheue Feng
*Department of Forensic Medicine, Hospital Kuala Lumpur, Malaysia*

Difficult forensic cases present many challenges to pathologists, not only in technical interpretation but also in legal and ethical aspects. While forensic work often centres on post-mortem examinations, clinical forensic assessment of living individuals can be equally complex and demands careful attention.

Inadequate documentation and incorrect assessment of injuries can lead to serious legal consequences. Such issues may arise during the initial assessment, when the first clinical team does not adequately evaluate or document the case. A case may also become more complex if police investigators' early involvement is limited before referral to the forensic team. These early shortcomings can complicate subsequent evaluations and further undermine the case. Another challenge arises when the next of kin or patient has unrealistic expectations that post-mortem or clinical forensic findings will support their own perspective.

In these situations, forensic doctors must balance technical expertise, legal expectations, and ethical responsibilities while upholding professional integrity. This requires not only knowledge and experience but also impartiality and an awareness of how their opinions may influence legal outcomes and public confidence. Close Collaboration with other medical teams, legal authorities, and investigative officers is essential to ensure fair and accurate conclusions. At the same time, they must remain vigilant against bias or external pressures that may affect their interpretations and expert testimony.

Expanding the role of forensic doctors from "speaking for the dead" to also protecting the living underscores their crucial contribution to justice and human dignity. Their responsibilities extend beyond the autopsy table, beginning wherever medicine and law intersect.

**Second Opinion in Forensic Pathology: Sharing Experience**

Bhupinder Singh
*Penang Medical College, Penang, Malaysia*

- A second opinion in forensic pathology refers to having a different forensic pathologist review or re-assess the findings, conclusions, or interpretations made by the initial pathologist in a post-mortem examination. It is relevant in cases that are complex, controversial, or have legal implications.
- Forensic pathologists must remain impartial, and a second opinion can help ensure that no bias or error has influenced the conclusions about the cause of death.
- The second forensic pathologist would carefully review autopsy reports, photographs, toxicology results, medical history, and any other available relevant materials to come to a conclusion.
- In cases where the cause of death is unclear or disputed, a second opinion can provide additional expertise or insights that may not have been initially considered.
- In some situations, families or legal teams may request a second opinion, particularly in high-profile or sensitive cases. They may perform an additional examination or review photographs and other evidence that the first pathologist may have missed.

**Mono-Discipline Postgraduate Training: Future Direction**

Razuin Rahimi
*Department of Forensic Medicine, Faculty of Medicine, Universiti Teknologi MARA, Sungai Buloh, Selangor, Malaysia.*

The evolving demands of healthcare and medico-legal system necessitate a focused, high-quality training pathway for future forensic pathologists. This presentation explores the current structure and future direction of the mono-discipline clinical postgraduate programme in Forensic Pathology in Malaysia. Traditionally part of a broader pathology training framework—encompassing medical microbiology, haematology, chemical pathology, and anatomical pathology, the shift towards a mono-discipline model allows forensic pathology to receive focused training emphasis from the very start of the programme. Key updates to the curriculum, assessment methods, and training rotations will be highlighted, emphasising the importance of competency-based education, interdisciplinary Collaboration, while at the same time giving more exposure to forensic casework. The programme continues to incorporate research, with increased emphasis on scientific writing and manuscript preparation. In conclusion, this presentation highlights the revamped postgraduate programme in Forensic Pathology as a response to national needs, equipping future professionals to adaptive roles in healthcare and medico-legal system.

**Postmortem Computed Tomography and Difficult Autopsies**

Grace Wong Yi-Li
*Faculty of Medicine and Health Sciences, University of Malaysia Sarawak, Kuching, Sarawak, Malaysia.*

PMCT serves as a useful adjunct to difficult autopsies, particularly in the evaluation of bone and gas distributions. Deaths resulting from suspected paediatric, adult or elderly abuse; deaths in custody, community centres or nursing homes require comprehensive multidisciplinary investigations and medicolegal documentation. Older neglected or healed bone fractures with callus formations may not always have external findings and can be missed without imaging. Additionally, PMCT can screen anatomical areas that are not routinely dissected, such as the spine and extremities, guiding targeted dissections or limited autopsies at regions of interest. For mass deaths, disasters, pandemics, blast or thermal related deaths, PMCT provides a quick means to triage cases, evaluate the extent of bone trauma/fragmentation and identify foreign bodies. Be aware that many PMCT findings can be equivocal and non-specific such as in the assessments of lung opacities, patterns of air distributions and fluid accumulations. PMCT findings of decomposition changes and resuscitation efforts often overlap with antemortem natural disease processes, iatrogenic injury, drowning and barotrauma e.g. diving, especially if the PMCT cannot be done soon after death, taking into consideration internal body and external environmental factors that may affect decomposition rate. The role of PMCT in identification for advanced decomposition, skeletonization, mummification and incomplete remain still requires large population-based research with comparisons to anthropological findings. For difficult autopsy cases, the combination of scene of death findings, postmortem imaging, autopsy, histopathologic and laboratory analysis are essential to extrapolate cause and manner of deaths more accurately.

**4. Haematology**

**Interesting Cases in Haemostasis: Exploring Acquired Bleeding and Thrombotic Disorders**

Lailatul Hadziah
*Haemostasis Unit, Department of Diagnostic Laboratory Services, Hospital Canselor Tuanku Muhriz, Kuala Lumpur, Malaysia.*

Haemostasis is a tightly regulated physiological process balancing clot formation and dissolution to maintain vascular integrity. Disorders of haemostasis, including both bleeding diatheses and thrombotic disorders, pose significant diagnostic and clinical challenges particularly when they present in previously healthy individuals. Accurate and timely diagnosis hinges on a combination

of clinical acumen and laboratory testing, which remains central in evaluating coagulation abnormalities and guiding targeted therapy. This session aims explore a series of intriguing haemostatic disorders, with a focus on two rare but clinically significant acquired conditions: acquired haemophilia A and catastrophic antiphospholipid syndrome (CAPS). Acquired haemophilia A is a rare bleeding disorder characterised by the development of antibodies against factor VIII, typically presenting with spontaneous soft tissue bleeding in patients with no prior history of bleeding. Diagnosis requires a high index of suspicion and relies on laboratory findings such as prolonged aPTT not corrected by mixing studies, and reduced factor VIII activity. Catastrophic antiphospholipid syndrome (CAPS) on the other hand, is a fulminant form of APS marked by widespread small-vessel thrombosis involving multiple organs over a short period. Despite its rarity, CAPS carries high morbidity and mortality. Prompt recognition, supported by laboratory detection of antiphospholipid antibodies and clinical correlation, is essential for initiating aggressive treatment, including anticoagulation, immunosuppression and plasma exchange. Through a case-based format, this session will highlight the critical role of the laboratory in detecting these rare entities and emphasise how timely recognition of these rare conditions can significantly alter patient outcomes.

**Morphologic, Immunophenotypic and Genetic Correlation for Refining Classification**

Rosline Hassan
*Department of Haematology, School of Medical Sciences, Universiti Sains Malaysia, Kota Bharu, Kelantan, Malaysia.*

Acute Myeloid Leukaemia (AML) is a heterogeneous group of blood cancers. In Malaysia, every year about 1,900 cases were diagnosed with ASR 6.3 per 100,000 population. It is one of the most common types of cancer with poor survival rates. The aetiologies are multifactorial and leukaemogenesis involve serial acquisition of genetic aberration leading to blocked in differentiation and clonal expansion of blast cells. It is necessary to make a correct diagnosis, and classifying the disease. The current classification of AML is based on WHO-HAEM5, International Consensus Classification (ICC), and European LeukaemiaNet (ELN) recommendations (2022), requiring the integration of immunophenotypic, cytogenetic, and molecular data, with clinical and morphologic findings. With the current classification, genetic testing is the upfront tool in suspected cases of AML based on clinical and blood morphology findings. Blast cell counts of less than 10% in peripheral blood is classified as AML in the present of recurrent genetic abnormalities. Those with blast counts between 10-19% but lacked defining genetic abnormalities is classified as MDS/AML. Multiparametric flow cytometry (FCM) is essential to identify and enumerate blast cells, and assign lineage hence crucial for the diagnosis. The other major advantages of FCM include detection of aberrant markers and specific surface marker which can be used for monitoring disease post-treatment, rapid turnaround time for prompt therapeutic decision-making and potential targeted immunotherapy, respectively. Strong correlations have been shown between immunophenotypic features and genetic aberrations, facilitating the prediction of the genotype based on flow cytometry data. In the future, this will provide an appropriate guide for the diagnostic workup and prompt clinical decision-making.

**Highlight from the Fifth Edition of the WHO Classification of Haematolymphoid Tumours (WHO-HEM-5): Evolving Understanding of Lymphoid**

Mardziah Mohamad
*Cytogenetics and Molecular unit, Division of Laboratory Medicine, University Malaya Medical Centre, Kuala Lumpur, Malaysia.*

The 5th edition of the World Health Organization (WHO) Classification of Haematolymphoid Tumours (WHO-HEM5), released in August 2022, represents a comprehensive update that reflects advances in diagnostics, molecular genetics, and pathobiology. This edition introduces a revised hierarchical, lineage-based classification system and integrates essential and desirable diagnostic criteria to promote global applicability while incorporating cutting-edge molecular insights. Notably, WHO-HEM5 includes stroma-derived lymphoid neoplasms and tumour-like lesions for the first time. In B-cell lymphoproliferative disorders, significant changes include the reclassification of B-cell prolymphocytic leukaemia and the introduction of "splenic B-cell lymphoma/leukaemia with prominent nucleoli" (SBLPN) as a placeholder entity. Refinements in the classification of B-lymphoblastic leukaemia/lymphoma (B-ALL) now emphasise ploidy and specific gene fusions, such as TCF::HLF and ETV6::RUNX1. Classic hairy cell leukaemia is now defined by the presence of BRAF p.V600E mutations, distinguishing it from related entities through immunophenotypic and molecular profiling. Follicular lymphomas are further stratified based on the presence or absence of BCL2 and BCL6 rearrangements, with new insights into their cell-of-origin, gene expression profiles, and potential transformation pathways. High-grade B-cell lymphomas (HGBL) are now more precisely Categorised, especially those with MYC, BCL2, and BCL6 rearrangements or 11q aberrations, improving diagnostic clarity and prognostic assessment. WHO-HEM5 underscores the need for standardised diagnostic approaches, integration of molecular diagnostics, and collabourative research to refine classification frameworks. These updates aim to enhance diagnostic accuracy and support the evolution of personalised treatment strategies in haematolymphoid malignancies.

**Navigating the Role and Challenges of Next-Generation Sequencing in Hereditary Hemolytic Anaemia**

Mohamed Saleem
*Cytogenomix Laboratory, George Town, Penang, Malaysia.*

Next-Generation Sequencing (NGS) has transformed the genetic diagnosis of hereditary haemolytic anaemia (HHA) by enabling rapid, high-resolution identification of causative variants. Despite its revolutionary potential, challenges persist, including variant

interpretation, cost-effectiveness, and bioinformatics complexity. This talk explores the role of NGS in molecular diagnosis of HHA, its impact on clinical decision-making, and the challenges associated with data analysis, ethical concerns, and accessibility across different healthcare settings. Case studies will illustrate both successful applications and pitfalls, offering real-world insights into genomic testing. By addressing these complexities, researchers and clinicians can refine the integration of NGS into routine haematological and genomic diagnostics, ultimately enhancing patient outcomes.

**AI and Transfusion Integration**

Mohammad Masrin Md Zahrin
*National Blood Centre, Kuala Lumpur, Malaysia*

The integration of Artificial Intelligence (AI) into transfusion medicine is revolutionising clinical practice by introducing sophisticated tools that support safer, more efficient, and patient-centred care. AI technologies are now embedded across the entire transfusion continuum from enhancing donor recruitment and selection processes to optimising blood inventory management, forecasting transfusion requirements, and mitigating adverse transfusion reactions. Machine learning models have demonstrated significant utility in predicting blood demand, identifying transfusion-related complications, and informing individualised strategies within Patient Blood Management (PBM) programs. Furthermore, AI-driven automation is streamlining laboratory operations, notably in blood grouping, antibody screening, and quality assurance workflows. For healthcare professionals, these advancements present valuable opportunities to enhance clinical decision-making, minimise unnecessary transfusions, and ultimately improve patient outcomes. Nevertheless, the successful deployment of AI in transfusion medicine depends on overcoming key challenges, including the acquisition and curation of high-quality data, seamless integration with existing clinical information systems, and strict compliance with regulatory and ethical standards.

**Overview of Regenerative Medicine**

Zalina Mahmood
*National Blood Centre, Kuala Lumpur, Malaysia*

Regenerative medicine is an emerging interdisciplinary approach focusing on repairing, replacing, or regenerating damaged or diseased tissues and organs following disease, trauma, or congenital abnormalities. It aims to reestablish tissue and organ function using external biological materials, such as stem cells and engineered tissues, gene therapy, biomaterials or cellular reprogramming. Promising preclinical and clinical data to date support the possibility for treating both chronic diseases and acute insults, including dermal wounds, cardiovascular diseases and traumas, treatments for certain types of cancer, and many more. Obstacles in the current therapy of transplantation of intact organs and tissues to treat organ and tissue failures and loss suffers from limited donor supply and often severe immune complications may potentially be bypassed using regenerative medicine strategies. Despite its exciting potential, regenerative medicine is still evolving, with challenges in cost, ethical concerns, and ensuring safety. But as technology advances, the possibilities for healing and transforming healthcare continue to expand.

**Radio-frequency Identification and Transfusion Safety**

Nor Amiza Mat Amin
*National Blood Centre, Kuala Lumpur, Malaysia*

Blood transfusion is a complex, vein-to-vein process that requires meticulous tracking of blood components to ensure both safety and efficacy. Various issues can arise throughout this process, including expired blood components, inventory management challenges, patient misidentification, and transfusion errors. Traditionally, barcode systems have been used to track blood components. However, radio-frequency identification (RFID) technology is emerging as a valuable tool for enhancing the efficiency and safety of the transfusion process across the entire blood supply chain, from collection to transfusion. The advantages of RFID include improved patient safety, reduced blood component wastage, increased supply chain efficiency, and enhanced traceability. Despite these benefits, widespread implementation faces obstacles, including high initial costs and concerns over patient privacy. Nevertheless, the significant improvements in transfusion safety and inventory control make RFID a worthwhile investment. Ultimately, RFID plays a critical role in modern Transfusion Medicine by enhancing transfusion safety and improving the efficiency of blood component management. With further development and broader adoption, RFID systems have the potential to significantly improve healthcare outcomes while simultaneously reducing costs.

**5. Genetic Pathology**

**Lung Cancer Today: Insights From an Oncologist**

Muthukumaran A/L Thiagarajan
*Department of Radiotherapy and Oncology, Hospital Kuala Lumpur, Malaysia*

At the wake of the 21st century, treatment options for advanced lung cancer stagnated with dismal outcomes with the use of platinum doublet chemotherapy. Subsequently, histologic classification served as a reliable predictive marker. But the breakthrough was later discovered with targeted therapies in the presence of targetable driver mutations. From an array of oral targeted therapies, intravenous immunotherapies and the most recent antibody-drug conjugates, it is highly challenging to treat lung cancer today without a molecular report. However, access to testing and subsequent novel treatment remains a hurdle due to exorbitant cost.

**Evolving Landscape of Cancer Diagnostics: Malaysian Journey**

Sayyidi Hamzi
*Premier Integrated Labs, Kuala Lumpur, Malaysia*

The field of cancer diagnostics is experiencing a rapid shift driven by the integration of artificial intelligence (AI), digital pathology, and next-generation sequencing (NGS). This presentation examines how these developments are transforming traditional diagnostic workflows, improving accuracy, and facilitating personalised cancer treatment strategies. By exploring key technologies—such as AI-powered image analysis, whole-slide imaging, and comprehensive genomic profiling—we demonstrate their combined impact on diagnostic accuracy, turnaround times, and clinical decision-making. Real-world case studies in lung, brain, and endometrial cancer demonstrate how combining histopathology, immunohistochemistry, and genomic data enhances biomarker detection and therapeutic decision-making. We will also discuss current limitations, ethical issues, and the changing role of pathologists in this data-driven era. This talk aims to offer a practical, future-focused perspective for pathologists and scientists navigating the evolution of cancer diagnostics.

**A Drop of Hope: AI-Enhanced Liquid Biopsy Promise and Challenges**

Roziana Ariffin
*Pantai Premier Pathology and Sunway Medical Centre, Kuala Lumpur, Malaysia.*

Liquid biopsies have proven their ability to inform treatment selection at diagnosis, monitor clonal evolution during treatment, sensitively detect minimum residual disease following local control, and provide sensitive posttherapy surveillance. Liquid biopsies encompass several components such as circulating tumour cells, circulating tumour DNA, exosomes, microRNA, circulating RNA, tumour platelets, and tumour endothelial cells. Advantages include reduced procedural anaesthesia, molecular profiling unbiased by tissue heterogeneity, and the ability to track clonal evolution. Traditional diagnostic measures require invasive procedures such as tissue excision using a needle, an endoscope, and/or surgical resection which can be unsafe, expensive, and painful. Additionally, the presence of comorbid conditions in individuals might render them ineligible for undertaking a tissue biopsy, and in some cases, it is difficult to access tumours depending on the site of occurrence. Being non-invasive liquid biopsy can now identify biomarkers for early diagnosis and targeted therapeutics. Liquid biopsies hold tremendous promise in oncology, enabling non-invasive serial surveillance with adaptive care. Recent advances in technologies and bioinformatics have improved applicability in the cancer landscape. This review also focuses on Premier Integrated Lab & Sunway mol lab experience i.e challenges and opportunities in liquid biopsy patient testing over the years.

**Fragile Foundations: Genomic Insights into Inherited Bone Marrow Failure**

Chin Loi Khim
*Pathology Department, Hospital Tunku Azizah, Kuala Lumpur, Malaysia*

Inherited bone marrow failure syndromes (IBMFS) represent a broad and intricate class of disorders that affect individuals due to the underlying genetic cause that disrupts normal haematopoiesis. Such disruption manifests clinically as a constellation of severe cytopenias or haematological malignancy transformations that pose considerable health risks. For this reason, prompt and precise genetic diagnosis is essential to their management.
Fanconi anaemia is due to a complex defect in the interstrand crosslink (ICL) repair process, a component of the DNA repair pathway. Congenital dyskeratosis is a diverse disorder caused by abnormalities in several genes vital for telomere preservation. Heterozygous mutations in the genes encoding ribosomal proteins, which are crucial structural and functional elements of ribosomes, the cell's machinery for protein synthesis, cause Diamond-Blackfan anaemia. The mutations in the SBDS gene, which is involved in ribosome biogenesis, lead to Shwachman Diamond syndrome.
Whole exome sequencing (WES) and whole genome sequencing (WGS) are advanced genomic technologies that aid in identifying disease-causing variants. Acknowledging these "fragile foundations," genomic profiling helps with genetic diagnosis, surveillance, and prognosis, as well as genotype-phenotype correlations. Some of these disorders address the intricate clinical and genetic landscape of IBMFS, important genetic functions, molecular pathways, inheritance patterns, and existing and new therapeutic approaches.

**Microarray Data Classification Using a Genetic Algorithm Optimised Extreme Learning Machine**

Shir Li Wang
*Faculty of Computing and Meta-Technology, Universiti Pendidikan Sultan Idris (UPSI), Tanjung Malim, Perak, Malaysia*

Microarray datasets are vital for medical diagnosis, especially in classifying diseases such as cancer based on gene expression patterns. However, their inherent high dimensionality, limited sample sizes, and class imbalance often present significant challenges to classification performance. This study proposes a hybrid classification framework that integrates the Extreme Learning Machine (ELM) with a Genetic Algorithm (GA) to address these issues. GA is employed to optimise feature selection and determine the optimal number of hidden neurons for ELM. At the same time, the Synthetic Minority Over-sampling Technique (SMOTE) is applied to address data imbalance. Materials and Methods: The proposed framework was evaluated using three leukaemia microarray datasets. Initially, feature selection was conducted using the Symmetric Uncertainty method, retaining the top 10% of the most informative genes. Subsequently, z-score normalization was applied, followed by data balancing using SMOTE. Classification was then performed using standard ELM and Kernel ELM (KELM), with GA utilised to optimise model parameters. Performance was assessed based on accuracy using a hold-out validation strategy with a 90 : 10 training-to-testing data split. Results: GA-ELM achieved an accuracy of 98.33% on the 2-class dataset, 96.11% on the 3-class dataset, and 95.83% on the 4-class dataset. On the other hand, standard ELM achieved 97.67%, 94.45%, and 94.17%, respectively. Both GA-KELM and standard KELM attained 100% accuracy across all datasets. Discussion: GA-ELM consistently outperformed standard ELM, with accuracy improvements of 0.66% for the 2-class dataset and 1.66% for the 3-class and 4-class datasets. Moreover, GA-ELM utilised fewer features and hidden nodes. For instance, in the 2-class dataset, GA-ELM selected 43 genes with 28 hidden neurons, compared to 72 genes and 33 hidden neurons for standard ELM. Similarly, GA-KELM selected 59 genes, fewer than the 72 genes used by standard KELM.

**AI: The intelligent Bridge Between Data and Diagnosis**

Anil Philip Kunnath
*Department of Applied Biomedical Science and Biotechnology, School of Health Sciences, International Medical University (IMU), Malaysia.*

Advancements in artificial intelligence (AI) and point-of-care testing (POCT) are transforming traditional laboratory systems, creating a more accessible, efficient, and cost-effective healthcare model. With the ability to perform diagnostics at home using optical, electrochemical, and magnetic sensors, a single drop of blood provides comprehensive analysis through AI algorithms. These systems enable real-time data interpretation and immediate feedback, bypassing the need for centralized laboratories and reducing diagnostic delays. One of the most transformative aspects of this approach is the application of deep learning to analyse genetic and biomarker data at a population scale. AI models are trained to predictively diagnose individuals by classifying them into disease-causing and non-disease-causing groups. By identifying high-risk individuals early, the system allows for targeted testing and early intervention, significantly reducing the burden of late-stage diseases. This predictive framework is not only empowering patients with personalised health insights, but it also enables healthcare systems and nations to allocate resources more effectively, focusing on those at the highest risk for developing serious conditions. By identifying diseases early, AI helps reduce medical costs through preventive care and early treatment, which lowers hospitalisation rates, avoids costly late-stage interventions, and improves overall public health outcomes. Moreover, AI-driven platforms enable remote consultations, allowing patients to receive real-time treatment recommendations without the need for clinic visits. Integrated with genomic analysis and pharmacogenomics, AI can predict adverse drug reactions and optimise therapy choices, enhancing patient safety and treatment effectiveness. Ultimately, this shift from reactive to predictive, personalised care will significantly reduce healthcare costs, streamline treatment workflows, and provide patients with more control over their health, all while driving the transition from traditional, centralized laboratory systems to a decentralized, AI-enabled healthcare model.

**Epigenetic Signatures in Adult Cancers: Biomarkers and Mechanistic Clues**

Felicia Chung Fei Lei
*Department of Biomedical Sciences, Faculty of Medical and Life Sciences, Sunway University, Kuala Lumpur, Malaysia.*

This talk will examine the role of epigenetic alterations in adult cancers from two interconnected perspectives: the utility of early epigenetic biomarkers for cancer risk stratification, and the use of epigenomic data to define disease heterogeneity and inform clinical management. The presentation begins with a prospective study on breast cancer, where DNA methylation profiling of buffy coat samples revealed subtle but consistent epigenetic changes in individuals years before diagnosis. A machine learning classifier trained on these features demonstrated predictive value, underscoring the potential of blood-based methylation markers for early detection. While promising, these findings remain exploratory, and future work is needed to validate such classifiers in larger, diverse cohorts and to assess their integration into population screening frameworks. The second half of the talk delves deeper into the molecular landscape of small intestinal neuroendocrine tumours (siNETs), where comprehensive multi-omics profiling uncovered four distinct molecular subtypes, each with unique epigenetic, transcriptomic, and genomic features. Notably, a mesenchymal-like subtype was associated with poor prognosis, resistance to therapy, and infiltration by cancer-associated fibroblasts. These findings challenge the clinical perception of siNETs as a homogeneous entity and open new avenues for subtype-specific treatment approaches and biomarker development. Future directions include functional validation of subtype-specific drivers, exploration of tumour-stroma interactions, and the design of clinical trials tailored to molecular subgroups.

Together, these studies highlight how epigenetic profiling can illuminate both the early phases of tumourigenesis and the complex diversity of established cancers, offering a dual lens for advancing personalised oncology.

**Malaysia Genome (MyGenom) Project: Unlocking the Future of Malaysia**

Zilfalil Alwi
*Human Genome Centre, School of Medical Sciences, Universiti Sains Malaysia, Kota Bharu, Kelantan, Malaysia*.

The MyGenom Project is Malaysia's first large-scale population genomics initiative, designed to decode the genetic diversity of the nation. By sequencing the genomes of Malaysian citizens from various ethnic backgrounds, the project aims to build a comprehensive Malaysian reference genome. Phase I will involve sequencing 2,400 genomes from healthy individuals, with a target of 10,000 genomes in Phase II. This foundational dataset will be critical for advancing precision medicine tailored to Malaysia's unique population. Currently, global genomic databases are dominated by European, American, and East Asian data. This underrepresentation of Southeast Asian populations leads to reduced diagnostic accuracy, ineffective treatments, and misinformed healthcare decisions for Malaysians. MyGenom addresses this gap by generating locally relevant genetic data. The project aims to deliver tangible benefits across multiple fronts. It will enhance understanding of the genetic basis of diseases common in the region, support pharmacogenomics to improve drug efficacy and safety, and enable personalised medicine approaches that optimise treatments for individual patients. Furthermore, MyGenom will support public health efforts by identifying at-risk populations and informing early screening and preventive strategies. By laying the groundwork for a more equitable and accurate healthcare system, the MyGenom Project marks a major step forward in national biomedical research and the future of personalised healthcare.

**6. Medical Microbiology**

**Leptospirosis: Current Status, Insights and Future Diagnostic Prospects in The Era of AI**

Zamberi Sekawi
*Department of Medical Microbiology, Faculty of Medicine and Health Sciences, Universiti Putra Malaysia, Serdang, Selangor, Malaysia*.

Leptospirosis, a zoonotic disease of global concern, poses significant public health challenges, particularly in tropical regions like Malaysia. Despite advances in surveillance and clinical management, the disease's diverse clinical manifestations and diagnostic limitations hinder effective control. Recent studies have shed light on the epidemiological landscape of leptospirosis in Malaysia, emphasising the need for enhanced diagnostic tools and region-specific insights. This presentation will provide an overview of the current status of leptospirosis, focusing on diagnostic challenges and recent research contributions. Furthermore, it will explore how emerging technologies, particularly artificial intelligence (AI), offer promising avenues for more rapid, accurate, and accessible diagnostics. The talk aims to bridge the gap between traditional diagnostic methods and future AI-enhanced tools, highlighting their potential to transform the detection and management of leptospirosis in Malaysia and beyond.

**A One Health Perspective on Hepatitis E**

Syafinaz Amin Nordin
*Department of Medical Microbiology, Faculty of Medicine and Health Sciences, Universiti Putra Malaysia, Serdang, Selangor, Malaysia.*

A One Health Perspective on Hepatitis E Syafinaz Amin-Nordin Hepatitis E, caused by the hepatitis E virus (HEV), is one of the most prevalent yet underdiagnosed forms of acute viral hepatitis, particularly in resource-limited settings. Four major genotypes of HEV are known to infect humans. Genotypes 1 and 2 are transmitted via the fecal-oral route and are primarily found in Asia and Africa. Genotypes 3 and 4, by contrast, infect both humans and animals and are more common in developed countries. These genotypes are primarily transmitted zoonotically through consumption of undercooked meat, contact with wild animals, and environmental exposure. Although often self-limiting, hepatitis E can occasionally result in liver failure, particularly in pregnant women. In some cases, it may lead to chronic infection, especially in immunocompromised individuals. Extrahepatic manifestations, such as neurological complications, have also been reported. Diagnosis is typically based on anti-HEV IgM detection, although molecular confirmation via RNA testing is essential due to serologic variability. Genomic sequencing supports genotype identification and outbreak tracking. Hepatitis E prevention requires coordinated attention to food safety, water sanitation, and environmental health. A One Health framework, recognising the interconnectedness of human, animal, and environmental systems, is essential. This approach supports integrated surveillance, molecular epidemiology, and cross-sectoral Collaboration to better understand transmission routes and control the spread of HEV. The application of artificial intelligence holds promising potential to strengthen HEV diagnostics, outbreak detection, and public health decision-making.

**The Utility of CMV Quantiferon in Monitoring Immunology-Based Assay in Assessing Clinical-Based Event among Post-Transplant Recipients**

Lim Soo Kun
*Department of Medicine, Faculty of Medicine, University Malaya, Kuala Lumpur, Malaysia.*

Cytomegalovirus (CMV) infection remains one of the most frequent and clinically significant complications following kidney transplantation, affecting up to 60% of high-risk recipients. Beyond its direct manifestations, such as CMV syndrome and tissue-invasive disease, CMV is associated with indirect adverse outcomes, including increased susceptibility to opportunistic infections, heightened risk of acute rejection, and potential long-term allograft dysfunction. While current management strategies, including antiviral prophylaxis and pre-emptive therapy guided by CMV PCR viral load, have significantly reduced CMV-related morbidity, they do not assess the recipient's immunological competence. The inability to gauge CMV-specific immune response presents a critical gap in individualised patient care, often leading to either overtreatment or under-recognition of those at highest risk of viral reactivation. The CMV QuantiFERON assay, an interferon-gamma release assay (IGRA), addresses this unmet need by measuring cell-mediated immunity specific to CMV. This immunology-based assay provides valuable insight into the transplant recipient's immune readiness to control CMV, independent of viral load, thereby enhancing clinical decision-making. This presentation will highlight the clinical utility of CMV QuantiFERON testing in the post-kidney transplant setting. Recent evidence and case-based discussions will illustrate how immune monitoring can inform duration of prophylaxis, predict recurrence risk, and support judicious use of antiviral therapies. Integrating immune function assays alongside traditional virological monitoring represents a promising advancement toward more personalised, risk-adapted CMV management - ultimately improving graft outcomes and patient survival.

**HCV Genotyping and Sequencing - Perspectives and Problems**

Rozainanee Mohd Zain
*Virology Unit, Institute for Medical Research, National Institutes of Health, Setia Alam, Selangor, Malaysia*

Hepatitis C virus (HCV) genotyping has been widely used to guide treatment regimens. However, in the era of pangenotypic direct-acting antivirals (DAAs), the clinical relevance of HCV genotyping has diminished. Furthermore, the limitations of currently available commercial kits for HCV genotyping have further reduced their clinical utility. This study aimed to determine the HCV genotype using an in-house Sanger sequencing method. A total of 59 samples with previously undetermined HCV genotypes were extracted, amplified via PCR, and sequenced at the targeted 5'-UTR region of the HCV genome. The sequencing results were analysed using the standard Nucleotide BLAST, and a phylogenetic tree was constructed to further assess the HCV genotypes. Of the 59 samples analysed, 50 (84.8%) were successfully amplified, sequenced, and genotyped. Nine samples failed to amplify the target region. In-house Sanger sequencing assays can be effectively utilised for HCV genotyping, helping to address certain diagnostic challenges. However, due to the quasispecies nature of HCV, these in-house assays may face limitations, including issues with accuracy, reliability, and technical complexity.

**EBV as a biomarker in NPC: current status and perspectives from Malaysia**

Yap Lee Fah
*Department of Oral and Craniofacial Sciences, Faculty of Dentistry, Universiti Malaya, Kuala Lumpur, Malaysia*

It is over 50 years since the discovery of Epstein-Barr virus (EBV), the first identified human cancer virus. Today, EBV remains the most common persistent viral infection worldwide, with approximately 95% of the global population carrying an asymptomatic life-long infection. Its strongest cancer link is with undifferentiated nasopharyngeal carcinoma (NPC), a malignancy endemic to southern China and Southeast Asia. In Malaysia, the Bidayuh people exhibit the highest incidence rates in the world. Indeed, many distinctive features of NPC may be attributed to EBV. The presence of EBV in virtually all NPC tumour cells provides unique opportunities for biomarker discovery and therapeutic intervention, spanning disease prediction, diagnosis, immunotherapy and targeting of EBV-driven oncogenic pathways. In particular, plasma EBV DNA has emerged as a valuable tool for early detection, patient stratification, and post-treatment surveillance. Meanwhile, the potential of EBV serology in screening continues to draw attention. Despite the promise of these approaches, their implementation into practice faces several challenges. This presentation will provide an overview of the NPC landscape in Malaysia and discuss opportunities for leveraging EBV-based biomarkers to improve patient management.

**EBV Serology in NPC Screening: Boon or Bane**

Nada Syazana Zulkifli
*Precision Diagnostics, Beacon Hospital, Petaling Jaya, Selangor, Malaysia.*

The link between Epstein-Barr Virus (EBV) and Nasopharyngeal Carcinoma (NPC) is well-documented, yet EBV serology for NPC screening remains uncertain in the local setting. This presentation examines the epidemiology, risk factors, symptoms, and screening methods for NPC, with particular emphasis on serological tests such as VCA IgA, EA IgA, EBNA1 IgA, and the role of EBV DNA in screening and diagnosis. The presentation concludes by presenting case studies and addressing challenges and strategies in NPC screening, highlighting the significance of early detection, inter-departmental Collaborations, and efficient serological screening.

**The Role of Artificial Intelligence in Mycological Diagnosis**

Ding Chuan Hun
*Department of Medical Microbiology and Immunology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Cheras, Kuala Lumpur, Malaysia*

Morphological identification is still widely used in Malaysia due to its low cost (compared to MALDI-TOF MS or DNA barcoding). Unfortunately, errors in identification are a real concern with microscopic identification. Also, not all microbiology laboratories have clinical mycologists. Artificial intelligence (AI) can potentially enhance the accuracy of fungal infection diagnosis through advanced image analysis techniques, which is critical in settings where rapid and accurate pathogen identification can influence clinical outcomes. Most AI models rely on supervised learning techniques – researchers provide algorithms with labelled training data and a smaller dataset for validation. AI has shown promise by automating the detection and classification of fungal pathogens in clinical and laboratory settings. Specifically, AI can assist in the detection of hyphae in KOH stained samples, the differentiation of aspergilli from Mucorales in histology slides, the diagnosis of onychomycosis from nail clippings, the identification of fungal keratitis in confocal microscopy images, the classification of tinea, the identification of yeast in cultures, and last but not least, the identification of moulds in cultures. Unfortunately, the performance of AI algorithms depends on the quality of the provided images and the accuracy of the gold labels, which are frequently based on the assessments of just a few mycology experts and most models have been retrospective or validated in silico rather than in real-world clinical settings. Also, AI models struggle to distinguish diagnostically meaningful structures from background or artefacts, even though algorithms have been developed to facilitate the detection of relevant fungal structures.

**Beyond Diagnostics: AI's Role in Fungal Research and Therapeutic Development**

Leslie Than Thian Lung
*Department of Medical Microbiology, Faculty of Medicine and Health Sciences, Universiti Putra Malaysia, Serdang Selangor, Malaysia.*

Artificial intelligence (AI) is rapidly transforming the landscape of biomedical research, extending far beyond its established role in diagnostics. In the context of fungal biology, AI offers unprecedented opportunities to accelerate discoveries and improve therapeutic strategies. Fungal infections present rising global health challenges due to increasing resistance and limited treatment options. AI-driven tools now enable the mining of complex genomic, transcriptomic, and metabolomic datasets to uncover novel pathogenic mechanisms, identify drug targets, and predict antifungal resistance patterns. Machine learning models are being used to screen large compound libraries in silico, significantly reducing the time and cost associated with antifungal drug discovery. Moreover, AI facilitates the design of personalised treatment regimens by integrating patient-specific data with fungal strain characteristics. In environmental and agricultural contexts, AI is aiding in fungal biodiversity mapping and predicting the impact of climate change on fungal pathogenicity. As these technologies advance, ethical and practical challenges including data quality, model transparency, and cross- disciplinary Collaboration must be addressed. The presentation will highlight AI's expanding role in fungal research, highlighting its potential to revolutionise therapeutic development and usher in a new era of precision mycology transitioning from pre-AI. By moving beyond diagnostics, AI paves the way for innovative interventions against one of the most underrecognised yet critical groups of pathogens.

**Malaria Diagnostics and Treatment: From Traditional Techniques to Cutting-Edge Solutions**

Roslinda Jaafar
*Pathology Department, Hospital Sultan Haji Ahmad Shah, Temerloh, Pahang, Malaysia*

Malaria continues to pose a significant global health challenge, affecting millions and hindering socio-economic development in endemic regions. This presentation will delve into the evolution of malaria diagnosis and treatment, tracing the journey from traditional techniques to cutting-edge solutions. It will begin by examining historical diagnostic methods, such as microscopy and blood smears, which laid the foundation for malaria detection but often faced limitations in sensitivity and accessibility. Transitioning to contemporary practices, the presentation will explore advancements in rapid diagnostic tests (RDTs) and molecular techniques, such as polymerase chain reaction (PCR), that enhance diagnostic accuracy and facilitate timely treatment. Furthermore, it will discuss innovative treatment strategies, including the development of new antimalarial drugs and combination therapies designed to combat emerging drug resistance. By integrating traditional knowledge with modern technology, effective strategies for malaria management can be formulated. This presentation aims to provide a comprehensive overview of current trends and future directions in malaria diagnostics and treatment, emphasising the necessity of collabourative efforts among researchers, healthcare providers, and policymakers to create sustainable solutions in the fight against malaria. Attendees will gain valuable insights into how these advancements can revolutionise malaria control efforts globally.

**Mapping the Landscape of Current to Future Diagnostic Tests For Arboviruses**

Jamal I-Ching
*Department of Medical Microbiology, Faculty of Medicine, University of Malaya, Petaling Jaya, Kuala Lumpur, Malaysia*

Mosquito-borne arboviruses cause a heavy burden of sporadic and epidemic disease globally, and pose continuous threats to spread to new areas. In Malaysia, there is endemic circulation of dengue, chikungunya, Zika and Japanese encephalitis viruses. The presence of abundant competent mosquito vectors also puts Malaysia at risk of arboviruses imported from other continents, such as yellow fever, Ross River and West Nile viruses. Greater clinical awareness, surveillance and diagnostics are critical to detect and mitigate arboviral spread. Laboratory diagnostics of arboviruses are still challenging, with many currently available tests are either limited in sensitivity and specificity, or too costly for widespread use. Only dengue rapid diagnostic tests for antigen and antibodies come close to fulfilling the WHO REASSURED criteria for impactful diagnostics in resource-limited settings where arbovirus risk is greatest. The risk of imported, non-endemic viruses has also increased the role of untargeted detection methods such as next-generation sequencing. As many arboviral diseases are zoonoses, diagnostic assays can also be extended beyond human patients for a One Health approach, using samples from the environment (e.g. wastewater), mosquito vectors, or animal reservoirs. Surveillance can be undertaken for endemic, newly imported, or novel pathogens, and to improve understanding of their epidemiology.

**Diagnostics Barrier of STH in the Underprivileged Population and Advances In Management**

Yvonne Lim Ai Lian
*Department of Parasitology, Faculty of Medicine, University of Malaya, Petaling Jaya, Kuala Lumpur, Malaysia.*

Soil-transmitted helminths (STH) remain a significant public health challenge, posing a high burden of morbidity, particularly among underprivileged populations like the Orang Asli (indigenous). Factors such as poverty, inadequate sanitation, and limited healthcare access exacerbate the impact of these infections. Diagnostic barriers, including the reliance on traditional microscopy methods and the lack of advanced portable diagnostic tools, hinder effective disease surveillance and management especially in low-resource settings. This talk will explore the socioeconomic and infrastructural challenges that contribute to diagnostic limitations, emphasising the need for innovative, cost-effective, and accessible diagnostic solutions tailored for field and clinic/hospital-based applications among Orang Asli populations in rural and remote areas. Furthermore, advances in the management of STHs, including preventive chemotherapy, integrated sanitation programs, and community-based interventions, have shown promise in reducing disease prevalence and improving health outcomes. The discussion will highlight the importance of multidisciplinary approaches in tackling STHs comprehensively. By addressing diagnostic barriers and leveraging advances in management, we can pave the way for sustainable solutions to combat STHs in vulnerable populations, resulting in transformative changes in public health for marginalised communities like the Orang Asli.

**An Overview of Newborn Screening in Inborn Error of Immunity**

Adli Ali
*Department of Pediatrics, Faculty of Medicine, Universiti Kebangsaan Malaysia, Cheras, Kuala Lumpur, Malaysia.*

Inborn Errors of Immunity (IEI) are a growing class of monogenic disorders with early-onset, life-threatening presentations. Newborn screening (NBS) for IEI, initially through T-cell receptor excision circles (TREC) and kappa-deleting recombination circles (KREC), has transformed early detection, enabling pre-symptomatic diagnosis of Severe Combined Immunodeficiency (SCID) and other profound lymphopenias. This presentation will provide a focused overview of current global practices and highlight recent developments in Southeast Asia, particularly Malaysia's SHINE initiative, the region's first public-private partnership for expanded NBS targeting IEI. SHINE demonstrates the feasibility of integrating molecular diagnostics into national programs in middle-income settings, and offers valuable insights on early implementation outcomes. The talk will also explore the next frontier: genomic newborn screening (gNBS) using targeted or whole genome sequencing to detect a broader spectrum of IEIs, including immune dysregulation and innate immunity defects. Additionally, advances in mass spectrometry-based platforms are enabling multiplexed, high-throughput detection of immune-related proteomic and metabolomic signatures. With the convergence of genomics, immunology, and population health, NBS for IEI is entering a new era-shifting from single-analyte detection to systems-based, precision screening. This session will highlight the critical role of pathology in leading this transformation toward equitable and data-driven early-life immune diagnostics.

**Approach to Anti-Neutrophil Cytoplasmic Antibody (ANCA) Testing**

Nurul Khaiza Yahya
*Department of Immunology, School of Medical Sciences, Universiti Sains Malaysia, Kota Bharu, Kelantan Malaysia.*

Antineutrophil cytoplasmic antibodies (ANCAs) are specific antibodies formed against cytoplasmic granules of polymorphonuclear neutrophil granulocytes (PMNs). ANCA-associated vasculitides (AAV) are multisystem disorders involving inflammation of the small blood vessels and include granulomatosis with polyangiitis (GPA, formally known as Wegener granulomatosis), microscopic

polyangiitis (MPA), and eosinophilic granulomatosis with polyangiitis (EGPA, formally known as Churg-Strauss syndrome). AAV damages blood vessels through a complex interplay of autoantibody binding, neutrophil activation, release of toxic substances, endothelial cell injury, and an amplified inflammatory response. This leads to vascular inflammation, necrosis, and ultimately organ damage.
The approach to ANCA testing involves a stepwise strategy, beginning with clinical suspicion based on symptoms, initial screening with IIF and followed by antigen-specific testing to confirm PR3-ANCA or MPO-ANCA positivity. Interpretation of results must consider the clinical context, as ANCA can also be present in other conditions, including infections, inflammatory bowel disease, and drug-induced vasculitis. The two main ANCA patterns detected by indirect immunofluorescence (IIF) are cytoplasmic (c-ANCA) and perinuclear (p-ANCA), which correspond to antibodies targeting proteinase 3 (PR3) and myeloperoxidase (MPO), respectively.
In summary, ANCA testing plays a pivotal role in diagnosing and managing AAV. However, it should always be used in conjunction with clinical evaluation and other laboratory or imaging tests for optimal patient management. Additionally, the role of ANCA titers in disease activity monitoring remains an area of ongoing research.

**Autoantibodies in Autoimmune Bullous Skin Diseases**

Masita Arip
*Medical Microbiology and Immunology Unit, Institute for Medical Research, National Institutes of Health, Setia Alam, Selangor, Malaysia.*

Autoimmune bullous skin diseases (AIBDs) are a heterogeneous group of disorders characterised by blistering of the skin and mucous membranes due to autoantibody-mediated disruption of structural proteins within the epidermis and basement membrane zone. These diseases exemplify the intersection of dermatology and immunology, where humoral autoimmunity plays a central pathogenic role.
This lecture delves into the molecular targets of autoantibodies across major AIBDs, including pemphigus vulgaris, pemphigus foliaceus, bullous pemphigoid, mucous membrane pemphigoid, epidermolysis bullosa acquisita, and dermatitis herpetiformis.
Pemphigus vulgaris (PV) and bullous pemphigoid (BP) are autoimmune blistering diseases, but they differ in the antibodies involved and the location of the blisters. PV is characterised by IgG antibodies targeting desmogleins (cell adhesion molecules), leading to intraepidermal blistering. BP, on the other hand, involves IgG and sometimes IgE antibodies targeting BP180 (Type XVII collagen) and BP230, which are components of the basement membrane, resulting in subepidermal blistering.
Emphasis will be placed on the mechanisms of acantholysis and subepidermal blister formation, serological and histological diagnostic techniques (ELISA, immunofluorescence, salt-split skin), and the clinical relevance of autoantibody profiles in disease monitoring. Additionally, the session will explore evolving biomarkers, overlapping antigenic patterns, and their implications for precision medicine.
Understanding the role of autoantibodies in AIBDs enhances diagnostic accuracy, informs prognosis, and enables targeted immunomodulatory therapies. As the field progresses, integration of novel immunologic tools and deeper insights into autoantigen-antibody interactions hold promise for improving patient outcomes. This lecture provides a comprehensive overview for clinicians, researchers, and students seeking to advance their understanding of immune-mediated dermatologic disorders.

**Abstracts of the oral and poster presentations are as follows:**

**AP02: From testis to metastasis: A rare case of metastatic germ cell tumour following spontaneous regression of non-teratomatous component**

Dahlia Munchar Elias[1], Julia Munchar Jajuli[2], Bala Sundaran Mariappan[3], Pathmanathan Rajadurai[2,4]
*[1]Department of Pathology, University Malaya Medical Centre, Kuala Lumpur, Malaysia; [2]Department of Pathology, Subang Jaya Medical Centre, Selangor, Malaysia; [3]Department of Urology, Subang Jaya Medical Centre, Selangor, Malaysia; [4]Jeffrey Cheah School of Medicine & Health Sciences, Monash University Malaysia, Selangor, Malaysia.*

Introduction: Germ cell tumours (GCTs) represent 90% of testicular tumours, classified into teratomatous and non-teratomatous components, with the latter being more aggressive. Spontaneous regression of non-teratomatous GCT components is exceedingly rare, but not unheard-of. We report a unique instance of metastatic spread following such regression. Case report: A 40-year-old man presented with abdominal pain and significantly elevated serum β-HCG and AFP levels. Imaging revealed a left testicular lesion (2.2cm) and hypermetabolic nodal disease involving the cervical, thoracic and para-aortic (4.5cm across) regions. Histopathological examination of the left testis showed only mature teratoma without immature elements or evidence of other GCT components. However, cervical lymph node biopsy revealed metastatic embryonal carcinoma, immunohistochemically positive for CD30, SALL4 and OCT3/4. Discussion: Spontaneous tumour regression has been reported in various neoplasms, including GCTs. In cases of 'burned-out' testicular tumours, the primary GCT regresses partially or completely without intervention, and secondary symptoms arise from metastatic mass effects. According to the WHO 2016 classification, spontaneous regression occurs in <5% of GCTs. The underlying mechanism remains unclear, with ischemic necrosis and immune-mediated regression being proposed hypotheses. Seminomas are most likely to undergo 'burn-out', followed by embryonal carcinoma, as observed here. Diagnosing burned-out tumours is challenging, as metastatic lesions are often mistaken for primary malignancies. This case underscores the importance of a multidisciplinary approach, integrating clinical, radiological, and biochemical findings to achieve accurate diagnoses. A pathologist focusing solely on the testicular findings may misinterpret it as a benign teratoma, potentially overlooking the malignant embryonal carcinoma, impacting treatment outcomes.

**AP03: Clear cell sarcoma of soft tissue in an elderly male**

Dayangku Norlida A. Ojep[1], Vernon Tan Sze Yuen[2], Than Than Aye[3], Mohamad Zulkarnaen Ahmad Narihan[1]
*[1]Department of Pathology, Faculty of Medicine and Health Sciences, Universiti Malaysia Sarawak, Sarawak, Malaysia; [2]Department of Orthopaedic, Faculty of Medicine and Health Sciences, Universiti Malaysia Sarawak, Sarawak, Malaysia; [3]Department of Pathology, International Medical School, Management and Science University, Selangor, Malaysia.*

*Introduction:* Clear Cell Sarcoma of Soft Tissue (CCSST) is a rare, aggressive sarcoma with melanocytic differentiation, often termed "malignant melanoma of soft parts." It primarily affects young adults aged 20–40 and commonly arises in tendons or aponeuroses of the extremities. Cases in older patients are uncommon, making diagnosis challenging. *Case report:* We describe a 68-year-old male who presented with a progressively enlarging, painless right thigh mass over five months, measuring 15×15 cm. He experienced weight loss and loss of appetite. MRI revealed an aggressive mass. Gross examination showed a poorly defined, greyish-tan tumour with areas of necrosis and haemorrhage. No obvious skin lesion was noted. Histologically, the tumour consisted of pleomorphic and spindle cells with vesicular nuclei, prominent nucleoli and focal melanin pigmentation. Immunohistochemistry was strongly positive for S100 and HMB45, with focal positivity for Melan A, supporting a diagnosis of CCSST. Surgical excision with clear margins was achieved. *Discussion:* CCSST primarily affects young adults, but occurrences in elderly patients are rare. The genetic hallmark, EWSR1-ATF1 fusion, remains consistent across age groups. Accurate diagnosis requires combining histology, immunohistochemistry, and molecular analysis. Surgical excision with clear margins remains the most effective treatment. However, systemic therapies offer limited benefit, especially in advanced cases. This case emphasises the need for considering CCSST in differential diagnoses across all age groups.

**AP04: Primary ductal adenocarcinoma, a rare and aggressive tumour of the lacrimal gland**

Mohd Farhan Omar[1], Nadiah Ahmad Sabri[1], Amizatul Aini Salleh[2]
*[1]Department of Pathology, Hospital Sultanah Bahiyah, Kedah, Malaysia; [2]Department of Pathology, Hospital Sultan Idris Shah, Selangor, Malaysia*

*Introduction:* Primary ductal adenocarcinoma (PDA) is a high-grade malignancy accounting for 2% of lacrimal gland epithelial tumour, and less than 40 reported cases up to date. It is the counterpart of salivary duct carcinoma and histologically resembles invasive ductal carcinoma of the breast. The 5-year survival rate is 44% with frequent nodal and distant metastases indicating an aggressive course of the tumour. *Case report:* A 56-year-old man presented with painless left eye swelling for 3 months associated with proptosis, binocular diplopia and ipsilateral preauricular swelling. CECT orbit and brain showed a heterogenous left lacrimal gland mass with extensive extraconal extension and metastases to the left pre-auricular and parotid lymph nodes. Left eye exenteration, total left parotidectomy and left neck dissection revealed a firm, solid greyish lacrimal gland tumour, measuring 38×32×24 mm with infiltrative borders extending into the surrounding fibroadipose tissue, skeletal muscles, and orbital bone. Optic nerve and orbit were uninvolved. Histological examination displayed epithelial tumour arranged in solid sheets, nests and cribriform pattern with frequent comedo necrosis. Lymphovascular and perineural invasions were present. The cells showed focal positivity for GCDFP-15 and androgen receptor (AR) immunostaining and focal weak immunopositivity for HER2 (1+). Ki67 proliferative index was 60%. The parotid gland showed similar tumour cells infiltrate. Sixty-four positive cervical nodal metastases were evident at all levels. *Discussion:* Awareness and recognition of this rare malignancy is important as its inherent poorer prognosis. GCDFP-15, AR and HER2 are among essential markers for diagnosis, and this offers targeted therapy for patients.

**AP05: Concurrent Chronic Lymphocytic Leukaemia and Anaplastic Large Cell Lymphoma in a 68-Year-Old Patient: Synchronous tumour or Richter transformation?**

Nurul Husna Mohd Dani, Norafifah Mohd Yusoff, Suria Hayati Md Pauzi
*Department of Pathology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia*

*Introduction:* Chronic lymphocytic leukaemia/small lymphocytic lymphoma (CLL/SLL) is an indolent B-cell lymphoproliferative disorder that can transform into more aggressive lymphomas. While Richter transformation into diffuse large B-cell lymphoma is well recognised, the occurrence of a synchronous or transformation to T-cell lymphoma is exceedingly rare. This report highlights a rare case of concurrent CLL/SLL and anaplastic large cell lymphoma (ALCL). *Case report:* A 68-year-old man with a recent diagnosis of CLL presented with a three-week history of persistent left parotid mass. Imaging revealed a hypermetabolic lesion in the left parotid and left cervical lymphadenopathy. Excisional biopsies of the left parotid and cervical lymph nodes were performed. Histopathological examination of both specimens shows different tumour morphology. The parotid tumour demonstrated large, pleomorphic lymphoid cells in diffuse sheets, with scattered hallmark cells. The cells were immunopositive for CD30, CD2, CD4, CD43, and TIA-1, while negative for CD20, CD79a, and ALK, the findings of which were consistent with ALCL. Nevertheless, the cervical lymph node was composed of monomorphic small neoplastic lymphoid cells in diffuse sheets with immunopositivity for CD20, BCL-2, CD5, CD23 and low proliferation fraction, consistent with CLL/SLL. *Discussion:* The clinical progression of CLL/SLL raises concerns about the potential transformation into aggressive B-cell lymphoma. Although de novo ALCL can occur synchronously in patients with CLL/SLL, a rare large cell transformation from CLL/SLL to ALCL cannot be excluded. Adequate tissue biopsy from all suspicious tumour areas and thorough morphological and immunophenotyping are crucial as the treatment strategies for ALCL differ significantly.

**AP06: An Incidental Histopathological Finding of Trichuris trichiura in a Surgical Specimen Following Blunt Abdominal Trauma: A Case Report**

Puvanesvari Purusothma Naido[1,2], Ahmad Faris Bin Ramli[1], Tham Joon Hi[1]
*[1]Department of Pathology, Hospital Queen Elizabeth 1, Sabah, Malaysia; [2]Department of Pathology, Hospital Duchess of Kent Sandakan, Sabah, Malaysia*

*Introduction:* Trichuris trichiura, or whipworm, is a common soil-transmitted helminth affecting low-income, rural populations in tropical regions. Infections are often asymptomatic, but heavy infections may cause chronic gastrointestinal symptoms. Histopathological identification is rare in surgical specimens and are usually incidental. This case illustrates an unexpected finding of Trichuris trichiura during evaluation of bowel resection following abdominal trauma. *Case report:* A 56-year-old male presented with abdominal pain and fever after falling forward and sustaining blunt abdominal trauma against the wooden part of a boat while fishing. Examination revealed signs of peritonitis. Imaging and intraoperative findings showed perforated ileum with mesenteric injury. He underwent exploratory laparotomy, right limited hemicolectomy, and double-barrel stoma. Gross examination of the resected specimen revealed dusky, gangrenous bowel serosa with ileal perforation. Numerous roundworms with tapered ends were seen; some with one end embedded within caecal mucosa. Microscopy confirmed the gross findings. Cross-sections of the roundworms show thick cuticle, transverse annulations, nucleated hypodermis, polymyarian musculature, and bacillary bands consistent with Trichuris trichiura. The muscle wall showed mild inflammatory infiltrates with very focal areas of moderate inflammation. The minimal to focal moderate inflammation observed suggests a chronic, low-burden infestation. *Discussion:* Incidental discovery of Trichuris trichiura in bowel specimens resected for trauma is rare but clinically significant. Although perforation was trauma-related, chronic infestation may weaken mucosal integrity through prolonged mucosal attachment and subclinical inflammation. In endemic areas, such parasitic burden may theoretically predispose bowel to injury particularly under stress, highlighting need for further investigation.

**AP07: Evaluation of Cell Block Quality in Cytodiagnosis of Body Fluid Effusions**

Mohd Hafiiz Bin Mohamad Rizan[1,2], Suria Hayati Md Pauzi[2], Azmawati Mohamed Nawi[2]
*[1]Department of Pathology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia; [2]Department of Pathology, Faculty of Medicine and Health Sciences, Universiti Malaysia Sarawak, Sarawak, Malaysia*

*Introduction:* Conventional cytology smears and cell block techniques are routinely used for cytologic assessment of serous body effusion. Each technique shows varying diagnostic yield, cellular preservation and architectural assessment. This study aimed to evaluate the diagnostic quality of cytology smear slides and cell blocks prepared from serous effusion samples. *Methodology:* A total of 144 cases of serous body effusion with its concurrent cell block between year 2021 and 2023 were obtained. In each case, the slides of the conventional smears and its cell block were assessed using the Mair Scoring System to determine the outcomes of diagnostic quality. Unsatisfactory cytology cases were excluded from sampling. *Result:* The majority of cases were from pleural fluid (n= 98, 68.1%) followed by peritoneal (n=40, 27.8%) and pericardial fluid (n= 6, 4.2%). The highest proportion of samples were categorised as malignant effusion (56.3%). Diagnostically superior quality was mainly observed in conventional cytological smears (n=80) as compared to cell block sections (n= 43). Furthermore, a high number of cell block samples were deemed diagnostically unsuitable (57 out of 144 samples, 40%). Statistical analysis showed a significant association between different preparation methods and diagnostic outcome ($p < 0.001$). *Conclusion:* The findings in this study emphasise the importance of good conventional smears and cell blocks in routine cytological examination. Since many cell block protocols are practiced worldwide, it is important for individual cytology laboratories to select the method most suitable for their needs, with ongoing quality monitoring.

**AP08: Salivary duct carcinoma: A rare case of high-grade carcinoma of the parotid gland**

Ameera Farisha Mohamad Ghazali[1], Reena Rahayu Md Zin[1], Qihui "Jim" Zhai[2]
*[1]Department of Pathology, Faculty of Medicine, Hospital Canselor Tuanku Muhriz UKM, Malaysia, [2]Department of Pathology and Translational Pathobiology, LSU (Louisiana State University) Health Shreveport, Shreveport, USA*

*Introduction:* Salivary duct carcinoma (SDC) is a rare, aggressive malignancy of the salivary glands that histologically resembles in situ and invasive ductal carcinoma of the breast. It predominantly affects males in the fifth to seventh decades and commonly involves the parotid gland. SDC often presents at an advanced stage with early regional and distant metastases. *Case report:* A 61-year-old woman with underlying diabetes, hypertension, and dyslipidemia presented with persistent left ear pain. Clinical examination was unremarkable. Fine-needle aspiration cytology suggested a salivary gland tumour of uncertain malignant potential. MRI revealed a well-defined lesion in the deep lobe of the left parotid gland. She underwent total parotidectomy with facial nerve preservation and selective neck dissection. Histopathology showed a high-grade carcinoma with cribriform architecture, comedo necrosis, perineural invasion and surgical margins involvement. The tumour cells are positive for CK7 and negative for p63 and S100. Initial differential diagnoses included poorly differentiated acinic cell carcinoma, adenocarcinoma and neuroendocrine carcinoma. Expert review confirmed salivary duct carcinoma. Androgen receptor (AR) immunostaining was recommended but unavailable. *Discussion:* SDC is a high-grade salivary malignancy that closely mimics breast ductal carcinoma, showing cribriform architecture, comedo necrosis and apocrine features. Diagnosis primarily relies on its distinct morphological features, supplemented by immunohistochemical staining. Strong and diffuse AR expression is a key diagnostic marker, while negative p63 and myoepithelial markers help exclude other salivary carcinomas. Absence of estrogen and progesterone receptor expression supports distinction from metastatic breast carcinoma. Early and accurate diagnosis is crucial for improving prognosis.

**AP09: Clinical Validation of UMS NodeReveal™ LymphoHarvest in Colorectal Cancer Specimen Processing: Bridging the Gap Between Innovation and Practice.**

Mohd Fariz Amri[1], Datu Agasi Mohd Kamal[2], Mohd.Hijaz Mohd Sani[2], Allia Najmie Muhammad Yusuf[2]
*[1]Department of Pathology and Microbiology, Faculty of Medicine and Health Sciences, Universiti Malaysia Sabah, Sabah, Malaysia;*
*[2]Department of Biomedical Sciences, Faculty of Medicine and Health Sciences, Universiti Malaysia Sabah, Sabah, Malaysia*

*Introduction:* Colorectal cancer (CRC) ranks as the second most common malignancy in Malaysia and most common type among Malaysian males. Precise lymph node examination is vital for staging and prognosis. However, manual harvesting often results in delays and suboptimal yields. This study aimed to evaluate the lymph node revealing solution (LNRS), UMS NodeReveal™ LymphoHarvest, to enhance lymph node detection during CRC specimen processing. *Methods:* A retrospective study was conducted on 35 archival colorectal carcinoma specimens in Hospital Queen Elizabeth, Sabah, Malaysia. Mesorectal fat was removed and submerged in UMS NodeReveal™ LymphoHarvest for 16 to 18 hours. Additional lymph nodes were extracted and histologically analysed for metastases. *Results:* UMS NodeReveal™ LymphoHarvest enabled the retrieval of 278 additional lymph nodes from the 35 specimens, averaging eight (8) additional nodes for each case. These additional lymph nodes were smaller, with an average size of 4.2 mm in contrast to the initial 7.7 mm ($p=0.142$). Among them, 10 additional metastatic lymph nodes were identified, resulting in upstaging for two (2) cases. Moreover, additional nodes were also successfully harvested from all specimens that underwent neoadjuvant treatment. *Discussion:* The LNRS increased lymph node yield and detection of smaller nodes that are frequently missed by conventional approaches. Its effectiveness in neoadjuvant-treated specimens is helpful to ensure proper staging and timely initiation of adjuvant therapy, thereby enhancing patient survival. Conclusion: UMS NodeReveal™ LymphoHarvest is a safe and effective method for detecting lymph nodes in challenging cases thus improving staging accuracy, and colorectal cancer management.

**AP10: Major Pathology Organisations Update on Lymph Node Assessment Standards: Practical Advances in Lymph Node Revealing Solutions**

Mohd Fariz Amri[1], Datu Agasi Mohd Kamal[2], Mohd.Hijaz Mohd Sani[2], Allia Najmie Muhammad Yusuf[2]
*[1]Department of Pathology and Microbiology, Faculty of Medicine and Health Sciences, Universiti Malaysia Sabah, Sabah, Malaysia;*
*[2]Department of Biomedical Sciences, Faculty of Medicine and Health Sciences, Universiti Malaysia Sabah, Sabah, Malaysia*

*Introduction:* A minimum of 12 lymph nodes must be examined to accurately stage colorectal cancer. However, minimally invasive surgeries and neoadjuvant therapy frequently limit lymph node yields, rendering routine gross examination ineffective. Lymph node revealing solutions (LNRS) offer a promising solution. *Methods:* A review was conducted using Scopus, MEDLINE, and Google Scholar, focusing on international guidelines published from 2000 to March 2025 regarding the use of LNRS in colorectal cancer pathology. Six main pathology organisations, including CAP, RCPath (UK), RCPA, International Collaboration on Cancer Reporting (ICCR), European Society of Pathologists (ESP), and Japanese Society of Pathologists (JSP), stress the significance of checking at least 12 lymph nodes. CAP suggests re-examination with or without visual enhancement methods if yields are low. The RCPA's 2020 protocol encourages the use of alternative fixatives and fat clearance solutions, whilst RCPath (UK) particularly suggests LNRS such as Carnoy's and GEWF solutions. Previous studies showed that LNRS greatly improves lymph node retrieval, especially for smaller nodes in cases post neoadjuvant therapy. *Discussion:* Neoadjuvant treatment reduces lymph node size and quantity; however, metastases can still be found in tiny nodes. Conventional examination may miss these, resulting in understaging. LNRS improves lymph node detection, especially small metastatic nodes, without affecting histological examination, resulting in more accurate staging. Conclusion: International guidelines recommend using LNRS to optimise lymph node retrieval in colorectal cancer, especially when the yield was low to begin with. Adoption of LNRS is necessary to improve staging precision and ultimately enhance patient outcomes.

**AP11: Laboratory Method Comparison in Developing an In-House Optimal Control Tissue for Fungal Stains**

Zarina S[1], Muhamad Idham M[1], Mardiana AA[1,2]
*[1]Department of Clinical Diagnostic Laboratories, Hospital Al-Sultan Abdullah, Universiti Teknologi MARA, Selangor, Malaysia.*
*[2]Department of Pathology, Faculty of Medicine, Universiti Teknologi MARA, Selangor, Malaysia*

*Introduction:* Detection of fungal elements in histopathology is done by histochemical stains such as Grocott-Gomori's Methenamine Silver (GMS). Histochemical stains require a positive tissue control, which may be difficult to obtain. This study aimed to establish the best method to develop an optimal positive control tissue for fungal stains. *Materials & Methods:* Colonies from two fungal species (Aspergillus and Candida) obtained from Microbiology laboratory were used. Two methods were used to develop the control blocks, which were the i) clotting and ii) direct method. In the clotting method, the fungal colonies underwent a fibrin clotting process with equal amounts of plasma and thrombin and subsequently placed in a biopsy bag and tissue cassette. For the direct method, the fungal colonies were directly placed in a tissue cassette and covered with biopsy sponge. Both cassettes underwent overnight tissue processing, sectioned at 3µm and stained with GMS. Ease of block sectioning, staining quality and demonstration of fungal elements were compared between the two. *Results:* For both methods, on GMS stain, the fungal elements were sharply delineated by a black colour, in dark grey and green background. However, the block produced using the clotting method was easier to section. *Discussion:* Both methods produced excellent GMS positive control tissue and are comparable in staining quality. The clotting method produced a block which was easier to section, as the fibrin clot provided an additional architectural support which facilitated sectioning. This is a useful and cost-effective method to produce an in-house fungal stain control tissue.

**AP12: Comparing the Diagnostic Performance of MRI-Targeted and Systematic Biopsy in Prostate Cancer and Exploring the Predictive Factors**

Norlisa Khalid[1,2], Huzlinda Hussin[1,2]
*[1]Department of Pathology, Hospital Sultan Abdul Aziz Shah, Selangor, Malaysia; [2]Department of Pathology, Faculty of Medicine and Health Sciences,Universiti Putra Malaysia, Selangor, Malaysia*

*Introduction:* Prostate cancer is a leading malignancy among men worldwide, including in Malaysia, with rising incidence and challenges in early detection. While transrectal ultrasound-guided systematic biopsy (SB) remains standard, its limitations have prompted the adoption of multiparametric MRI (mpMRI) and MRI-targeted biopsy (MRI-TB) to improve diagnostic accuracy. *Materials & Methods:* This retrospective study analysed 258 patients who underwent both MRI-TB and SB at Hospital Sultan Abdul Aziz Shah, Selangor, from January 2023 to October 2024. A total of 308 biopsy samples were examined to compare diagnostic accuracy and identify predictive factors for clinically significant prostate cancer (csPCa). Diagnostic accuracy metrics, McNemar's test, and logistic regression were performed. *Results:* MRI-TB demonstrated superior sensitivity (80.3%) and negative predictive value (89.3%) compared to SB (59.0% and 79.9%, respectively), while both achieved 100% specificity. MRI-TB detected a higher rate of csPCa (30.5%) than SB (22.4%) ($p < 0.001$). SB missed 11.7% of csPCa cases, whereas MRI-TB missed 3.6%. Multivariate analysis identified PI-RADS 5 (OR=3.73, p=0.001), smaller prostate volume (OR=0.98, p<0.001), suspicious digital rectal examination (DRE) findings (OR=2.80, p=0.028), age (OR=1.10, p<0.001), and Chinese ethnicity (OR=1.85, p=0.047) as independent predictors. *Discussion:* MRI-TB offers superior diagnostic performance over SB, with fewer missed csPCa cases. However, SB remains complementary. PI-RADS 5, prostate volume, and suspicious DRE findings significantly predict csPCa. Integrating MRI-TB and SB while refining risk stratification may enhance diagnostic precision and reduce unnecessary biopsies. Future research should focus on MRI standardisation and optimising biopsy strategies.

**AP13: A Rare Case of Partial Hydatidiform Mole with Co-existing Living Foetus**

Marini M[1,2], Nadiah AS[1]
*[1]Department of Pathology, Hospital Sultanah Bahiyah, Alor Setar, Malaysia; [2]Department of Pathology, Hospital Canselor Tuanku Muhriz Universiti Kebangsaan Malaysia, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* Molar pregnancy with a viable foetus is a rare occurrence, estimated to occur in approximately 1 in 22,000 to 1 in 100,000 pregnancies. In most reported cases, it is associated with multiple maternal and foetal complications. We report a case of partial mole with coexisting living foetus, delivered at 33 weeks of gestation. *Case report:* A 25-year-old woman, 33 weeks pregnant with her second child, presented with a smaller-than-expected uterus. Antenatal ultrasound revealed foetal growth restriction with abnormal blood flow. Cardiotocography (CTG) indicated foetal distress, and meconium-stained liquor was observed during labour, prompting an emergency caesarean section. The baby, born prematurely, weighing 1120 grams, was reported to be stable under neonatal intensive care. Gross examination of the placenta showed multiple small fluid-filled vesicles on the placenta bed, occupying approximately 10% of the placenta surface. The histopathological finding revealed two populations of chorionic villi with large villi having central cistern formation and circumferential trophoblastic growth; which were in keeping with partial mole. The remaining areas demonstrated accelerated villous maturity with distal villous hypoplasia, features suggestive of maternal vascular malperfusion. *Discussion:* The most common type of molar pregnancy coexisting with a viable foetus is a twin pregnancy with one healthy foetus and a complete mole. Meanwhile twin pregnancy with a healthy foetus and partial mole is less common. The rarest type is a healthy single foetus with a partial molar placenta. The awareness of this rare condition and early detection during antenatal follow-up may aid in better treatment plans and foetal survival.

**AP15: Spectrum of histopathological diagnoses of lymph node biopsies – A private hospital experience**

Henry Rantai Gudum[1], Siow-Phing Tay, Muhamad Harith Izzat Mohamad Akbar[1], Jing-Loc Leong[1], Ashley Debra Branja[1], Zarith Faressa Azureen Md Zaki[1], Joseph Uchang[2]
*[1]Faculty of Medicine and Health Sciences, Universiti Malaysia Sarawak, Sarawak, Malaysia; [2]Borneo Medical Centre, Sarawak, Malaysia*

*Introduction:* Lymphadenopathy is a common clinical problem, and biopsies are required to confirm the diagnosis when it cannot be determined solely on clinical grounds. Histopathological patterns vary geographically, impacting clinical decision-making. However, recent data describing these patterns in Sarawak, Malaysia, are lacking. Understanding the local spectrum of LN pathology is essential for optimising diagnostic strategies in this region. This study aimed to determine the histopathological diagnoses of LN biopsies and evaluate trends over a 5-year period at a private hospital in Sarawak. *Materials & Methods:* This retrospective study reviewed all LN biopsies submitted to the pathology laboratory of Borneo Medical Centre (BMC), Kuching, Sarawak, over a five-year period (2016–2020). *Results & Discussion:* A total of 129 LN biopsies were analysed. The most common biopsy site was the cervical LN group (52.7%), followed by supraclavicular (14.7%) and inguinal (9.3%) regions. Neoplastic disorders comprised the majority (61.2%), while benign disorders were present in 37.2%. Neoplastic disorders that included lymphoma (34.8%) and metastatic diseases (26.4%) were more commonly seen above 40 years old. Reactive hyperplasia (17.1%) was the predominant benign disorders, followed by granulomatous disease (10%). Over the 5-year period, there were decreasing trends of granulomatous diseases and reactive hyperplasia. However, increasing trends were noted in neoplastic diseases for both Hodgkin's and Non-Hodgkin's lymphomas, as well as metastatic diseases. Overall diagnostic yield was 98.5% with two inconclusive findings. *Conclusions:* Neoplastic conditions, particularly lymphoma and metastatic disease, represent the majority of diagnoses in LN biopsies in this cohort, especially in patients over 40. These findings provide crucial contemporary data to guide clinical practice and diagnostic approaches for lymphadenopathy in Sarawak.

**AP 16: Profiling of Histopathological Specimens' Rectification in Anatomic Pathology Unit, Hospital Al-Sultan Abdullah UiTM**

Muhamad Idham M[1], Nurfareha MH[1,2], Awla MA[1,2]
*[1]Department of Clinical Diagnostic Laboratories, Hospital Al-Sultan Abdullah Universiti Teknologi MARA, Selangor, Malaysia; [2]Department of Pathology, Faculty of Medicine, Universiti Teknologi MARA Sungai Buloh, Selangor, Malaysia*

*Introduction:* Rectification of specimens is one of the most important pre-analytical steps in Anatomic Pathology laboratory for histopathological examination (HPE). Following the 'No Rejection Policy' for HPE specimens, rectification is crucial to prevent any discrepancy which might violate the integrity of patients' results. Rectifiable issues included error with specimen (i.e. inadequate fixative, wrong specimen container), request form (i.e. inadequate clinical history, no accompanying request form), and labelling (i.e. mislabelled, no label). Hence, this warrants the study of root causes with subsequent prevention and control measures. *Materials & Methods:* This retrospective study reviewed the 4 years documented rectification data from 2021 to 2024 at our institution, which was then tabulated and categorised according to the source of errors. *Results:* There were 37 cases of rectification recorded which included 18 types of erroneous requests. In general, two predominant types of rectification were documented, namely mislabelling of specimens (21 cases or 63.33%) and inadequate fixative (5 cases or 15.15%). Notably, there was a reducing trend of specimen rectification cases over the years. *Discussion:* Relevant precautionary measures were enforced in ensuring reduction of the rectification of specimens including scheduled customer education series program, orientation checklist for newly appointed clinical personnel, and immediate incidence reporting through official portal. These interventions are important in preventing errors and delay of laboratory turn-around-time. With the decreasing pattern of specimen rectification cases over the years, it could be concluded that the precautionary measures have succeeded in reducing the cases of rectification for HPE specimens at our institution.

**AP17: Cancer Incidence and Distribution of Common Cancer Types in Anatomic Pathology Laboratory, Department of Clinical Diagnostic Laboratories, Hospital Al-Sultan Abdullah Universiti Teknologi MARA (HASA UiTM)**

Muhammad Nor Hidayat MN[1], Muhamad Idham M[1], Nor Salmah B[1,2], Awla MA[1,2]
*[1]Department of Clinical Diagnostic Laboratories, Hospital Al-Sultan Abdullah Universiti Teknologi MARA, Selangor, Malaysia; [2]Department of Pathology, Faculty of Medicine, Universiti Teknologi MARA Cawangan Selangor, Selangor, Malaysia*

*Introduction:* Understanding cancer incidence distribution in anatomic pathology is essential for identifying cancer trends within specific regions or populations. Well-documented incidence supports research, healthcare planning, diagnostic improvements, and targeted treatment. This study aimed to estimate the incidence and distribution of various cancer types over a three-year period. *Materials & Methods:* This observational study was conducted over a three-year period (2020–2022) by documenting diagnosed cancer cases retrieved from the Laboratory Information System (Specimen Management System). Diagnoses were Categorised based on the organ or system involved, and the distribution of cases was presented as percentages. *Results:* A total of 1,034 cancer cases were reported during the study period. Breast cancer represented the most frequent diagnosis, accounting for 32.21% of cases, followed by digestive tract cancers (24.66%), lung cancer (15.86%), and gynaecological cancers (8.32%). Other cancer types including, but not limited to, those of the nasopharynx, thyroid, soft tissues, oral cavity, and prostate collectively constituted 18.96% of the cases. *Discussion:* Epidemiological data on cancer incidence are crucial for improving the understanding of cancer trends within defined populations. The findings of this study may assist public health authorities in assessing the cancer burden in specific regions and facilitate more informed healthcare planning. By identifying cancer types with the highest incidence rates, healthcare systems can more effectively allocate resources and prioritize interventions. Furthermore, such data support the formulation of strategies for early detection and targeted screening programs, ultimately contributing to improved cancer outcomes.

**AP19: When Common Symptoms Conceal a Rare Tumour: Primary Synovial Sarcoma of the Pericardium in a Young Patient**

Yessy Setiawati[1,2], Yuliza Ariani[1], Rahmi Ramadhani[1], Nani[3], Aan Ardiansyah[4]
*[1]Department of Anatomical Pathology, Faculty of Medicine, Andalas University, Padang, Indonesia; [2]Department of Anatomical Pathology, Dr. M. Djamil Hospital, Padang, Indonesia; [3]Department of Cardiology Faculty of Medicine, Andalas University, Padang, Indonesia; [4]Department of Thoracic Surgery Faculty of Medicine, Andalas University, Padang, Indonesia*

*Introduction:* Synovial sarcoma is a rare and aggressive malignancy most commonly occurring in the soft tissues of the extremities. Primary synovial sarcoma in the pericardium is extremely rare and poses significant diagnostic challenges. *Case report:* A 21-year-old female patient presented with progressively worsening chest pain and shortness of breath. An electrocardiogram showed a complete atrioventricular (AV) block. Echocardiography revealed a large mass measuring 39 × 33 mm, with an area of 17.7 cm², firmly banded to the posterior wall of the right atrium with massive pericardial effusion and cardiac tamponade, initially suspected to be a giant myxoma. Histopathology of the biopsy obtained via video-assisted thoracoscopic surgery revealed spindle cell proliferation in a fascicular-storiform pattern resembling fibrosarcoma. Immunohistochemical staining showed strong positivity for vimentin and CD99, a high Ki-67 proliferation index (>20%), and focal positivity for CKAE1/AE3, confirming a diagnosis of monophasic synovial sarcoma. Unfortunately, the patient died due to complications from the tumour's aggressiveness. *Discussion:* Primary synovial sarcoma of the pericardium is uncommon, especially in young adults. Due to nonspecific symptoms, a thorough diagnostic approach is crucial. With panel immunohistochemistry, the absence of molecular testing (e.g., SYT-SSX fusion gene) did not alter the conclusion. The patient's rapid decline after chemotherapy highlights the difficulties in managing tumours in critical locations. There was a need for early detection and Collaboration with a multidisciplinary team.

**AP20: Enhancing Lymphoma Diagnosis through Adaptive Variable Length Particle Swarm Optimisation for Feature Selection in Cancer Classification**

Siti Ramadhani[1,2], Muhammad Fikri[1,2], Theam Foo Ng[3], Sumayyah Dzulkifly[1], Roziana Ariffin[4,5], Shir Li Wang[1,6*]

*[1]Department of Software Engineering and Smart Technology, Faculty of Computing and Meta-Technology, Universiti Pendidikan Sultan Idris, Perak, Malaysia; [2]Department of Informatics Engineering, Faculty of Science and Technology, Universitas Islam Negeri Sultan Syarif Kasim Riau, Indonesia; [3]Centre for Global Sustainability Studies, Universiti Sains Malaysia, Penang, Malaysia; [4] Premier Integrated Lab, Pantai Hospital Ampang, Kuala Lumpur, Malaysia; [5]Sunway Medical Centre, Subang Jaya, Selangor, Malaysia; [6]Data Intelligence and Knowledge Management Special Interest Group, Faculty of Computing and Meta-Technology, Universiti Pendidikan Sultan Idris, Perak, Malaysia; [8]Department of Information system, Faculty of Science and Technology, Universitas Islam Negeri Sultan Syarif Kasim Riau, Pekanbaru - Indonesia.*

*Introduction:* Cancer, including lymphoma, is a leading global health challenge, with complex molecular and genetic factors making diagnosis and classification difficult. Lymphoma, a malignancy of the lymphatic system, is particularly challenging due to its heterogeneous nature. Recent advancements in artificial intelligence (AI), particularly evolutionary algorithms (EAs), have shown promising results in improving cancer diagnosis using high-dimensional datasets like Gene Expression Profiles (GEPs). Given the high feature-to-sample ratio in cancer data, effective feature selection (FS) is crucial for improving classification accuracy, reducing data complexity, and enhancing model interpretability. *Materials & Methods:* This study explores the use of an enhanced variant of the Particle Swarm Optimisation (PSO) algorithm called Adaptive Variable Length PSO (Adaptive-VLPSO) for feature selection in cancer classification. Adaptive-VLPSO dynamically adjusts chromosome lengths, enabling more efficient solution space exploration and avoiding stagnation in local optima. By incorporating adaptive inertia weights and acceleration factors, Adaptive-VLPSO improves parameter optimisation, yielding more robust and accurate models. *Results:* Evaluations on lymphoma datasets show that Adaptive-VLPSO significantly outperforms traditional methods, with a 50% improvement in generalization consistency and a 40% enhancement in model quality and effectiveness. This improvement aligns with the increased accuracy observed in the training and testing phases. *Discussion:* Adaptive-VLPSO optimisation minimises overfitting and enhances model generalization, crucial in cancer diagnosis. This method has the potential to revolutionise medical diagnostics, offering a more efficient and accurate assisting tool for cancer classification.

**AP21: Histopathological landscape and heterogeneity of paediatric neuroblastic tumours in Malaysia: preliminary data from the NBMY-1 study**

Fang Chyi Fong[1], Yin Ping Wong[2], Geok Chin Tan[2], Doris Sie Chong Lau[3], Betty Lee Sue Ho[4], Aisyah Muhammad Rivai[5], Ming Ping Ang[6], Ay Jiuan Teng[7], Norsarwany Mohamad[8,9], Ahmad Zafrullah Afham Ahmad Fikri[8,9], Jen Chun Foo[10], Rasheila Ganapathi[11], Che Hadibiah Che Mohd Razali[11], Nazzlin Dizana Din[12], Soon Keng Cheong[1,13], Kok Hoi Teh[14], C-Khai Loh[3]

*[1]HCTM-MAKNA Cancer Centre, Universiti Kebangsaan Malaysia, Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia; [2]Department of Pathology, Faculty of Medicine, Hospital Canselor Tuanku Muhriz, Universiti Kebangsaan Malaysia, Wilayah Persekutuan Kuala Lumpur, Malaysia; [3]Department of Paediatrics, Hospital Tunku Ampuan Besar Tuanku Aishah Rohani, Universiti Kebangsaan Malaysia, Wilayah Persekutuan Kuala Lumpur, Malaysia; [4]Department of Paediatrics, Hospital Umum Sarawak, Sarawak, Malaysia; [5]Department of Paediatrics, Hospital Raja Permaisuri Bainun, Perak, Malaysia; [6]Department of Paediatrics, Hospital Pulau Pinang, Pulau Pinang, Malaysia; [7]Department of Paediatrics, Hospital Wanita Dan Kanak-Kanak Sabah, Sabah, Malaysia; [8]Department of Paediatrics, School of Medical Sciences, Universiti Sains Malaysia, Kelantan, Malaysia; [9]Hospital Pakar Universiti Sains Malaysia, Health Campus, Kelantan, Malaysia; [10]Department of Paediatrics, Universiti Malaya Medical Centre, Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia; [11]Department of Paediatrics, Hospital Sultan Ismail, Johor Bahru, Johor, Malaysia; [12]Department of Paediatrics, Hospital Sultanah Nur Zahirah, Kuala Terengganu, Terengganu, Malaysia; [13]Department of Medicine, M. Kandiah Faculty of Medicine and Health Sciences, Tunku Abdul Rahman University, Selangor, Malaysia; [14]Department of Paediatrics, Hospital Tunku Azizah, Wilayah Persekutuan Kuala Lumpur, Malaysia.*

*Introduction:* Neuroblastoma, ganglioneuroblastoma, and ganglioneuroma represent a spectrum in differentiation and maturation of sympathoblast-derived neoplasms. This often results in complexities for prognostication and patient management. *Materials & Methods*: Preliminary data from the national Neuroblastoma Malaysia (NBMY-1) study was obtained through retrospective review of paediatric clinical case notes for neuroblastic tumours diagnosed between 1 January 2014 to 31 December 2023. *Results:* A total of 82/134 (61.2%) patients with available data were subtyped by the International Neuroblastoma Pathology Classification (INPC) system, where 12 were subtyped retrospectively. The remaining 52 cases (38.8%) were reported as neuroblastoma without further specifications. The subtypes reported include ganglioneuroma (n=5, 6.1%); ganglioneuroblastoma, intermixed (n=3, 3.7%); ganglioneuroblastoma, nodular or unspecified (n=11, 13.4%); differentiating neuroblastoma (n=4, 4.9%); poorly-differentiated neuroblastoma (n=36, 43.9%); undifferentiated neuroblastoma (n=22, 26.8%); and conflicting interpretations (poorly-differentiated vs. undifferentiated neuroblastoma; n=1, 1.2%). Eighty-four cases were classifiable as either favourable (n=27, 32.1%) or unfavourable (n=57, 67.9%) based on INPC criteria. Eleven cases had their primary site reported as ganglioneuroma at diagnosis, of which five had distant metastases detected. After histopathological examination of excised primary tumours or metastatic sites, five cases were found to harbour immature components and were thus revised to a higher grade, with two having progressed, and one died. Three cases with concurrent examination of primary and metastatic sites found less differentiated components in the latter. *Discussion:* Heterogeneity is an important consideration in histopathological diagnosis of neuroblastic tumours, as favourable findings do not preclude the existence of unfavourable subclones that can drive disease progression.

**AP22: A Rare Case of Metastatic Ovarian Leiomyosarcoma with Concomitant Metastatic Squamous Cell Carcinoma of Unknown Primary**

Lik Xian Tang[1], Shahanee Khadheeja[1], Stephen Jink Yang Chew[1], Yin Ping Wong[1], Geok Chin Tan[1].
*Department of Pathology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia.*

*Introduction:* Primary ovarian leiomyosarcoma is exceedingly rare, accounting for less than 1% of all ovarian tumours. It carries poor prognosis, with a 5-year survival rate of less than 20%. *Case report:* We reported an unusual case of metastatic ovarian leiomyosarcoma involving sigmoid colon nodules, along with a concomitant metastatic squamous cell carcinoma of unknown primary origin to the pelvic lymph nodes. Result: A 41-year-old lady, previously diagnosed with a high-grade mesenchymal malignancy of the left ovary, presented with a fluorodeoxyglucose (FDG)-avid right adnexal lesion and abdominopelvic lymphadenopathy. She underwent hysterectomy with right salpingo-oophorectomy, and excision of sigmoid mesenteric nodules and pelvic lymph nodes. Histological examination of the sigmoid nodules showed neoplastic spindle cells arranged in intersecting fascicles with areas demonstrating bizarre nuclear morphology and brisk mitotic activity, morphologically similar to the left ovarian tumour. The spindle cells stained positive for SMA and desmin, and negative for CKAE1/AE3,S100,DOG1,CD117 and CD34. A diagnosis of metastatic leiomyosarcoma was rendered. Interestingly, the lymph nodes revealed neoplastic cells arranged in sheets, positive for CK5/6,p63 and p53(mutant), consistent with metastatic squamous cell carcinoma. No residual malignancy was identified in the right ovary, fallopian tube, uterus or cervix. *Discussion:* Ovarian leiomyosarcomas are exceedingly rare, aggressive neoplasms that resemble uterine counterparts histologically. Diagnosis is often supported immunohistochemically by positive immunoreactivity for smooth muscle markers. The presence of a second epithelial malignancy in this patient is intriguing, raising the possibility of a previously unsampled epithelial component within the initial left ovarian tumour, or alternatively, a separate primary carcinoma of unknown origin.

**AP23: Rare synchronous occurrence of large intestinal adenocarcinoma and small intestinal extranodal marginal zone lymphoma: a case report**

Emira AR[1], Haza Syakirin MZ[1], Zalifah PR[1], Gan[2]
*[1]Department of Pathology, Hospital Selayang, Selangor, Malaysia; [2]Department of Surgery, Hospital Sungai Buloh, Selangor, Malaysia*

*Introduction*: Colonic adenocarcinoma is one of the most common types of colorectal neoplasms, accounting for over 95% of cases, while primary lymphomatous forms are unusual, comprising only 0.2-0.4% of cases. However, the simultaneous synchronous appearance of adenocarcinoma with lymphoma in the same patient is a rare entity, and the event is even rarer when two different gastrointestinal organs are involved. *Case report:* A 70 year-old Chinese gentleman with no known pre-morbid presented with two years history of perianal swelling and one month bleeding per-rectum. Computed tomography (CT) scan showed circumferential nodular thickening at the descending colon and wall thickening with 'aneurysmal dilatation' at the distal jejunum. Preoperative biopsy of the descending colon mass disclosed a tubulovillous adenoma with high-grade dysplasia. Subsequently, left hemicolectomy and small bowel resection were performed. Histopathological examination and immunohistochemical testing revealed a moderately differentiated adenocarcinoma of the descending colon with synchronous extranodal marginal zone lymphoma of mucosa-associated lymphoid tissue (MALT) of the small intestine. *Discussion:* While there is no known common etiological factor between adenocarcinoma and lymphoma, other than advanced age, it was suggested that the presence of lymphoma disrupts the patient's immune competence that may induce the development of a secondary malignant lesion. Non-metastatic lymph node on dissection should raise the suspicion of lymphomatous infiltration apart from systematic reactive reaction. Conclusion: It is important to recognise this occurrence as it impacts the therapeutic decision of treatment choice, surgical resection, assessment of tumour extension, prognosis and monitoring of recurrence and metastasis.

**AP24: Clear Cell Sarcoma Masquerading as Melanoma: A Molecular Diagnostic Revelation**

Geethanjali Makenthiran[1], Suria Hayati Md Pauzi[1], Geok Chin Tan[1], Yin Ping Wong[1]
*[1]Department of Pathology, Faculty of Medicine, Universiti Kebangsaan Malaysia, 56000 Kuala Lumpur, Malaysia*

*Introduction:* Clear cell sarcoma of soft tissue (CCSST) is a rare, aggressive soft tissue malignancy with melanocytic differentiation, often posing diagnostic challenges due to its morphological and immunohistochemical overlap with malignant melanoma. Accurate diagnosis is essential, as treatment and prognosis for these entities differ significantly. *Case report:* A 31-year-old man presented with progressive lower back pain, sudden paraplegia, and a progressively enlarging left chest wall mass. Imaging revealed multiple destructive bone lesions, soft tissue masses and spinal cord oedema at T9–T10, raising suspicion of a metastatic malignancy. Biopsies from spinal and chest wall masses were obtained. Histological examination showed loose cohesive nests and sheets of neoplastic cells arranged in pseudopapillary patterns with vague perivascular accentuation. The neoplastic cells had eccentrically placed round to ovoid nuclei, moderate eosinophilic cytoplasm and inconspicuous nucleoli. Scattered binucleated cells and coarse brown pigmentation were noted. The stroma displayed haemangiopericytoma-like vessels and mild inflammatory infiltrate. Tumour necrosis was focally noted, while mitotic activity remained low, counted up to 2 per 10 high power fields. Immunohistochemically, the neoplastic cells showed diffuse positivity for MUM1, HMB-45 and BCL2, with focal Melan-A immunoexpression, and were negative for S100, myogenin, desmin, CD3, CD20, and CD138 – features raising suspicion for plasmacytoid malignant melanoma. Nonetheless, the absence of primary cutaneous/mucosal lesion prompted further investigation. Molecular analysis using fluorescence in situ hybridization (FISH) analysis revealed EWSR1 gene rearrangement, confirming the diagnosis of CCSST. *Discussion:* This report highlights the indispensable role of molecular diagnostics in resolving morphologically ambiguous melanocytic tumours.

**AP25: Aggressive Benign Tumour: Maxillary Osteoblastoma - A Detailed Report**

Nadia Najwa Shuhairi[1], Wan Asmat Mahussin[2], Rashima Ali @ Ibrahim[2], Mukhriz Hamdan[3], Khamisah Awang Kechik[4]
*[1]Oral Pathology & Oral Medicine Unit, Oral & Maxillofacial Surgery Department, Hospital Taiping, Perak, Malaysia; [2]Department of Paediatric Dentistry, Hospital Taiping, Perak, Malaysia; [3]Oral & Maxillofacial Surgery Department, Hospital Taiping, Perak, Malaysia; [4]Oral Pathology & Oral Medicine Unit, Oral & Maxillofacial Surgery Department, Hospital Raja Permaisuri Bainun, Perak, Malaysia.*

*Introduction:* Osteoblastoma is a benign yet locally aggressive bone tumour, with approximately 10% occurring in the craniofacial region, most commonly the mandible. It primarily affects individuals in the second to third decades of life. *Case report:* We report a rare case of osteoblastoma in a 13-year-old boy, with a one-year postoperative follow-up. The patient complained of a progressively enlarging mass at the right upper gingiva, preceded by a toothache on tooth 16, six months earlier. Intraoral examination revealed a firm, expansile bucco-palatal lesion extending from tooth 14 to the maxillary tuberosity. Contrast-enhanced computed tomography (CT) showed a heavily calcified right palatine mass with bony erosion of the right maxillary sinus floor and right maxilla. The patient underwent right hemimaxillectomy including teeth 14 to 17. Grossly, the tumour was well-circumscribed with solid and cystic haemorrhagic areas. Histology showed a multinodular tumour with osteoid trabeculae rimmed by plump osteoblasts, marked blue bone matrix and cystic haemorrhagic degeneration. Several osteoclast-like giant cells are present. No atypia or atypical mitoses were observed. Immunohistochemistry revealed strong diffuse vimentin expression and a Ki-67 index <5%. However, the tumour is observed at the superior surgical margin. *Discussion:* This case underscores the rarity of maxillary osteoblastoma in a young Malaysian. Comprehensive clinical, radiological and histopathological evaluation is crucial for accurate diagnosis and treatment planning. At one-year follow-up, the surgical site shows no recurrence. However, there is a new radiopaque lesion at the anterior maxilla, near the midline. The lesion is currently under investigation.

**AP26: Electron Microscopy Elucidates the Glomerular Basis of Atypical Nephrotic Syndrome in a Child: A Case Suggestive of Alport Syndrome**

Nur Afrina Muhamad Hendri[1], Tengku Rogayah Tengku Abdul Rashid[1], Siti Zainab Salim[1], Latifah Ibrahim[1], Balvinder S.G. Pradhaman Singh[2], Chuah Ming Jie[3], Haidi Mohamad[4]
*[1]Electron Microscopy Unit, Institute for Medical Research, National Institutes of Health, Ministry of Health Malaysia;[2] Special Research Centre, Institute for Medical Research, National Institutes of Health, Ministry of Health Malaysia; [3]Department of Paediatrics, Hospital Sultanah Bahiyah, Kedah, Malaysia; [4]Department of Pathology, Hospital Sultanah Bahiyah, Alor Setar, Kedah*.

*Introduction:* Nephrotic syndrome in children presents a diagnostic challenge. While light microscopy (LM) and immunofluorescence (IF) provide valuable information, electron microscopy (EM) is crucial for detailed evaluation of glomerular pathology. This case report highlights EM's importance in characterising an atypical presentation. *Case Presentation:* A child with atypical nephrotic syndrome underwent renal biopsy. Light microscopy (LM) showed focal global glomerulosclerosis, and immunofluorescence (IF) revealed only focal weak (1+) mesangial IgM deposition. *Results:* EM revealed significant ultrastructural glomerular basement membrane (GBM) abnormalities (thin to thick areas, lamellation, fraying) and focal foot process effacement (15-20%). These findings raised suspicion for collagen IV abnormalities, especially given a family history of nephrotic syndrome in the patient's older brother. *Discussion:* The EM findings of GBM ultrastructural abnormality, atypical nephrotic syndrome, and relevant family history strongly suggest X-linked Collagen IV α5 abnormality (Alport syndrome). This should prompt clinicians to investigate hearing and visual abnormalities. LM and IF were limited in characterising the glomerular pathology, highlighting EM's necessity for accurate diagnosis. *Conclusion:* EM is essential in evaluating atypical nephrotic syndrome in children. In this case, EM revealed significant GBM abnormalities, suggesting a possible underlying genetic disease (Alport syndrome) and emphasising the need for further investigations, including collagen IV and genetic studies, as well as family screening for urinary abnormalities. Without EM, the patient might have been misdiagnosed with podocytopathy and inappropriately treated with steroids and immunosuppressants, which is not the mainstay of treatment in Alport's disease.

**AP27: Revolutionising DLBCL diagnosis: In silico design of DNA-Aptamers for detection of c-Myc translocated oncoprotein**

Nur Nadhira Izyani Asmera[1], Ummi Atikah Ayub[1], Normayazi Mohamed Ali[1], Siti Norasikin Mohd Nafi[1], Hany Haqimi Wan Hanafi[2], Aidy Irman Yajid[1], Shazana Hilda Shamsuddin[1], Faezahtul Arbaeyah Hussain[1]
*[1]Department of Pathology, [2]Department of Internal Medicine, School of Medical Sciences, Health Campus, Universiti Sains Malaysia, Kelantan, Malaysia*

*Introduction:* Diffuse Large B-cell Lymphoma (DLBCL) is an aggressive subtype of non-Hodgkin's lymphoma (NHL) marked by translocations involving the c-Myc oncogene. While Fluorescence in situ Hybridization (FISH) remains the diagnostic gold standard, it is hindered by high costs, labour-intensive protocols, and inconsistent specificity and sensitivity. Consequently, there is a critical demand for a cost-effective, rapid, and highly accurate protein-level diagnostic alternative. *Objective:* This study pioneers the development of DNA-Aptamer-based assays targeting the c-Myc oncoprotein in DLBCL. By combining biocomputational design with Aptahistochemical (AHC) validation, we benchmarked these assays against FISH for gene translocation detection, directly comparing their diagnostic specificity and sensitivity. *Methods:* DNA-Aptamers targeting c-Myc translocated oncoprotein were computationally designed (in silico), followed by comprehensive bioinformatics analyses to characterise their binding mechanisms. The specificity and sensitivity of these DNA-Aptamers were validated using AHC assays on 20 DLBCL-positive tissue samples, with results benchmarked against oncogene translocations detected via Fluorescence in situ Hybridization (FISH). *Results:* Three DNA-Aptamers, ranging from 35 to 50 nucleotides, demonstrated high stability and strong affinity for c-Myc, with binding energies between -18.3 and -17.8 kcal/mol. AHC analysis confirmed that these DNA-Aptamers specifically bound to nuclear-localised c-Myc in DLBCL tissue samples. The protein-level detection results were consistent with those obtained by FISH, and comparative analysis showed that DNA-Aptamer-based assays achieved specificity and sensitivity comparable to the current

gold standard for detecting translocated oncoproteins. *Conclusion:* These findings indicate that DNA-Aptamer-based assays have great potential as alternative protein-focused diagnostic tools, offering a promising avenue to transform the diagnosis of DLBCL.

**AP30: Clear cell odontogenic carcinoma: EWSR1 gene rearrangement is the golden key to diagnosis**

Geethanjali Makenthiran [1], Nurul Inaas Mahamad Apandi[2], Nurwahyuna Rosli[1]
*[1]Department of Pathology, Faculty of Medicine, Universiti Kebangsaan Malaysia Medical Centre, Kuala Lumpur, Malaysia; [2]Department of Craniofacial Diagnostics and Biosciences, Universiti Kebangsaan Malaysia Medical Centre, Kuala Lumpur, Malaysia*

*Introduction:* Clear cell odontogenic carcinoma (CCOC) is rare, malignant odontogenic tumour that often is not the first entity to be considered when presented in a patient with jaw swelling. *Case report:* We report a case of a 72-year-old female patient who presented with right mandibular swelling for 2 weeks causing pain and numbness at the site. CT neck revealed a right mandibular expansile lytic bony lesion with enhancing soft tissue component, making it locally aggressive. Initial clinical differential diagnoses included salivary gland carcinoma, metastatic disease, or osteosarcoma. CCOC was not considered at presentation due to its rarity and overlapping features with more common entities. Histology revealed infiltrative malignant tumour with heterogeneous appearance composed of mixed epithelial cells with clear cytoplasm and eosinophilic cytoplasm. Immunohistochemistry showed strong positivity for p63, CK5/6, and EMA, with focal weak CK19 staining. Fluorescence in-situ hybridisation (FISH) demonstrated EWSR1 gene rearrangement, supporting a diagnosis of CCOC. *Discussion:* CCOC poses a diagnostic challenge due to its histological and immunohistochemical overlap with other clear cell neoplasms, including salivary gland carcinoma, metastatic renal cell carcinoma, and clear cell variant of calcifying epithelial odontogenic tumour. Although not exclusive, EWSR1 rearrangement is a highly characteristic feature that helps distinguish CCOC from its mimics. Given CCOC's significant potential for both local recurrence and distant metastasis, aggressive surgical resection and vigilant follow-up are imperative, therefore an accurate diagnosis is extremely critical for effective patient management. Molecular testing is useful in confirming the diagnosis in cases where histopathological and immunohistochemical findings are inconclusive.

**AP31: Diagnosing metastatic testicular seminoma on fine needle aspiration cytology (FNAC)**

Lik Xian Tang[1], Rosli Nurwahyuna[1]
*Department of Pathology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia.*

*Introduction:* Seminoma is a common form of testicular germ cell tumour, and frequent metastasis to retroperitoneal, mediastinal and cervical lymph nodes. Cervical lymph node metastasis occurs in approximately 4% to 15% of cases. While the use of fine needle aspiration cytology (FNAC) in diagnosing primary testicular tumours remains controversial, it is particularly effective in evaluating metastatic lesions. *Case Report:* We present a case of a 59-year-old man with a history of left testicular seminoma, previously treated with orchidectomy and chemotherapy. He presented with left cervical lymphadenopathy. FNAC of the lymph node revealed moderately cellular smears containing discohesive malignant cells scattered singly in a haemorrhagic background mixed with lymphocytic infiltration. The malignant cells exhibited enlarged round nuclei, high nuclear-cytoplasmic ratios, prominent single to multiple nucleoli and scant to moderate cytoplasm with occasional clearing. The typical "tigroid" background characteristic of seminoma was absent, likely due to low cellular yield. Histopathological examination of the lymph node biopsy showed malignant cells with similar morphology. Immunohistochemical staining was positive for PLAP and CD117, and negative for CKAE1/AE3, CD3, and CD20, confirming the diagnosis of metastatic seminoma. *Discussion:* This case underscores the importance of recognising FNAC features of seminoma, which are infrequent in routine cytology practice. Given that the classical "tigroid" background may not always be present, use of ancillary techniques like cell block preparation and immunohistochemistry can enhance the diagnostic accuracy. In cases with uncommon presentations such as cervical node metastasis with unknown primary, early identification can prompt timely investigation for a testicular primary tumour.

**AP32: Littoral cell angioma of the spleen: A rare vascular tumour with dual-lineage differentiation**

Norafifah Mohd Yusoff[1], Noraidah Masir[2], Yong Kar Ying[3], Suria Hayati Md Pauzi[1]
*[1]Department of Pathology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Wilayah Persekutuan Kuala Lumpur, Malaysia; [2]Prince Court Medical Centre, Wilayah Persekutuan Kuala Lumpur, Malaysia; [3]Hospital Miri, Sarawak, Malaysia*

*Introduction:* Littoral cell angioma (LCA) is a rare splenic vascular tumour that originates from the lining cells of the splenic red pulp sinuses with both endothelial and histiocytic differentiation. *Case report:* A 65-year-old woman with no known medical history presented with epigastric pain. She was otherwise well, with no constitutional symptoms. Abdominal CT imaging revealed multiple lesions in the liver and spleen. A splenectomy was subsequently performed. Microscopic examination showed multiple ill-defined nodular lesions composed of proliferations of tortuous vascular channels with irregular lumina and occasional papillary-like projections into cystic spaces. These vascular channels were lined by plump to tall endothelial cells. Immunohistochemistry showed that the endothelial cells were positive for CD31 and CD68, focally positive for CD34, and negative for CK AE1/AE3 and CD8. A diagnosis of Littoral Cell Angioma was made based on these findings. *Discussion:* Littoral cell angioma remains a diagnostic challenge due to its rarity and nonspecific clinical presentation. In most cases, a definitive diagnosis relies on histopathological examination and immunohistochemistry. The current clinical understanding of LCA is limited, and no standardised treatment guidelines exist. This case highlights the importance of considering LCA in the differential diagnosis of splenic lesions.

**AP33: A large renal angiomyolipoma causing hydronephrosis**

Wei Meng Phang[1], Eng Hong Goh[2], Yin Ping Wong[1], Geok Chin Tan[1,2]
*[1]Department of Pathology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia; [2]Department of Urology, Prince Court Medical Centre, Kuala Lumpur. Malaysia*

*Introduction:* Renal angiomyolipomas is one of the PEComa tumours with characteristic triphasic morphology featuring varying proportions of dysmorphic blood vessels, smooth muscle cells, and mature adipose tissue. The majority of angiomyolipomas are sporadic, with a female-to-male ratio of 2-4:1. They typically affect adults with a mean age of 43 years. Large angiomyolipomas pose a risk of haemorrhagic complication. Post-embolisation nephrectomy may alter the histological features, making comprehensive analysis challenging. *Case report:* A 47-year-old lady presented with right abdominal pain for 2 months, and investigation found a 14.2cm renal mass causing hydronephrosis. Following arterial embolisation, persistent symptoms necessitated nephrectomy. The specimen weighed 1441.8grams with a well-circumscribed yellowish mass confined within Gerota's fascia. Histological examination revealed classic triphasic morphology comprising mature adipose tissue (80-90%), dysmorphic vessels, and smooth muscle components. Post-embolisation changes included extensive fat necrosis and foreign body giant cell reaction. Immunohistochemistry demonstrated expressions of HMB45, MelanA, and SMA while negative for PAX8 and cytokeratins. Multiple perinephric lymph nodes showed reactive hyperplasia without tumour involvement. *Discussion:* The management approach with initial embolisation followed by surgical resection reflects current evidence-based protocols. The reactive lymph node hyperplasia confirms the benign biological behaviour of classic angiomyolipomas. Post-embolisation artefacts should not be misinterpreted as malignancy. Classic angiomyolipomas has excellent prognosis following complete resection.

**AP34: Desmoid Fibromatosis of the Post-Auricular Region with APC Mutation: An Unusual Location in a Previously Irradiated Field**

Muhd Afif Mohd Yusof[1], Ng Pui Foong[2], Subasri Armon[3]
*[1]Department of Pathology, Hospital Raja Perempuan Zainab II, Kelantan, Malaysia; [2]Department of Pathology, Hospital Pulau Pinang, Pulau Pinang Malaysia; [3]Advanced Genomics Technology Centre (AGTC), Kuala Lumpur, Malaysia.*

*Introduction:* Desmoid-type fibromatosis (DTF) is a rare, benign, but locally aggressive neoplasm characterised by infiltrative fibroblastic proliferation and associated with high recurrence rates. Mutations in APC or CTNNB1 genes, involving the Wnt/β-catenin signalling pathway, drive tumourigenesis. Desmoid tumours are classified as either sporadic with CTNNB1 mutations or hereditary, linked to familial adenomatous polyposis (FAP) APC mutations. *Case Report:* A 61-year-old male with a prior history of nasopharyngeal carcinoma treated with radiation therapy approximately two years prior, presented with a right post-auricular mass at the radiation field. Histopathological evaluation revealed hypocellular bland spindle cell proliferation in long sweeping fascicles with nuclear positivity for beta-catenin, consistent with desmoid-type fibromatosis. Next-generation sequencing identified an APC (p.D1519fs*4) frameshift mutation at a high variant allele fraction of 66%. Considering the patient's age and clinical history, the APC mutation is likely radiation-induced rather than hereditary. *Discussion:* DTFs arise from dysregulated Wnt/β-catenin signalling, commonly driven by mutations in the CTNNB1 or APC genes. APC mutations strongly suggest either a hereditary predisposition (FAP/Gardner syndrome) or somatic events possibly induced by radiation exposure. While radiation-induced desmoid tumours are rare, a documented history of prior irradiation supports this pathogenesis. A thorough evaluation for FAP-associated manifestations, including colonoscopy, is recommended when an APC mutation is detected. However, given the patient's age and clinical background, a somatic mutation due to radiation is favoured.

**AP35: Proximal-type Epithelioid Sarcoma: The Importance of Early Recognition and Intervention**

Muhd Afif Mohd Yusof[1], Mohd Salahuddin Abdul Latif[2], Muhd Rifqi Rahim[3]
*[1]Department of Pathology, Hospital Raja Perempuan Zainab II, Kelantan, Malaysia; [2]Department of Orthopedics, Hospital Raja Perempuan Zainab II, Kelantan, Malaysia; [3]Department of Radiology, Hospital Raja Perempuan Zainab II, Kelantan, Malaysia.*

*Introduction:* Proximal-type epithelioid sarcoma (PES) is a rare, aggressive soft tissue malignancy frequently missed due to its clinical resemblance to benign inflammatory lesions. Early recognition is challenging but critical, as delayed diagnosis worsens prognosis significantly. *Case report:* An 18-year-old female presented with a tender mons pubis swelling initially diagnosed as an abscess and managed with antibiotics. Persistence and growth of the lesion prompted incision and drainage, but recurrence occurred rapidly. Subsequent biopsy revealed high-grade proximal-type epithelioid sarcoma characterised by rhabdoid morphology, necrosis, brisk mitotic activity, and complete INI1 loss. Imaging demonstrated a lobulated, heterogeneously enhancing subcutaneous mass with bilateral inguinal lymphadenopathy. MRI confirmed necrotic, haemorrhagic components involving skin without deeper invasion. Six months after initial presentation, wide local excision and inguinal node dissection were performed, with clear but close margins and reactive nodes. Recurrence appeared after three months, progressing to pelvic nodes. Extensive hospital management exceeding eight weeks involved further surgery and complex wound care. The disease rapidly advanced, metastasizing subcutaneously and to lungs and bones. Chemotherapy with doxorubicin was initiated, but was complicated by hospital acquired pneumonia. Despite multidisciplinary interventions, the patient expired approximately one year post-presentation. *Discussion:* PES presents significant diagnostic challenges, frequently masquerading as benign inflammatory lesions, which may delay accurate diagnosis and appropriate management. Prognosis remains poor, particularly with nodal or distant metastases. Early biopsy for persistent or atypical inflammatory lesions, comprehensive imaging assessment, and aggressive multidisciplinary intervention are essential for better outcomes.

**AP36: Chest clue to a renal riddle: Cast nephropathy in a background of multiple comorbidities**

Awla Mohd Azraai[1,2], Anas Mat Asis[3], Muhammad Iqbal Abdul Hafidz[3,4] Norina Kassim[5]
*[1]Department of Clinical Diagnostic Laboratories, Hospital Al-Sultan Abdullah Universiti Teknologi MARA, Selangor, Malaysia; [2]Department of Pathology, Faculty of Medicine, Universiti Teknologi MARA Sungai Buloh, Selangor, Malaysia; [3]Department of Internal Medicine, Hospital Al-Sultan Abdullah Universiti Teknologi MARA, Selangor, Malaysia; [4]Department of Internal Medicine, Faculty of Medicine, Universiti Teknologi MARA Sungai Buloh, Selangor, Malaysia; [5]Department of Pathology, Hospital Selayang, Selangor, Malaysia*

*Introduction:* Light chain cast nephropathy (LCCN) is the most common cause of acute kidney injury (AKI) in patients with plasma cell myeloma (PCM). *Case report:* We present the case of a 58-year-old man with multiple comorbidities who was admitted due to AKI. His comorbidities include diabetes mellitus, hypertension, dyslipidaemia, and chronic kidney disease secondary to left ureteric calculi. A chest wall mass, noticed two months before, was biopsied revealing a PCM with lambda restriction. Bone marrow aspiration and trephine biopsy showed similar findings. A renal biopsy was performed to determine the main cause of his AKI which showed LCCN, diabetic nephropathy, acute tubular injury with tubular rupture, giant cell reaction, moderate chronic tubulointerstitial inflammation and hypertensive vasculopathy. Congo red stain was negative. Immunofluorescence test showed tubular casts with lambda light chain restriction. *Discussion:* Renal biopsy was crucial in this case to determine the main cause of renal impairment. The hallmark of LCCN is the presence of light chain casts, which form in the distal nephron segments, obstructing tubular flow and causing direct tubular damage. Acute tubular injury results from the toxic effects of light chains and subsequent ischaemic injury, leading to cellular dysfunction and necrosis. Tubulointerstitial lesions are caused by the inflammatory response to the light chain deposits and tubular damage. The number of casts per square millimeter and the degree of interstitial fibrosis and/or tubular atrophy are important predictors of renal function. The patient was treated with Bortezomib, Thalidomide, and Dexamethasone. His renal function improved gradually with regular haemodyalisis.

**AP37: Expression of LRRC15 in the placenta of pregnancies complicated with preeclampsia and foetal growth restriction**

Wei Meng Phang[1], Muaatamarulain Mustangin[1], Nur Maya Sabrina Tizen[1], Shamsul Azhar Shah[2], Yin Ping Wong[1], Geok Chin Tan[1]
*[1]Department of Pathology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia; [2]Department of Community Health, Universiti Kebangsaan Malaysia Medical Centre, Kuala Lumpur, Malaysia*

*Introduction:* Preeclampsia affects 2-8% of pregnancies globally, with maternal vascular malperfusion (MVM) as classical histomorphological features in the placenta. Leucine-rich repeat-containing protein 15 (LRRC15) plays a crucial role in remodeling of the maternal uterine tissue during early pregnancy. However, its associations with preeclampsia (PE) are largely unexplored. This study investigated the expression of LRRC15in preeclamptic pregnancies across various placental cell types and its association with adverse perinatal outcomes. *Materials & Methods:* This was a retrospective cross-sectional study analysed 110 placental specimens (54 preeclamptic, 56 normotensive controls). LRRC15 immunohistochemistry was evaluated in eight placental cell types. MVM was classified into low and high-grade based on Amsterdam criteria. *Results:* LRRC15 was upregulated in the placenta of mother with preeclampsia with cell-type specificity. Cytotrophoblast positivity was significantly higher between PE and control (92.6% versus 5.4%) (OR 215.8, p<0.001). Similarly, syncytiotrophoblast expression was significantly higher in PE compared to control (94.4% versus 1.8%) (OR 1273.0, p<0.001). High-grade MVM was observed exclusively in preeclamptic cases (37.0% vs 0%, p<0.001). LRRC15 expression was observed in all high-grade MVM lesions (100% vs 0%, p<0.001). LRRC15 expression was significantly associated with adverse perinatal outcome including prematurity (83.3% vs. 21.4%) (p<0.001), NICU admission (61.1% vs. 10.7%) (p<0.001), and foetal growth restriction (22.2% vs. 1.8%) (p<0.001). Multivariable regression identified LRRC15 positivity (OR 8.2, p=0.003) as an independent predictor of adverse outcomes. *Discussion:* LRRC15 may play a role in the pathogenesis of PE and could be biomarker for PE. It might also be biomarker for adverse perinatal outcomes in PE.

**AP38: Differential expression of RANK, RANKL, and OPG in prostate cancer: Correlation with PSA and Gleason Score**

Nasrin Shahifar[1], Intan Nureslyna Samsudin[1], Razana Mohd Ali[1], Noraina Muhamad Zakuan[2]
*[1]Department of Pathology, Faculty of Medicine and Health Sciences, Universiti Putra Malaysia, Selangor, Malaysia; [2]Department of Biomedical Sciences, Faculty of Medicine and Health Sciences, Universiti Putra Malaysia, Selangor, Malaysia.*

*Introduction:* Prostate cancer (PrCa) carries a high risk of invasion and metastasis. The receptor activator of NF-κB (RANK), its ligand RANKL, and osteoprotegerin (OPG) are thought to be key mediators implicated in tumour progression. This study compared the expression of RANK, RANKL, and OPG in prostate biopsy specimens of patients with and without PrCa and examined their correlation with Gleason score and serum prostate-specific antigen (PSA) levels. *Materials & Methods:* Fifty patients who underwent transrectal ultrasound-guided (TRUS) prostate biopsy were included. Demographic and clinical, including pre-procedural serum PSA levels, were recorded. Immunohistochemistry (IHC) for RANK, RANKL, and OPG were performed on formalin-fixed paraffin-embedded (FFPE) specimens, and immunoreactive scores (IRS) were calculated. Associations between marker expression and PSA levels or Gleason scores were analysed using Spearman's correlation tests. *Results:* Of the 50 patients, 28 (56%) had PrCa and 22 (44%) were non-PrCa. There was no significant difference in age and race between groups, but PSA levels were significantly higher in PrCa patients (90.50 (IQR=153.75) vs 14.15 (IQR=13.04), p<0.001). The median IRS for RANK [4(IQR=5) vs 2(IQR=2), p=0.003] and RANKL [12(IQR=4) vs 8(IQR=0), p=0.003] were significantly higher in PrCa. The IRS OPG expression showed no significant difference. Moderate positive correlations were observed between PSA and both RANK (R=0.44, p=0.002) and RANKL (R=0.39, p=0.002). Similarly, RANK (R=0.45, p=0.001) and RANKL (R=0.46, p=0.001) also showed moderate correlations with the Gleason score. *Discussion:* RANK, RANKL, and OPG are expressed in both PrCa and non-PrCa tissues, but significantly higher IRS for RANK and RANKL in PrCa suggests their potential role in tumour progression.

**AP39: Benign and malignant soft tissue tumour of the extremities: A histopathological review in a tertiary hospital in Sarawak**

Mohammad Zulkarnaen Ahmad Narihan[1,2], Dayangku Norlida Awang Ojep[1,2], Yusri Yusuf[2] , Muhammad Zawawi Zuhardi[1], Nur Syafiqah Mohd Fazeri[1], Angelina Allan[1], Maria Wee Soo Ting[1]
[1]Department of Pathology, Faculty of Medicine and Health Sciences, Universiti Malaysia Sarawak, Sarawak, Malaysia; [2]Department of Pathology, Hospital Umum Sarawak, Sarawak, Malaysia

*Introduction:* Soft tissue tumours (STTs) are neoplasms arising from non-epithelial, extra-skeletal connective tissue, including adipose tissue, muscle, fibrous tissue and peripheral nerves. This study aims to evaluate the histopathological spectrum of extremity STTs, with a focus on tumour classification and distribution by age, gender, and anatomical site. *Materials & Methods:* A retrospective study was conducted over a five-year period (2019-2023) at the Department of Pathology, Sarawak General Hospital. All histologically confirmed cases of soft tissue tumours located in the extremities were reviewed and analysed for tumour type, age, gender and anatomical site. *Results:* A total of 210 cases of STTs of the extremities were identified. Of these, 118 were benign (56.2%) and 92 were malignant (43.8%). The most common benign tumours were lipoma (53/118), followed by haemangioma (15/118), schwannoma (15/118), tenosynovial giant cell tumour (15/118) and fibromatosis (6/118). The most common malignant tumours were atypical lipomatous tumour (16/92), undifferentiated pleomorphic sarcoma (12/92), myxofibrosarcoma (9/92), myxoid liposarcoma (8/92) and leiomyosarcoma (7/92). The most affected age group was 31 -40 years (32/210), while malignant tumours were most prevalent in the 51-60 age group (22/92). A female predominance was noted in overall STT, with a male-to-female ratio of 0.75:1. whereas slight male predominance was seen in malignant tumours (1.09:1). Malignant tumours demonstrated a predilection for the lower limbs (70/92), compared to the upper limbs (22/92). *Discussion:* Benign STTs were more prevalent than malignant ones in the extremities. Malignant STTs of the extremities predominantly affecting older individuals, males and were commonly located in the lower limbs. These findings highlight the relevance of demographic and anatomical factors in the diagnostic evaluation of soft tissue tumours.

**AP40: Histopathological Evidence of Listeria monocytogenes in Early Pregnancy Loss**

Zalifaah Pajaru Rahman[1], Abdullah[1], Siti Noraisyah Othman[2], Diana Mutusamy[3], Nur Syahrina Rahim [1,4]
*[1]Department of Pathology, Hospital Selayang, Selangor, Malaysia; [2]Department of Pathology, Hospital Lahad Datu, Sabah, Malaysia; [3]Department of Obstetric and Gynaecology, Hospital Selayang, Selangor, Malaysia; [4]Faculty of Medicine & Health Science, Universiti Sains Islam Malaysia, Negeri Sembilan, Malaysia*

*Introduction:* Listeria monocytogenes is a potentially lethal pathogen with serious implications for both maternal and foetal health. During pregnancy, listeriosis may present non-specific symptoms but can lead to severe outcomes, including septic miscarriage, preterm labour, and intrauterine foetal demise. We present a case of placental listeriosis identified through histopathological examination following a first trimester pregnancy loss. *Case Report:* A 33-year-old woman, gravida 3 para 1+1, at approximately 11 weeks' gestation, presented with a short history of flu-like symptoms, per vaginal bleeding, abdominal pain, and vomiting. During admission, she spontaneously expelled products of conception, which were non-foul smelling. Sections of the placenta were submitted for histopathological evaluation. Microscopic examination revealed intervillous necrotising abscesses, acute villitis, and dense chorioamnionitis. Numerous Gram-positive bacilli were visualised on the placental surface and highlighted with Warthin-Starry staining. Microbiological culture of placental tissue subsequently confirmed Listeria monocytogenes via MALDI-TOF mass spectrometry (Bruker Biotyper, IVD database). *Discussion & Conclusion:* Listeriosis during pregnancy may be clinically silent or present with vague, non-specific symptoms, often leading to delayed diagnosis. Despite its subtle presentation, the potential consequences ranging from early pregnancy loss to neonatal mortality demand heightened clinical vigilance. Histopathological examination of placental tissue is a valuable diagnostic tool, especially in cases of unexplained early miscarriage. Timely recognition is critical, as Listeria monocytogenes responds well to targeted antimicrobial therapy, significantly improving maternal and foetal outcomes. This case underscores the pivotal role of pathologists in uncovering occult infectious causes of pregnancy loss through careful histological evaluation.

**AP41: Co-existence of immature teratoma and extraovarian implant: A case report**

Nabilah Huda Hamzah[1], Nadzrin Md Yusof[1]
*[1]Department of Pathology, Hospital Sultanah Bahiyah, Kedah, Malaysia*

*Introduction:* Immature teratoma (IT) only occurs in <1% of all teratomas and associated extraovarian tumour implant is even rarer. We present a rare case of IT with multiple peritoneal implants of mature components. *Case report:* A 20-year-old-woman was incidentally found to have an ovarian mass following a motor-vehicle-accident in early 2023, during which she sustained a splenic injury. Imaging revealed a pelvic mass measuring 15 cm, which expanded to 18 cm by the end of the year. Elevated tumour markers were noted. Surgical intervention by an excision of the ovarian tumour was performed along with excision of multiple peritoneal deposits. Gross examination showed an intact capsule with a solid-cystic, gritty cut surface, areas of haemorrhage, necrosis with fat and bone components. The peritoneal and omental deposits exhibited similar characteristics of bone and fat tissue on cut surface. Histological examination confirmed an immature ovarian teratoma with multiple peritoneal implants consisting solely of mature components. The patient recovered well postoperatively and commenced chemotherapy. *Discussion:* Clinically, IT grows rapidly and can penetrate its capsule, form adhesions and spreads to the surrounding peritoneal cavity. While may be due to haematogenous metastasis peritoneal implants may also result from intraoperative spillage during tumour resection or, as in this case, possibly due to tumour rupture from abdominal trauma. These metastases and peritoneal implants may also be affected by chemotherapy resulting in growing teratoma syndrome. IT co-existing with peritoneal implants is extremely rare. However, with current advancements in both surgical and chemotherapeutic treatment, it still has a good curative and survival rate.

**AP42: SARS-CoV-2–Associated Stillbirth: Recognising the Placentitis Triad and Diagnostic Utility of Immunohistochemistry**

Nur Syahrina Rahim [1,2], Nur Aini Abu Bakar[1], Salmi Abdullah[1], Zalifaah Pajaru Rahman[1], Abd Rahman Hayati[2]
[1]*Department of Pathology, Hospital Selayang, Selangor, Malaysia;* [2]*Faculty of Medicine & Health Science, Universiti Sains Islam Malaysia.*

*Introduction:* With the recent global surge in SARS-CoV-2 activity, the emergence of new variants, and ongoing vaccine hesitancy, infection during pregnancy presents significant maternal and perinatal risks. Although not individually specific, the proposed histopathological diagnostic triad offers valuable morphological clues suggestive of SARS-CoV-2 placentitis. Further laboratory techniques may confirm the infectious origin, effectively excluding other clinicopathological entities with similar features, such as massive perivillous fibrin deposition and chronic histiocytic intervillositis, which are known to cause recurrent stillbirths. *Methodology:* We analysed the histopathological features and immunohistochemical profiles of SARS-CoV-2 placentitis in cases of stillbirth at 23 and 29 weeks of gestation. Both presented with maternal COVID 1 and 2 categories respectively. They showed the characteristic triad of extensive perivillous fibrin with trophoblasts necrosis and histiocytic intervillositis. Other findings include frequent intervillous thrombi and concomitant chronic villitis. SARS-CoV-2 immunohistochemistry showed strong positivity for both spike and nucleocapsid proteins, localised to the villous surface trophoblasts. Expression of ICAM-1 was additionally observed. The intervillositis infiltrates showed predominant CD68 histiocytes followed by CD3 T-lymphocytes. *Discussion & conclusion:* The diffuse involvement in SARS-CoV-2 placentitis leading to foetal demise is often not associated with severe maternal COVID-19 infection. Necrosis and shedding of the villous trophoblasts promote fibrin deposition and thrombosis, compromising intervillous circulation and impairing placental function. Immunohistochemistry serves as a robust and widely available diagnostic method for confirming SARS-CoV-2 infection in placental tissue.

**AP44: A Rare Case of Diffuse Large B-cell Lymphoma of the Parotid Gland with Aberrant p63 Expression**

Raniza Musily[1], Nurul Husna Mohd Dani[1], Suria Hayati Md Pauzi[1], Nordashima Abd Shukor[1]
[1]*Department of Pathology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia.*

*Introduction:* Diffuse large B-cell lymphoma (DLBCL) is the commonest subtype of non-Hodgkin lymphoma. While extranodal involvement is frequently observed, DLBCL of the parotid gland is a rare presentation. The diagnosis of DLBCL in this location is challenging due to its rarity and the need to distinguish it from other salivary gland neoplasms. This report aims to present a rare case of primary DLBCL in the parotid gland with notable p63 expression. *Case report:* An 84-year-old lady with a 6-week history of painless left infra-auricular swelling. Fine needle aspiration cytology (FNAC) was performed which revealed atypical lymphoid cells suggestive of lymphoproliferative disorder. CT neck showed an enlarged left parotid mass involving the superficial and deep lobes. She underwent a left total parotidectomy. Histopathological examination showed infiltration by sheets of malignant cells exhibiting pleomorphic, large and vesicular nuclei with conspicuous nucleoli. Immunohistochemical stains showed the malignant cells were positive for LCA, CD20, CD79a, p63 and BCL6. They were negative for CKAE1/AE3, CD10, MUM 1, CD3 and CD5. *Discussion:* Diffuse large B-cell Lymphoma (DLBCL) involving the parotid gland is uncommon. The rarity of this presentation, coupled with aberrant immunohistochemical findings of p63 positivity which are more commonly expressed in squamous or myoepithelial neoplasms can lead to diagnostic confusion and potential misclassification as an epithelial malignancy. The present case underscores the importance of recognising atypical immunohistochemical profiles in salivary gland lymphomas. Awareness of such diagnostic pitfalls is essential to avoid misdiagnosis and to ensure prompt and appropriate treatment.

**AP46: Can artificial intelligence replace pathologists in tumour infiltrating lymphocyte (TIL) assessment? A comparative study of manual versus AI-based scoring in triple-negative breast cancer (TNBC)**

Nurkhairul Bariyah Baharun[1,2], Mohamed Afiq Hidayat Zailani[1], Afzan Adam[3], Reena Rahayu Md Zin[1], Nasir M. Rajpoot[4], Qiaoyi XU[3], Muaatamarulain Mustangin[1]
[1]*Faculty of Medicine, The National University of Malaysia;* [2]*Faculty of Health Sciences, Universiti Selangor* [3]*Centre for Artificial Intelligence Technology (CAIT); Faculty of Information Science & Technology, The National University of Malaysia;* [4]*Department of Computer Science, University of Warwick, United Kingdom*

*Introduction:* Tumour-infiltrating lymphocytes (TILs) are established as a robust prognostic biomarker in triple-negative breast cancer (TNBC). However, their clinical utility is hindered by the subjectivity and interobserver variability inherent in manual assessment. Artificial intelligence (AI)-based models offer a promising, reproducible alternative for TIL quantification; but their performance in complex histopathological landscape remains to be fully validated. This study aims to evaluate the performance of an AI-based model in assessing stromal (sTILs) and intratumoural (iTILs) lymphocyte density in TNBC. *Materials & Methods:* A total of 64 H&E-stained TNBC whole-slide images (WSIs) was independently assessed by two pathologists using standardised sTILs scoring guidelines. Interobserver agreement was quantified using intraclass correlation coefficients (ICCs) and Cohen's Kappa. Discrepant cases (n=36) were reviewed by a third pathologist. An AI model, trained on annotated regions of interest (ROIs), was evaluated against manual scores using ICCs and Bland–Altman analysis. *Results:* Initial agreement was moderate for sTILs (ICC = 0.57) and substantial for iTILs (ICC = 0.70), improving after consensus (sTILs = 0.70; iTILs = 0.81). AI-manual agreement was moderate (sTILs = 0.48; iTILs = 0.51; $p < 0.01$). Notably, 28 of 43 AI-manual discrepant cases overlapped with those that were also discordant between pathologists. Contributing factors to discrepancies included heterogeneous TIL distribution, poorly-defined tumour-stroma interface, and focal dense lymphoid infiltrates. Limitations of the AI model included restricted ROI sampling and difficulty detecting clustered lymphocytes. *Discussion:* Discrepancies were more prevalent in in moderate-to-high TIL cases. While AI demonstrates potential to improve reproducibility and efficiency, it lacks the nuanced interpretative ability of the human eye. These findings support AI as complementary decision-support In TIL assessment.

**AP47: Performance Evaluation of Automated Tumour-Infiltrating Lymphocytes (TILs) Assessment Against Manual Assessment in Triple-Negative Breast Cancer for Artificial Intelligence Algorithm Validation**

Nurkhairul Bariyah Baharun[2], Mohamed Afiq Hidayat Zailani[1], Afzan Adam[3], Nasir M. Rajpoot[4], Reena Rahayu Md Zin[1].
*[1]Department of Pathology, Faculty of Medicine, Hospital Canselor Tuanku Muhriz, Universiti Kebangsaan Malaysia (UKM), Wilayah Persekutuan Kuala Lumpur, Malaysia; [2]Department of Medical Diagnostic, Faculty of Health Sciences, Universiti Selangor, Selangor, Malaysia; [3]Centre for Artificial Intelligence Technology (CAIT), Faculty of Information Science & Technology, Universiti Kebangsaan Malaysia (UKM), Selangor, Malaysia; [4]Department of Pathology, Hospital Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* Triple-negative breast cancer (TNBC) accounts for approximately 15% of all breast cancer. Tumour-infiltrating lymphocytes (TILs) are significant biomarkers in TNBC, potentially predicting immunotherapy responses and guiding treatment. Deep learning and digital pathology-based automation have emerged to overcome the limitations of manual TILs assessment (mTILs). This study evaluates the performance of automated TILs assessment (aTILs) against mTILs for artificial intelligence (AI) algorithm validation. *Materials & Methods:* A new deep learning-based aTILs model was developed and validated using a public dataset. The model was trained using 70% of digitized TNBC slides. Sequential algorithms were employed, first for tissue segmentation, and second for quantifying TILs across 320 selected regions of interest. The model's performance for tissue segmentation was assessed using the Dice score, while TILs quantification was evaluated using intraclass correlation (ICC), Cohen's kappa (κ), and Spearman's rank correlation coefficient (ρ). *Results:* The aTILs model exhibited excellent performance in segmenting tumour (Dice = 0.909) and stromal (Dice = 0.897) regions in H&E-stained TNBC tissue sections. However, for TILs quantification, the model showed low to moderate agreement for both stromal (ICC = 0.434, $\kappa = 0.04$, $\rho = 0.475$) and intratumoural (ICC = 0.469, $\kappa = 0.28$, $\rho = 0.363$) TILs. *Discussion:* The high concordance in tissue segmentation indicates a strong foundation for automated analysis, but the lower concordance in TILs quantification highlights a critical area for future development. Further refinement of the aTILs model is warranted, as it holds significant potential to enhance its clinical application for TNBC cases. Future studies should also explore the model's predictive value for TNBC patient prognosis.

## CHEMICAL PATHOLOGY (CP)

**CP1: Optimising HbA1c testing requests: A clinical audit to enhance resource stewardship and improve efficiency**

Khadijah Noh[1], Muhammad Adib Ayob[1], Ling J-Cyn[1], Nurul Huda Osman[1], Paula Anthonysamy[1], Nasirah Nasiruddin[1], Zafaruddin Ismail Zulkifli[1]
*[1]Department of Pathology, Hospital Seri Manjung, Perak, Malaysia*

*Introduction:* Glycated haemoglobin (HbA1c) is an essential marker for diagnosing and monitoring type 2 diabetes mellitus (T2DM). However, its convenience often leads to overuse. In 2021, Hospital Seri Manjung (HSM) recorded the second-highest HbA1c testing volume in Perak, despite ranking fourth in total chemical pathology workload, highlighting a disproportionate demand. This audit aimed to evaluate the appropriateness of HbA1c test requests, assess shifts in clinician practices, and examine the financial implications. *Materials & Methods:* All HbA1c requests from January 2021 to December 2024 were reviewed using manual request forms and workload data. Requests were assessed based on the 2020 T2DM Clinical Practice Guidelines (CPG) and the 2017 Diabetes in Pregnancy CPG. In April 2023, an improved request form was introduced, requiring clinicians to specify diagnostic or monitoring indications. Trained personnel screened all submissions to ensure compliance with CPG criteria. Comparative analysis of test volumes and costs before and after this intervention was conducted across five major Perak hospitals. *Results:* HSM's HbA1c testing decreased from 12,947 in 2021 to 9,377 in 2024, post-intervention. Correspondingly, testing costs declined from RM100,986.60 to RM73,140.60, saving approximately RM28,000 annually. The HbA1c workload trend became more consistent with the overall chemical pathology trend in the state. *Discussion:* The revised form improved compliance with guidelines and reduced unnecessary testing. Although effective, this process depends on trained staff. Incorporating AI-based clinical decision support systems could enhance future efficiency and clinical outcomes.

**CP2: Non-reportable biochemical results in cold autoimmune haemolytic anaemia: A case of severe haemolysis and sample rejection**

Najmul Aufa Mohamad Zulkipli[1,2], Subashini Chellappah Thambiah[1,2], Yin Ye Lai[1,2], Intan Nureslyna Samsudin[1,2], Muhamad Syahmi Nazli[1]
*[1]Department of Pathology, Hospital Sultan Abdul Aziz Shah, Universiti Putra Malaysia, Selangor, Malaysia; [2]Faculty of Medicine and Health Sciences, Universiti Putra Malaysia, Selangor, Malaysia*

*Introduction:* Cold autoimmune haemolytic anaemia (cAIHA) is a rare disorder in which IgM autoantibodies bind to red blood cell (RBC) antigens at low temperatures, causing agglutination and complement-mediated haemolysis. It is often associated with cold agglutinin disease (CAD) and is more common in the elderly. cAIHA can be idiopathic or secondary to infections, autoimmune diseases, or malignancies. Both in vivo and in vitro haemolysis pose significant clinical challenges, including artefacts such as pseudohyperkalaemia that can confound biochemical results. *Case report:* A 77-year-old man with diabetes mellitus, chronic kidney disease, and hypertension presented with neurological deficits, jaundice, and Raynaud's phenomenon. Laboratory tests revealed anaemia (Hb 10.5 g/dL), acute kidney injury and hyperkalaemia (8.7 mmol/L), inconsistent with his clinical presentation. A full blood picture showed RBC agglutination, which raised suspicion of cAIHA, and this was confirmed by a positive direct antiglobulin test for C3d. Standard blood sample processing caused severe in vitro haemolysis, resulting in non-reportable biochemical results. Blood was subsequently collected in pre-warmed tubes at 37°C and processed with low-speed centrifugation (1500g, 15 minutes), reducing haemolysis. This approach improved potassium levels to 6.2 mmol/L, which was consistent with the patient's clinical condition. *Discussion:* This case illustrates the diagnostic challenge of cAIHA, particularly pseudohyperkalaemia due to in vitro

haemolysis. Pre-analytical measures like pre-warming and low-speed centrifugation are crucial to minimise haemolysis and ensure accurate results. Early detection and management of these artefacts are key to proper diagnosis and patient care.

**CP3: Comparison of capillary electrophoresis with agarose gel electrophoresis techniques for the identification of monoclonal proteins in human serum samples**

Sharmila Vani Kallipermalu[1], Subashini C. Thambiah[1], Lai Yin Ye[1], Lim Chee Hoe[2], Mohd Jamsani Mat Salleh[2], Muhammad Syahmi Nazli [1], Intan Nureslyna Samsudin[1]
*[1]Department of Pathology, Hospital Pulau Pinang, Pulau Pinang, Malaysia; [2]Department of Pathology, Faculty of Medicine and Health Sciences, Universiti Putra Malaysia, Selangor, Malaysia*

*Introduction:* Serum protein electrophoresis (SPE) is a cornerstone for screening, diagnosing and monitoring plasma cell dyscrasias. Agarose gel electrophoresis (AGE) separates proteins into distinct fractions, while immunofixation (IF) confirms monoclonal proteins (M proteins). Capillary electrophoresis (CE) offers higher resolution and automated M protein identification with immunosubtraction (IT). *Materials & Methods:* The study aimed to compare protein fractions (albumin, α-1, α-2, β, γ globulins) between AGE and CE, evaluate M protein characterisation between IT and IF, and assess the correlation and mean difference in M protein concentrations. A total of 40 serum samples, including 10 normal samples, 20 samples with M proteins, and 10 samples with polyclonal paraproteinaemia were collected from patients suspected of MM. The sample size was determined based on the Clinical and Laboratory Standards Institute guidelines, ensuring a balance between statistical reliability and laboratory capacity. *Results:* The median age of the subjects was 67.5 years. Significant differences in protein fraction concentrations between AGE and CE methods were observed for α-1, α-2, and β globulins, with CE yielding higher α-1 and AGE showing higher α-2 and β concentrations. Concordance was found in M protein (heavy chain) characterisation across IT and IF methods. A moderate positive correlation was evident between AGE and CE for M protein concentrations ($r = 0.714$, $p < 0.001$), with no consistent bias detected. *Discussion:* This study confirms that AGE and CE are reliable and complementary methods for assessing M protein, supporting the use of either technique for the screening, diagnosis, and monitoring of monoclonal gammopathy.

**CP4: Drug-induced haemolytic anaemia in tuberculosis treatment: A rare case report**

Muhammad Khair bin Ali[1,2], Yin Ye Lai[1,2], Subashini Chellappah Thambiah[1,2], Intan Nureslyna Samsudin[1,2], Muhamad Syahmi Nazli[1]
*[1]Department of Pathology, Hospital Sultan Abdul Aziz Shah, Universiti Putra Malaysia, Selangor, Malaysia; [2]Faculty of Medicine and Health Sciences, Universiti Putra Malaysia, Selangor, Malaysia*

*Introduction:* Drug-induced immune haemolytic anaemia (DIIHA) is a rare but potentially fatal cause of autoimmune haemolytic anaemia (AIHA), commonly implicated with the use of antimicrobials, anti-inflammatory agents, and platinum-based chemotherapy. *Case report:* A 32-year-old woman, recently started on rifampicin/isoniazid for latent tuberculosis, presented to the hospital with lethargy and dizziness. She was pale and tachycardic on examination. Laboratory findings showed pancytopenia, reticulocytosis and a positive direct antiglobulin test. Peripheral blood film revealed agglutination and rouleaux formation. Infectious screening and autoimmune workup were negative. DIIHA was suspected based on the temporal relationship between drug commencement and the development of illness. Rifampicin/isoniazid were discontinued, and corticosteroid therapy was initiated, resulting in clinical and laboratory improvement within a week. *Discussion:* DIIHA in our case is likely attributed to rifampicin or isoniazid, with rifampicin being more probable due to a higher reported incidence. However, a synergistic effect of both drugs cannot be ruled out. Risk factors for the development of DIIHA may be patient or drug-specific and remain poorly understood. A positive drug-dependent antibody screening, though not widely available, distinguishes between drug-independent DIIHA from drug-dependent cases. Biochemical findings in DIIHA are similar to those in AIHA. Haemolysis raises intracellular markers like lactate dehydrogenase, aspartate aminotransferase, and alanine aminotransferase while diluting plasma sodium, leading to hyponatraemia. An unexpectedly low HbA1c discordant with clinical presentation and plasma glucose reflects erythrocyte destruction. Management of DIIHA involves immediate drug cessation, corticosteroids, and supportive care. This case highlights the importance of awareness and prompt intervention in DIIHA.

**CP5: Gene co-expression analysis of organic anion transporter polypeptide 2 *(OATP2)* and UDP-glucuronosyltransferase 1A1 *(UGT1A1)* variants in significant neonatal hyperbilirubinaemia in Malaysia**

Shwe Sin[1], Ong Han Kiat[1], Boo Nem Yun[1], Chee Seok Chiong[2], Maslina Mohamed[2], Michelle Ling Min Min[2], Anita Kaur Ahluwalia[2]
*[1]M. Kandiah Faculty of Medicine and Health Sciences, Universiti Tunku Abdul Rahman (UTAR), Kajang, Malaysia; [2]Department of Paediatrics, Hospital Selayang, Selangor, Malaysia*

*Introduction:* Significant neonatal hyperbilirubinaemia (SigNH) is diagnosed when the total serum bilirubin (TSB) level reaches 17 mg/dL (≥291 μmol/L) in term infants. Variations of the UDP-glucuronosyltransferase 1A1 *(UGT1A1)* and organic anion transporter 2 *(OATP2)* genes have been reported as risk factors associated with neonatal hyperbilirubinaemia. This study aimed to investigate the association between the co-expression of OATP2 and *UGT1A1* gene variants and SigNH in Malaysia. *Materials & Methods:* Patients were recruited from Selayang Hospital over an 18-month period. The inclusion criteria included all full-term infants admitted for hyperbilirubinaemia treatment following parental consent. Dried blood spots (DBS) were collected from each infant. The PCR-RFLP method was used to detect *OATP2* gene variants (388G>A, 521T>C) and *UGT1A1* gene variants (211G>A, promoter $A(TA)_nTAA$, c.-3279T>G, 686C>A, 1091C>T, and 1456T>G). *Results:* A total of 1121 neonates were recruited (696 with SigNH and 425 without). A total of 234 co-expression cases (20.9%) were detected across both SigNH and non-SigNH groups, with a higher proportion observed in the SigNH group (54.7%). The highest number of co-expression cases were observed for the c.388G/A and c.-3279T/G mutations, followed by the c.521T/C and c.-3279T/G mutations. However, only c.521T/C and c.3279T/G co-expression showed a significant difference in frequency among cases with *OATP2* and *UGT1A1* mutations (p=0.03). Discussion: Co-expression of *OATP2* and *UGT1A1* gene mutations was more frequently detected in the SigNH group compared

to the non-SigNH group. Additionally, co-expression of the heterozygous c.521T/C and c.3279T/G mutations was identified as a significant risk factor for neonatal hyperbilirubinaemia.

**CP6: Diagnostic discordance in primary aldosteronism: Imaging versus adrenal venous sampling**

Nurul Husna Zulkifli[1,2], Subashini C. Thambiah[2], Nor'ashikin Othman[1], Normaizuwana Mohamed Mokhtar[1], Intan Nureslyna Samsudin[2], Yin Ye Lai[2]

*[1]Department of Pathology, Hospital Kuala Lumpur, Ministry of Health Malaysia; [2]Department of Pathology, Faculty of Medicine & Health Sciences, Universiti Putra Malaysia, Selangor, Malaysia*

*Introduction:* Adrenal venous sampling (AVS) remains the gold standard method for diagnosing primary aldosteronism (PA), offering superior sensitivity over imaging in distinguishing unilateral from bilateral aldosterone hypersecretion. While computed tomography (CT) scan has a sensitivity and specificity of 78% and 75%, respectively, AVS provides superior accuracy (95% sensitivity, 100% specificity). *Case report:* A 57-year-old man with a 20-year history of hypertension presented with hypokalaemia, increased plasma aldosterone concentration, and an elevated aldosterone-renin ratio. An adrenal CT scan suggested bilateral adrenal hyperplasia. However, AVS showed a lateralisation index of greater than or equal to 4, indicating unilateral aldosterone hypersecretion from the right adrenal gland. Despite the CT findings, AVS confirmed unilateral aldosterone hypersecretion from the right adrenal gland. The patient subsequently underwent right retroperitoneoscopic adrenalectomy, resulting in normalisation of potassium levels and improved blood pressure control. *Discussion:* PA is the leading endocrine cause of hypertension and is often associated with treatment-resistant hypertension. Once PA is confirmed, subtype evaluation including an adrenal CT scan and AVS is essential for determining the appropriate treatment strategy. In this case, while CT imaging suggested bilateral adrenal hyperplasia, AVS confirmed unilateral aldosterone excess from the right adrenal gland. This underscores the limitations of CT, which lacks functional specificity and may misclassify PA subtypes. AVS remains essential for accurate subtyping and treatment planning, particularly when considering surgery. Here, AVS guided a right adrenalectomy, resulting in improved clinical outcomes and highlighting its pivotal role in resolving diagnostic discordance in PA.

**CP7: Determining the diagnostic values of procalcitonin (PCT), C-reactive protein (CRP) and CRP/PCT ratio as markers of infection in febrile patients with solid tumours in Hospital Kuala Lumpur**

Muhammad Farhan Salleh[1,2], Intan Nureslyna Samsudin[1], Yin Ye Lai[1], Subashini C. Thambiah[1], Normaizuwana Mohamed Mokhtar[2], Ibtisam Muhamad Nor[3]

*[1]Department of Pathology, Faculty of Medicine & Health Sciences, Universiti Putra Malaysia, Selangor, Malaysia; [2]Department of Pathology, Hospital Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia; [3]Department of Radiotherapy and Oncology, Hospital Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* Differentiating infectious from non-infectious fever in patients with solid tumours is crucial but challenging. C-reactive protein (CRP) and procalcitonin (PCT) are commonly used biomarkers of infection, with recent studies suggesting that the CRP/PCT ratio may improve diagnostic specificity. This study evaluated the use of PCT, CRP, and the CRP/PCT ratio in differentiating between infectious and non-infectious causes of fever in patients with solid tumours. *Materials & Methods:* This cross-sectional study included 123 adult febrile patients with solid tumours admitted to Hospital Kuala Lumpur (HKL) between September 2023 and August 2024. PCT, CRP, and the CRP/PCT ratio were measured prior to antibiotic administration, and their values were compared between infectious and non-infectious groups. The diagnostic accuracy and optimal cut-off values for the biomarkers were determined by analysing the Receiver Operating Characteristic (ROC) curve. *Results:* Infection was identified as the underlying cause of fever in 80 (65.0%) patients. Patients with infection had significantly elevated median PCT (0.65 vs 0.12 ng/mL, $p<0.001$) and CRP (106.7 vs 60.4 mg/L, $p=0.001$) levels. Additionally, the median CRP/PCT ratio was markedly lower in this group (104.42 vs 443.33, $p<0.001$) than in patients with non-infectious fever. The optimal cut-off values were 0.305 ng/mL for PCT [area under the curve (AUC) 0.823, sensitivity 71.25%, specificity 86.05%) and 274.8 for the CRP/PCT ratio (AUC 0.771, sensitivity 72.5%, specificity 81.4%). In contrast, CRP alone exhibited the lowest diagnostic performance (AUC 0.675, sensitivity 67.5%, specificity 62.8%). *Discussion:* Utilising a PCT cut-off of 0.305 ng/mL and a CRP/PCT ratio of 274.8 in febrile patients with solid tumours aids in ruling out infections and may enhance antibiotic stewardship within this patient population.

**CP8: A case of insulinoma: The role of arterial stimulation venous sampling**

Nik Salwani Nik Wan[1], Samuel D. Vasikaran[2], Siti Sharina Anas[3], Nur Shafini Che Rahim[4]

*[1]Department of Pathology, Hospital Sultanah Nur Zahirah, Terengganu, Malaysia; [2]PathWest Laboratory Medicine, Fiona Stanley Hospital, Murdoch, WA, Australia; [3]Department of Pathology, Hospital Putrajaya, Wilayah Persekutuan Putrajaya, Malaysia; [4]Department of Pathology, Hospital Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* Insulinoma is a functional neuroendocrine tumour of the pancreas which can lead to hypoglycaemia. CT scan is the preferred imaging modality for tumour localisation. Arterial stimulation venous sampling (ASVS) helps to localise the lesion when conventional imaging fails. *Case report:* A 37-year-old man presented with a history of loss of consciousness and recurrent seizures due to hypoglycaemia. His hypoglycaemic episodes were alleviated by the intake of sweet food. The following results were obtained during evaluation: fasting blood glucose: 2.0 mmol/L, C-peptide: 1016 pmol/L (366-1466), insulin: 24.11 pmol/L (17.8-173), serum cortisol: 270 nmol/L and prolactin: 185.7 mIU/L (45-375). A CT scan of the pancreas was performed but no lesion was identified. Endoscopic ultrasound revealed an ambiguous lesion at the pancreatic head-neck junction. Following these investigations, he was diagnosed with insulinoma and started on T. diazoxide 100 mg BD. ASVS was performed to further localise the tumour and guide definitive surgical management. Localisation was based on a twofold elevation in insulin levels in the 30 and 60-second samples obtained from the hepatic veins following calcium gluconate injection for gastroduodenal artery, with a concordant C-peptide gradient of 1.6. It was possible to locate the tumour in the head of the pancreas. He underwent a Whipple's

procedure and histopathological examination demonstrated a well-differentiated neuroendocrine tumour. *Discussion:* ASVS is a useful approach for localisation of insulinoma that necessitates a coordinated multidisciplinary approach. While insulin gradients following calcium gluconate injection aid tumour localisation, C-peptide gradients can provide additional diagnostic clarity, particularly when the insulin gradient is equivocal.

**CP9: Weak positive urine pregnancy test in a perimenopausal woman: A cause for concern?**

Nurhazrina Hashim[1], Nadzimah Mohd Nasir[1,2]
*[1]Department of Clinical Diagnostic Laboratories, Hospital Al-Sultan Abdullah, Universiti Teknologi MARA, Puncak Alam, Selangor, Malaysia; [2]Department of Pathology, Faculty of Medicine, Universiti Teknologi MARA, Sungai Buloh, Selangor, Malaysia*

*Introduction:* In a perimenopausal woman, hormonal fluctuations and irregular menstrual cycles can make interpretation of the urine pregnancy test (UPT) results challenging. A faintly positive UPT in such cases may be further complicated by the presence of gestational trophoblastic disease, as illustrated in this case. *Case report:* A 54-year-old woman, para 5, with last childbirth 19 years ago presented with a 1-month history of prolonged vaginal bleeding, varying from fresh clots to brownish discharge, associated with a palpable abdominal mass. Examination revealed a mobile uterine mass approximating 22-week gestational age. UPT, repeated twice, were weakly positive with a corresponding serum beta human chorionic gonadotropin (β-hCG) level of 1,230 IU/L. CA 125 was significantly raised (190.6 U/mL). Ultrasound showed a large, bulky uterus with a characteristic snowstorm appearance, consistent with histopathological findings of a complete hydatidiform mole. Two weeks after a total abdominal hysterectomy and bilateral salpingo-oophorectomy, the β-hCG level was 9,847 IU/L, dropping to 2,464 IU/L one week later. *Discussion:* This case depicts a rare occurrence of molar pregnancy in a perimenopausal woman. The initial β-hCG level was unexpectedly low for a complete hydatidiform mole, which often exceeds 100,000 IU/L. The postoperative β-hCG was significantly higher, raising the possibility of high-dose hook effect in the initial β-hCG reading in retrospect. Extremely high β-hCG levels can saturate antibodies in sandwich immunoassays, causing falsely low results. This phenomenon can be revealed by dilution of the sample, which unfortunately was not available for this case.

**CP10: Unmasking in vivo haemolysis in a patient with end-stage renal failure**

Nurul Ainn Absul[1,2], Intan Nureslyna Samsudin[1], Ana Daliela Masiman[2], Yin Ye Lai[1], Subashini C. Thambiah[1]
*[1]Department of Pathology, Faculty of Medicine and Health Sciences, Universiti Putra Malaysia, Selangor, Malaysia; [2]Department of Pathology, Hospital Melaka, Melaka, Malaysia*

*Introduction:* Haemolytic samples, either in vivo or in vitro, can interfere with the analysis of certain biochemical tests, leading to inappropriate test cancellations and delays in clinical management. Distinguishing between these causes is essential for accurate diagnosis and appropriate patient care. *Case report:* We report the case of a 49-year-old man with diabetes mellitus (DM), hypertension, and end-stage renal failure (ESRF) on regular haemodialysis, who presented to the Emergency Department (ED) with a hypertensive emergency during the third hour of dialysis. Apart from a headache, the patient denied other symptoms. On examination, his blood pressure was markedly elevated (218/133 mmHg), with no other significant clinical findings. Initial and subsequent blood samples collected in ED were grossly haemolysed, with a haemolysis index (HI) of 4+, and a normal potassium level of 4.1 mmol/L (reference interval: 3.5 – 5.1). Haemolysis was further evidenced by elevated lactate dehydrogenase (LDH) and aspartate aminotransferase (AST). Predominantly increased indirect bilirubin suggested the possibility of in vivo haemolysis. However, the absence of anaemia, a normal reticulocyte count, and no evidence of schistocytes or spherocytes on the peripheral blood smear were inconsistent with typical in vivo haemolysis. *Discussion:* This case emphasises the importance of distinguishing in vitro and in vivo haemolysis. Persistent haemolysis with normal potassium should prompt consideration of in vivo causes. It also highlights haemodialysis as a potential cause of in vivo haemolysis, and the underlying mechanisms should be further investigated. Future studies should also examine the bone marrow response to haemodialysis.

**CP11: Improvement of sample registration at Central Diagnostic Laboratory Hospital Pakar Universiti Sains Malaysia: A cost-saving measure**

Wan Mohd Saifuhisam Wan Zain[1,2], Tan Say Koon[1,2], Iwani A. Rozak[1,2], Siti Noria Mansor[1,2], Lydia Michael Ijang[1,2], Nuru Asyikin Mamat Saman[3,2], Wan Norlina Wan Azman[1,2]
*[1]Department of Chemical Pathology, School of Medical Sciences, Universiti Sains Malaysia Health Campus, Kelantan, Malaysia; [2]Hospital Pakar Universiti Sains Malaysia, Kelantan, Malaysia; [3]Pusat Pengetahuan Komunikasi & Teknologi, Universiti Sains Malaysia Health Campus, Kelantan, Malaysia*

*Introduction:* Sample registration in the Laboratory Information System (LIS) is important to ensure proper identification and tracking of samples throughout the laboratory workflow. Unregistered samples in the LIS can lead to an unnecessary increase in sample rejections and wastage of consumables and human resources. *Materials & Methods:* This retrospective study was conducted over a six-month period, from August 2023 to January 2024. The percentage of sample rejections and the waste cost of consumables and human resources were compared before and after improvements were made to the sample registration process in the LIS. The improvement required users to first register the samples in LIS before the stickers for tube labelling can be printed. *Results:* There was a significant reduction in the percentage of sample rejection following the improvement of sample registration in LIS, decreasing from 0.3% to 0.2% ($p < 0.01$). Additionally, the waste cost of consumables and human resources was significantly reduced, from RM 15,720.93 before the improvement to RM 8,403.38 after the improvement ($p < 0.01$). This resulted in a cost saving of 46.5%, amounting to RM 7,317.55. The cost associated with preparing a single sample was calculated to be RM 47.21. *Discussion:* Unregistered samples in the LIS contributed approximately 40-60% of total sample rejections in our laboratory. The improved sample registration process significantly reduced the percentage of sample rejection and the waste cost of consumables and human resources. This cost-saving measure is necessary given the increasing cost of laboratory operations.

**CP13: Implementation of an electronic minimum retesting interval gating in a teaching hospital: An early experience**

Yin Ye Lai [1,2], Intan Nureslyna Samsudin [1,2], Subashini C. Thambiah[1,2].
*[1]Department of Pathology, Faculty of Medicine & Health Sciences, Universiti Putra Malaysia, Selangor, Malaysia; [2]Department of Pathology, Hospital Sultan Abdul Aziz Shah, Serdang, Selangor*

*Introduction:* With the global increase in healthcare expenditure, various approaches have been taken to optimise laboratory testing. The use of minimum retesting interval (MRI) enables laboratory staff to identify and deal with inappropriate, redundant testing. This study evaluated the performance and usefulness of electronic minimal retesting interval gating (eMRIG), an institutionalised, electronic gating system to block repeat testing of selected biochemical tests in Hospital Sultan Abdul Aziz Shah (HSAAS). *Materials and Methods:* This retrospective cross-sectional study over a 6-month duration involved all patients who had biochemical testing at HSAAS. The eMRIG setting within the hospital laboratory system automatically compares a new laboratory test request with the previous request for the same individual and blocks test requests within the minimum retesting interval (MRI). The total number of tests and the number of test requests violating eMRIG were collected. Analysis of percentage reduction in tests performed and total cost savings were performed. *Results:* Within the panel of 12,495 tests subjected to eMRIG, an overall 6.2% cost reduction and 7.4% test reduction was recorded. The annulment of test requests blocked by the eMRIG resulted in an overall financial saving of RM 18,985 with thyroid function test contributing the most to overall cost reduction. *Discussion:* eMRIG is a simple and cost-effective method of demand management to reduce repetitive, inappropriate laboratory testing. The outcome of this study serves as a stepping stone to further improve and utilise the eMRIG for a wider list of laboratory tests in the near future.

**CP14: Unravelling the mystery: Serum aspartate aminotransferase elevation without clear aetiology**

Nor Amani Ashari[1], Rosemawati Arifin[1], Nik Salwani Nik Wan[1], Rabiatul Adawiyyah Mohamad[1], Mohd Jamsani Mat Salleh[2]
*[1]Department of Pathology, Hospital Sultanah Nur Zahirah, Kuala Terengganu, Terengganu, Malaysia; [2]Department of Pathology, Hospital Pulau Pinang, Pulau Pinang, Malaysia*

*Introduction:* Elevated serum aspartate aminotransferase (AST) levels are often associated with liver injury or muscle damage but, persistent isolated AST elevation without a clear cause can pose diagnostic challenges. *Case report:* We present the case of a 41-year-old man with a medical history of cerebrovascular accident (CVA) and non-ST elevation myocardial infarction (NSTEMI), who was found to have persistently elevated AST and creatine kinase (CK) levels during routine follow-up. Despite a comprehensive evaluation - including screening for viral hepatitis, autoimmune disease, and haemolysis - no definitive cause was identified. The patient reported no history of myalgia, strenuous physical exertion, or the use of traditional medicines or supplements. Serial laboratory results showed AST levels ranging from 147–176 U/L and CK levels between 228–427 U/L. Other liver enzymes (ALT, ALP, GGT) and CK-MB remained normal, supporting the hypothesis of non-hepatic and non-muscular origins for the elevated AST and CK. Macro-AST was suspected, and the sample was sent for polyethylene glycol (PEG) precipitation testing, revealing a percent PEG-perceptible activity (%PPA) of 80%, confirming the diagnosis. *Discussion:* Macro-AST is generally benign but can complicate clinical assessments. The laboratory's role in detecting this rare condition is crucial, particularly in distinguishing macro-AST from other causes of enzyme elevation. The PEG precipitation method proved essential in diagnosing macro-AST in this case. While alternative methods, such as assessing AST activity upon refrigeration, can also aid diagnosis, they were not utilised here. Recognising macro-enzymes helps avoid unnecessary further investigations and ensures accurate diagnosis.

**CP15: Implementing plasma uracil test to enhance fluoropyrimidine safety in Hong Kong**

Elaine YL Wong[1], Florence Fung[1], Felix CK Wong[1], Jacky TK Ling[1], Justin CF So[1], Timothy Yeung[1], CW Lam[1,2]
*[1]Division of Chemical Pathology, Department of Pathology, Queen Mary Hospital; [2]Department of Pathology, Li Ka Shing Faculty of Medicine, University of Hong Kong*

*Introduction:* Patients with dihydropyrimidine dehydrogenase (DPD) deficiency face an increased risk of severe toxicity from fluoropyrimidine-based chemotherapy due to impaired drug metabolism. The European Medicines Agency recommends pre-treatment DPD deficiency screening, while China's National Medical Products Administration (2025 No. 18) mandates safety information on fluorouracil packaging. This study develops and validates a liquid chromatography tandem mass spectrometry (LC-MS/MS) method to measure plasma uracil, 5,6-dihydrouracil (DHU), and 5-Fluorouracil (5-FU) levels. *Materials & Methods:* Plasma samples were extracted via protein precipitation and mixed-solvent extraction, followed by $N_2$ drying and reconstitution. Chromatographic separation was performed using a UPLC C18 column. The extracted samples were analysed using LC-MS/MS with multiple-reaction-monitoring for precise quantification. *Results:* The validated LC-MS/MS assay measures plasma uracil (2–250 ng/mL), DHU (10–1000 ng/mL), and 5-FU (20–2500 ng/mL), with $R^2$>0.99 for all analytes. Within-batch and between-batch precision (%CV) remained within 10%. No matrix suppression or enhancement was observed in the retention time period by post-column infusion study. The validated method has participated in an external quality assurance program based in France (ASQUALAB) and meets international standards. *Discussion:* This is the first validated LC-MS/MS assay for DPD deficiency screening implemented at Queen Mary Hospital under the Hong Kong Hospital Authority. It supports pre-treatment testing for fluoropyrimidine chemotherapy, which helps clinicians to identify patients with full DPD deficiency who should avoid the drug and those with partial deficiency for adjusted dosing, improving safety and chemotherapy outcomes.

**CP16: When hypoglycaemia strikes without ketones: A rare case of CPT1A deficiency in a 10-month-old Orang Asli boy**

Rahidatul Fairuz I[1], Ting HY[1], Vani M[1], Lina Wati D[1], Huzaimah AS[1], Ainul Liza A[1], Nur Haidar Z[1], Hafizah A[1], Yusnita Y[2], Nor Azimah AZ[2], Lee JN[3]

*[1]Biochemical Genetics Unit, Department of Pathology, Hospital Tunku Azizah, Wilayah Persekutuan, Kuala Lumpur; [2]Unit of Molecular Diagnostics, Institute of Medical Research, Wilayah Persekutuan, Kuala Lumpur; [3]Department of Genetic, Hospital Kuala Lumpur, Wilayah Persekutuan, Kuala Lumpur*

*Introduction:* Carnitine palmitoyltransferase 1A (CPT1A) deficiency is a rare autosomal recessive disorder of long-chain fatty acid oxidation (FAOD). It typically presents in infancy with non-ketotic hypoglycaemia, liver dysfunction, and metabolic decompensation. *Case report:* We describe a 10-month-old Orang Asli boy, the third child of a consanguineous marriage, who presented with acute gastroenteritis. He had several hospitalisations since birth, including presumed neonatal sepsis with non-ketotic hypoglycaemia requiring ventilation, and recurrent episodes of gastroenteritis, transaminitis, and coagulopathy. Examination revealed gross developmental delay, small for age, and hepatosplenomegaly. Echocardiogram showed a small atrial septal defect and patent foramen ovale. Biochemical investigations revealed metabolic acidosis and markedly elevated liver enzymes, with normal ammonia and lactate levels. The acylcarnitine profile demonstrated elevated free carnitine (C0), low levels of long-chain acylcarnitines (C16, C18, C18:1), increased C0/C16+C18 ratio, and decreased (C16+C18:1)/C2 ratio—results consistent with CPT1 deficiency. Urine organic acids showed a moderate increase in dodecanedioate and a slight increase in 3-methylglutaconate, 3-hydroxyisovalerate, and 3-methylglutarate. Plasma amino acids were unremarkable. Genetic testing revealed a homozygous c.2125G>A variant in the CPT1A gene. *Discussion:* This case highlights the need to consider inborn errors of metabolism (IEM) in infants with recurrent metabolic crises, even if ammonia and lactate levels are normal. Early diagnosis through expanded newborn screening is essential to initiate timely interventions, reducing the risk of life-threatening complications and long-term developmental delays. Clinical and biochemical findings strongly support CPT1 deficiency, consistent with a previous report which identified heterozygous c.2246G>A and c.2125G>A mutations in the CPT1A gene.

**CP19: Relationship between waist circumference and random blood glucose level in healthy young adults**

Arlizan Baizura binti Ariffin[1], Syah Jahan Putera bin Ahmad[2], Jessica Lim Hui Min[2], Nur Aina Fariesya binti Sofian[2], Anarina Anak Thomas[2], Norashikin binti Samsudin[1], Madzlifah binti Ahadon[1]

*[1]Department of Pathology, Faculty of Medicine and Health Sciences, Universiti Malaysia Sarawak, Sarawak, Malaysia; [2]Faculty of Medicine and Health Sciences, Universiti Malaysia Sarawak, Sarawak, Malaysia*

*Introduction:* The prevalence of obesity in young adults is increasing globally. Waist circumference (WC) is a simple anthropometric measurement for assessment of body composition and associated health risks, including diabetes mellitus. This study aimed to investigate the association between WC and random blood glucose (RBG) levels in healthy young adults. *Materials & Methods:* A total of 98 healthy students aged 19 to 23 years in UNIMAS participated in this cross-sectional study. Demographic data, and measurements of WC (in cm) using a flexible measuring tape, and RBG levels (in mmol/L) using glucometer were collected. Statistical analysis was carried out using SPSS (version 29). *Results:* Of the participants, 62% were female and 38% were male. 19.4% of participants had abnormal WC while 10.2% had abnormal RBG levels. Median (IQR) for WC was 73.0 cm (15.5) and RBG was 5.8 mmol/L (1.6). WC was statistically significant ($p < 0.05$), while RBG level was statistically insignificant ($p=0.259$) between genders. Spearman's rho correlation indicated a weak negative correlation between WC and RBG, which was not statistically significant ($\rho = -0.138$, $p = 0.175$). *Discussion:* Increased WC is associated with increased metabolic syndrome and diabetes risk. This study found no significant correlation between WC and RBG in healthy young adults, despite central obesity often being associated with an increased risk of elevated blood glucose. While WC is a quick tool to assess the risk of diabetes, its usefulness in young adults and Southeast Asian populations requires further evaluation.

**CP20: Comparison of data analysis using Deming (Analyse-it) and linear regression (Excel) for method comparison study**

Aminatul Alisya Ahmad Saifuddin, Sharifah Khairul Atikah Syed Kamaruddin, Rozita Abdullah, Cecelia Gillian Ling Huong Gene, Siti Nurranis Omar, Norsyuhadah Musa

*Chemical Pathology Unit, Department of Pathology, Hospital Sungai Buloh, Selangor, Malaysia*

*Introduction:* Method comparison is usually performed in laboratories as part of new equipment installation. Currently, the laboratory uses linear regression (using Excel) to analyse method comparison data. However, linear regression assumes the old method as reference and does not have measurement errors. This assumption is incorrect, as both the new and old methods do have errors. With regard to this, Deming regression should be used as it meets the assumption that both methods have errors. We embark to investigate the differences in outcomes when different statistical methods are applied. *Materials & Methods:* Method comparison data for 70 analytes that were tested in both Atellica (old method) and Roche Cobas Pro (new method) were subjected to analysis using Deming and linear regression method. *Results:* Most assays were comparable and demonstrated no clinically significant differences. However, a group of tests showed clinically significant differences (acetaminophen, AST, ALT, FT3, β-hCG, prolactin, vitamin B12, folate, ferritin, oestradiol, progesterone, cortisol, procalcitonin, CEA, Ca19-9, urine total protein, urine chloride, urine phosphate, urine amylase, urine creatinine). It is also important to highlight that in some cases, not only were the differences significant, but the direction of error can also be opposite (total bilirubin, CA125, oestradiol, testosterone). *Discussion:* This study highlights the importance of choosing the appropriate statistical method for method comparison. Failure to select appropriate statistical methods may result in incorrect estimation of bias, hence a wrong conclusion of the method comparison study.

**CP21: Evaluation of serum tumour markers: A six-month audit of requesting and retesting intervals**

Wan Norlina Wan Azman[1,2], Wan Mohd Saifuhisam Wan Zain[1,2], Aniza Mohammed Jelani[1,2], Hanim Afzan Ibrahim[1,2,3], Ahmad Ezam Zainan[1,2], Tengku Zulkhairuazha Tuan Yahya[1,2], Tan Say Koon[1,2]

*[1]Department of Chemical Pathology, School of Medical Sciences, Universiti Sains Malaysia, Health Campus, Kelantan, Malaysia; [2]Central Diagnostic Laboratory, Hospital Pakar Universiti Sains Malaysia, Kelantan, Malaysia; [3]Basic Sciences and Medical Unit, School of Dental Sciences, Universiti Sains Malaysia, Kelantan, Malaysia*

*Introduction:* Serum tumour markers are valuable in cancer management, providing insights into disease progression and treatment response. However, inappropriate requests and short retesting intervals raise costs without adding clinical value. This study evaluates the frequency and cost of serum tumour marker retesting within 28 days to improve clinical practice and resource use. *Materials & Methods:* This cross-sectional study investigated carcinoembryonic antigen (CEA), alpha-fetoprotein (AFP), cancer antigen 125 (CA125), prostate-specific antigen (PSA) and combinations of multiple tumour markers requested simultaneously. The data set comprised patients who presented at Hospital Pakar Universiti Sains Malaysia between November 2024 and April 2025. Costs were estimated by multiplying test frequency by their charges. *Results:* 2866 tumour markers were requested. Retesting intervals <28 days were observed in 203 requests (7%). CEA was most repeated (14.6%), followed by CA125 (9.8%), PSA (1.8%), and AFP (3.7%). The most common repeated marker combinations were CEA+CA125 (7.8%), AFP+CEA (6.9%), AFP+CEA+PSA (4.3%), CEA+PSA (4.5%), and AFP+CA125+CEA (2.9%). Mean ± SD retesting intervals (days) were: CEA, 15 ± 5; CA125, 12 ± 6; AFP, 11 ± 8; PSA, 14 ± 7; and CEA+CA125, 14 ± 7. The most common repeat diagnoses were colon cancer (48.8%), inappropriate requests (16.3%) and rectal cancer (5.4%). Total cost of repeat testing was RM2734.30. *Discussion:* This study shows a high frequency of serum tumour marker retesting within 28 days, especially for CEA. It highlights the need to establish minimum retesting intervals to improve patient management, reduce financial burdens on healthcare facilities and optimise laboratory resources.

**CP22: Optimisation of a fast protein liquid chromatography method for efficient isolation of native iduronate-2-sulphatase protein**

Rosnani Mohamed[1], Azreena Mamat[1,2], Affandi Omar[1], Fatimah Diana Amin Nordin[1], Norashareena Mohamed Shakrin[1], Saliza Asman[2], Julaina Abdul Jalil[1]

*[1]Inborn Errors of Metabolism and Genetic Unit, Nutrition Metabolism Cardiovascular Research Centre, Institute for Medical Research, National Institutes of Health, Selangor, Malaysia; [2]Department of Physics & Chemistry, Faculty of Applied Science and Chemistry, Universiti Tun Hussein Onn Malaysia (UTHM), Hab Pendidikan Tinggi Pagoh, Johor, Malaysia*

*Introduction:* Iduronate-2-sulphatase (IDS) is a lysosomal enzyme involved in degradation of glycosaminoglycans. IDS deficiency leads to mucopolysaccharidosis type II (MPS II), a rare X-linked lysosomal storage disorder. Existing methods for isolating native IDS protein yield low purity, limiting its use in reliable assays for MPS II drug discovery. This study aimed to develop an optimised fast protein liquid chromatography (FPLC) method to isolate native IDS protein from human embryonic kidney (HEK) cells for downstream applications. *Materials & Methods:* IDS was isolated using automated FPLC with an anion exchange column. The elution buffer was optimised by varying sodium chloride (NaCl) concentrations (200, 500 and 1000 mM) and pH (5.0, 6.0 and 7.5). Protein elution was monitored at 280 nm and collected fractions were analysed by SDS-PAGE, using commercial IDS as a reference. *Results:* Native IDS was successfully isolated using an elution buffer containing 1000 mM NaCl at pH 5.0. The mean peak areas at 1000 mM NaCl concentration were 97.913 ± 21.89, 92.23 ± 12.62 and 70.25 ± 15.05 for pH 5.0, 6.0 and 7.5, respectively ($p<0.05$). SDS-PAGE analysis confirmed the presence of native IDS protein in the 50-70 kDa range. *Discussion:* Higher NaCl concentrations and acidic pH reduce protein-resin interactions, allowing effective elution of native IDS. This optimised FPLC protocol enables reliable recovery of active IDS protein, supporting its application in MPS II drug screening and functional studies.

**CP24: Multiple acyl-CoA dehydrogenase deficiency (MADD) in Malaysia: Bridging clinical, biochemical and genetic approach**

Noornatisha Salleh[1], Norzahidah Khalid[1], Nur Afiqah Ismail[1], Nur Ayuni Ratmi[1], Imran Abdul Kadir[1], Muhd Irfan Bukhari Ahmad Nazri[1], Huzaimah Abdullah Sani[2], Lua Seok Hian[1], Yusnita Yakob[1], Azzah Hana Abu Yamin[1], Leong Huey Yin[3], Anasufiza Habib[1], Saraswathy Apparow[1]

*[1]Specialized Diagnostic Centre, Institute for Medical Research, National Institute of Health, Ministry of Health Malaysia; [2]Department of Pathology, Hospital Tunku Azizah, Kuala Lumpur, Ministry of Health Malaysia; [3]Department of Genetic, Hospital Kuala Lumpur, Ministry of Health Malaysia*

*Introduction:* Multiple acyl-CoA dehydrogenase deficiency (MADD) (OMIM #231680), is a rare autosomal recessive fatty acid oxidation disorder with heterogeneous manifestations from severe neonatal to mild late-onset forms. The clinical disease is based on the electron transfer flavoprotein (ETFA, ETFB) or ETF dehydrogenase (ETFDH) gene variants. This cross-sectional exploratory study highlights the spectrum of Malaysian MADD patients. *Materials & Methods:* The records of 42 suspected MADD patients diagnosed from urine organic acids analysis and dried blood spot (DBS) acylcarnitines profiling were reviewed. Molecular studies were conducted on the suggestive cases. *Results:* DBS acylcarnitines profile showed multiple acylcarnitines elevation. Urine organic acids analysis demonstrated massive excretion of glutarate, dicarboxylic acids and acylglycines. Clinically, these patients were diagnosed mainly during infancy, presenting with lethargy, metabolic acidosis, hypoglycaemia and developmental delay. Molecular analysis identified ETFDH gene variants in four patients. In silico prediction analysis revealed likely pathogenic variants in Patient A (c.353G>T and c.783_787del), Patient C (c.341T>C and c.992A>T) and Patient D (c.1469-1G>T), while Patient B harboured pathogenic variants (c.250G>A and c.770A>G). The c.341T>C variant in Patient C is possibly a novel variant, while the c.1469-1G>T variant in Patient D is not sufficient to cause the disease as only one heterozygous variant was detected. *Discussion:* The synergistic biochemical analysis and genetic testing provides a comprehensive diagnostic tool for clinicians to differentiate MADD from other diseases for early management and ultimately improve patient outcomes.

**CP25: Re-evaluation of urinary cystine cut-offs for improved detection of subclinical or carrier cystinuria in adults**

Marleena M[1], Nur Fatin Syakirah MR[1], Siti Nur Farah Adibah R[1], Azzah Hana AY[1], Saraswathy A[2], Anasufiza Habib[1]
*[1]Biochemistry Unit, Specialised Diagnostic Centre, Institute for Medical Research, National Institute of Health, Kuala Lumpur; [2]Endocrine Unit, Specialised Diagnostic Centre, Institute for Medical Research, National Institute of Health, Kuala Lumpur*

*Introduction:* Cystinuria (OMIM 220100) is a hereditary disorder caused by mutations in SLC3A1 (OMIM 604144) or SLC7A9 (OMIM 604278), leading to defective renal reabsorption of cystine. This leads to elevated urinary cystine levels and increases the risk of cystine kidney stone formation. While severe cases are typically diagnosed early, subclinical individuals and adult carriers may exhibit only mild elevations in urinary cystine, increasing the risk of misdiagnosis or underdiagnosis. This study aims to reevaluate urinary cystine cut-off values in adults to improve the detection of carriers and subclinical cystinuria, while minimising false negatives. *Materials & Methods:* Urine samples from three groups were analysed using liquid chromatography–mass spectrometry (LC-MS/MS): 311 healthy adults, three confirmed cystinuria patients, and one confirmed carrier. Urine cystine concentrations were normalised to creatinine. Cut-off values were defined using percentile analysis of the healthy cohort, and diagnostic thresholds were evaluated based on clinical correlation and intergroup overlap *Results:* A revised cut-off of <31.1 mmol/mol creatinine (99th percentile) was established, replacing the previous threshold of <50.0 mmol/mol creatinine. Three borderline cases were initially flagged as false positives by the new screening method but were later confirmed through follow-up analysis using ion-exchange liquid chromatography (IEC) for urine amino acids. *Discussion:* Subclinical or carrier cystinuria may be missed due to subtle biochemical findings. Updating diagnostic cut-offs based on current population data enhances early detection, enables timely preventive measures, and supports appropriate monitoring of at-risk individuals.

**CP26: Early detection of dihydropteridine reductase deficiency: Diagnostic value of urine and cerebrospinal fluid for biogenic amines and pterins profiling**

Nurul Aina K[1], Norzahidah K[1], Ameliya Bhandal ASN[1], Jia Ni Lee[2], Saraswathy A[1]
*[1]Biochemistry Unit, Specialized Diagnostic Centre, Institute for Medical Research, National Institute of Health, Ministry of Health Malaysia, Kuala Lumpur, Malaysia; [2]Genetic Department, Hospital Kuala Lumpur, Ministry of Health Malaysia, Kuala Lumpur, Malaysia*

*Introduction:* Dihydropteridine reductase (DHPR) deficiency is a rare autosomal recessive neurotransmitter disorder that disrupts tetrahydrobiopterin (BH4) metabolism, resulting in hyperphenylalaninaemia and reduced synthesis of monoamine neurotransmitters. Clinically, it manifests as developmental delay, seizures and other neurological impairments. Although there is currently no curative therapy, dietary management and supplementation with neurotransmitter precursors remain the standard of care. Diagnosis requires a combination of biochemical profiling and genetic analysis. The Institute for Medical Research, as the national referral laboratory, offers urine and cerebrospinal fluid (CSF) analysis for biogenic amines and pterins using high-performance liquid chromatography (HPLC) with electrochemical detector. *Case report:* We report a case of a one-year-old girl, born to non-consanguineous parents, who presented with hypotonia, developmental delay and oculogyric crisis starting at four months of age. She was initially treated for seizures; however, an elevated plasma phenylalanine level (516 µmol/L; reference range: 39–134 µmol/L) prompted further investigation. Paired urine and CSF samples for biogenic amines and pterins demonstrated low levels of 5-hydroxyindolacetic acid (5-HIAA) and homovanillic acid (HVA) alongside elevated biopterin levels. Whole exome sequencing (WES) confirmed a pathogenic mutation in the QDPR gene. *Discussion:* This case underscores the diagnostic value of urine and CSF analysis of biogenic amines and pterin, particularly in settings with limited access to molecular diagnostic facilities. While CSF provides greater diagnostic sensitivity, urine remains a non-invasive and accessible first-line screening tool for patients with suspected neurometabolic disorders.

**CP27: Stability study of plasma Krebs von den Lungen-6 (KL-6) biomarker under different storage conditions and time periods**

Noor Hafizah Hassan[1], Ili Karmila Norazli[1], Siti Nurwani Ahmad Ridzuan[1], Muhammad Nursyazwan Zamre[1], Nurul Izzati Hamzan[1], Hamadah Mohammad Shariff[1], Fadzlyasraf Shaari[2] Hanna Nadhirah Mohd Radzi[2] Anasufiza Habib[3]
*[1]Special Protein Unit Specialised Diagnostic Centre, Institutes For Medical Research, Wilayah Persekutuan Kuala Lumpur, Malaysia; [2]Alfa Diagnostic Sdn Bhd, Selangor, Malaysia; [3]Specialised Diagnostic Centre, Institutes For Medical Research, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* Specimen quality, especially from human-derived clinical samples is critical for ensuring accurate laboratory results and effective patient care. Improper handling or storage can lead to sample instability resulting in degraded or altered biomarker concentrations. This study assessed the long-term stability of Krebs von den Lungen-6 (KL-6) in human plasma stored at −20°C and −80°C over extended durations using manufacturer-recommended handling procedures. *Materials & Methods:* Twenty-one plasma samples were stored at −20°C and −80°C and analysed at seven time points from Day 1 (T0) to Day 132 (T6). Samples were thawed once and allowed to reach room temperature (15–30°C) before analysis. KL-6 concentrations were measured and absolute bias (in U/mL) from T0 values was calculated, using ±10% of the theoretical value as the acceptance threshold. *Results:* All samples across both storage conditions and time points demonstrated absolute bias within the ±10% criterion. Samples stored at −80°C showed consistent results with minimal variability. Those stored at −20°C exhibited slightly more variation, particularly at later time points and higher concentrations but were within acceptable limits. *Discussion:* Plasma samples for KL-6 testing remained stable for up to 132 days when stored at −20°C or −80°C, thawed properly and analysed following a single freeze–thaw cycle. These results surpass the manufacturer's 4-week guideline for −80°C storage and support the use of −20°C as a viable short- to mid-term alternative. Findings may inform updated internal storage protocols and enhance flexibility in laboratory sample management.

**CP28: Optimising early thyroid disorder detection: A paradigm shift in cord TSH reporting using autoverification and streamlined sample handling**

Nur Aasyirah Zakariah[1], Hanisah Abd Hamid[1], Nurul Hidayah Hashim[1], Noriha Sanusi[1]
*Department of Pathology, Hospital Tengku Ampuan Rahimah, Selangor, Malaysia*

*Introduction:* Timely reporting of cord blood thyroid stimulating hormone (TSH) levels is critical for the early detection of congenital hypothyroidism. Historically, the workflow involved batching of sample deliveries by ward and asynchronous laboratory analysis with manual result verification. This resulted in reporting delays of up to 48 hours, often post-discharge, necessitating manual tracing by the Paediatric Clinic and subsequent dissemination of results to Klinik Kesihatan for patient follow-up. Such delays increased the risk of postponed clinical follow-up and delayed initiation of appropriate management. *Materials & Methods:* A revised workflow was introduced involving continuous sample submission and laboratory processing. Autoverification rules were configured based on analyte thresholds, enabling automated result release. For results that failed autoverification, Medical Laboratory Technologists consulted the on-call pathologist for urgent review. If TSH exceeded 60 mIU/L, the on-call paediatrician was immediately informed. *Results:* In a four-month period, 3,982 cord TSH samples were processed. Of these, 98% (3,935) were autoverified. Median laboratory turnaround time (LTAT) decreased from 5 hours to 46 minutes. All results were available prior to discharge, eliminating the need for post-discharge tracing. *Discussion:* The revised workflow enhanced result availability and reduced delays, ensuring all reports were ready before discharge. The high autoverification rate demonstrated system efficiency with a small subset of manual review, allowing rapid response to abnormal results. This initiative illustrates how a small adjustment in workflow i.e. integrating real-time processing and autoverification, can have a significant impact on clinical operations, reducing manual workload and improving patient care.

**CP29: From suspicion to diagnosis: A six-year journey of urinary organic acid analysis for inborn errors of metabolism at Hospital Tunku Azizah**

Vani Munusamy[1], Lina Wati Durani[1], Sivasangkari Supermaniam[1], Ainul Liza Ahmat[1], Nik Aishah Nik Hitam[1], Huzaimah Abdullah Sani[1], Ting Huong Yew[1], Hafizah Abdullah[1], Ngu Hock Lock[2],
*[1]Department of Pathology, Hospital Tunku Azizah, Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia; [2]Department of Genetics, Hospital Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* Inborn errors of metabolism (IEMs) present significant diagnostic challenges due to their heterogeneous and non-specific clinical manifestations. Urinary organic acid analysis (UOA) is a crucial diagnostic tool that enables early and accurate identification, facilitating timely medical intervention. *Materials & Methods:* A six-year cross-sectional study analysed urine samples from patients with suspected IEMs referred from various hospitals. Primary indications for UOA included hyperammonaemia, hyperlactataemia, hypoglycaemia, metabolic acidosis, neurological or hepatic dysfunction, family history of IEMs, and neonatal deaths. Samples were processed through oximation, extraction and trimethylsilyl derivatization, followed by gas chromatography-mass spectrometry (GC-MS) detection. *Results:* Among 5,112 urine samples tested, 93 (2%) showed IEM-specific profiles, 70 (1%) inconclusive and required further investigation and 4,949 (97%) were non-diagnostic. Aminoacidopathies were the most common (44%), followed by organic acidurias (29%), fatty acid oxidation defects (11%), purine/pyrimidine disorders (10%), and mitochondrial disorders (6%). Most diagnoses occurred in neonates (44%) and infants (39%), compared to children (14%) and adults (3%), with no adolescent cases. The cohort had a male predominance (69% male, 31% female; 2:1 ratio) and was primarily Malay (73%), followed by Chinese (12%), Bumiputera (9%), Indian (4%), and other ethnicities (2%). *Discussion:* This study highlights the diagnostic utility of GC-MS-based UOA analysis in detecting IEMs, especially in neonates and infants, where early intervention is vital. High prevalence of aminoacidopathies and organic acidurias reflects the metabolic disorders in our population. Gender and ethnic distributions align with national demographics, suggesting unbiased sampling. Enhanced diagnostic precision and timely management are facilitated by complementing UOA analysis with acylcarnitine, plasma amino acid and purine/pyrimidine testing.

**CP30: Utility of high-sensitivity cardiac troponin T in cardiovascular risk assessment across age groups and lipid risk indices**

Atiqah Mokhsin[1], Sarina Ali[2], Rafezah Razali[3], Rahal Yusoff[4], Rohana Abd Ghani[4], Aletza Ismail[4], Sazzli Shahlan Kasim[1,4], Thuhairah Abdul Rahman[1,3,4]
*[1]Cardiovascular Advancement and Research Excellence (CARE) Institute, Universiti Teknologi MARA, Sungai Buloh, Selangor, Malaysia; [2]Department of Clinical Diagnostic Laboratories, UiTM Medical Specialist Centre, Sungai Buloh, Selangor, Malaysia; [3]Department of Clinical Diagnostic Laboratories, Hospital Al-Sultan Abdullah, Bandar Puncak Alam, Selangor, Malaysia; [4]Faculty of Medicine, Universiti Teknologi MARA, Sungai Buloh, Selangor, Malaysia*

*Introduction:* High-sensitivity cardiac troponin T (hs-cTnT) is a widely used biomarker for myocardial injury, but its utility in cardiovascular (CV) risk stratification across age groups and lipid indices remains unclear. This study evaluates the relationship between hs-cTnT, age, lipid parameters, and their performance in discriminating CV risk levels. *Materials & Methods:* This retrospective study analysed 228 participants categorised into hs-cTnT CV risk groups: low (<5 ng/mL), moderate (5.0–9.9 ng/mL), and high (>9.9 ng/mL). Participants were stratified by age (<50, 50–70, >70 years) and lipid-based indices (Castelli I, Castelli II, Atherogenic Index of Plasma [AIP]). Statistical analyses included descriptive tests, Kruskal-Wallis, Spearman correlation, logistic regression, and ROC curve analysis. *Results:* hs-cTnT levels increased significantly with age ($p < 0.001$) and differed by gender ($p = 0.046$). Positive correlation was observed with age ($r = 0.34$, $p < 0.001$); while negative correlations were found with HDL-c ($r = –0.27$, $p < 0.001$) and LDL-c ($r = –0.25$, $p < 0.001$). Logistic regression showed that individuals <50 years were more likely to have low CV risk (OR = 3.17–4.90, $p < 0.01$), while those >70 had increased odds of high CV risk (OR = 3.53, $p = 0.003$). A significant association was found between hs-cTnT and Castelli I index ($p = 0.022$). ROC analysis showed moderate discriminatory power for high CV risk (AUC = 0.668) and older age (AUC = 0.672), but poor performance for distinguishing low/moderate risk. *Conclusion:* hs-cTnT shows moderate utility in identifying high CV risk, particularly in older adults, supporting its use as a complementary marker with lipid indices.

**CP31: From tube to diagnosis: Uncovering multiple myeloma through a floating gel phenomenon**

Nor Atikah Mohamad[1,2], Fathimah Mohamad[1], Nadzimah Mohd Nasir[1], Arjoanna Farra Azizi[1], Wan Nur Aimi Wan Mohd Zamri[2]
*[1]Faculty of Medicine, Universiti Teknologi MARA, Sungai Buloh Campus, Selangor, Malaysia; [2]Chemical Pathology Unit, Department of Pathology, Hospital Selayang, Selangor, Malaysia*

*Introduction:* Blood collection tubes with separator gel are widely used in many laboratories for chemistry analyses due to their ability to form a stable barrier that prevents the bridging of molecules and proteins released from cells into the serum or plasma. However, in rare pathological states such as hyperproteinaemia, increased serum or plasma density can lead to aberrant gel flotation may occur, compromising sample integrity. *Case report:* We report a case of a floating gel phenomenon in a primary blood collection tube. A blood sample was collected into a BD Vacutainer LH PST II Plus tube from a 51-year-old man who presented to the emergency department with progressive lethargy for three months. Following manual centrifugation, the separator gel was observed floating above the plasma, indicating abnormal phase separation. This unexpected finding prompted further biochemical investigations, which revealed high serum protein level and elevated serum IgG concentration. Serum protein electrophoresis subsequently identified a monoclonal IgG Kappa band, confirming a diagnosis of multiple myeloma, IgG Kappa subtype. *Discussion:* Timely recognition of the gel flotation phenomenon by laboratory personnel through direct visual inspection before analysis significantly accelerates diagnosis by guiding clinicians toward more diagnostically relevant testing and appropriate confirmatory tests. Awareness of such preanalytical anomalies is crucial, as it not only helps prevent analytical issues such as probe blockage or gel aspiration but also supports the early identification of clinically significant conditions. This case highlights the diagnostic value of preanalytical vigilance in chemical pathology.

**CP32: Misreading the peak: Haemoglobin variant co-migrating with HbA0 obscures HbA1c**

Umi Khalsom Abd. Aziz[1], Hani Ajrina Zulkeflee[1,3], Alina Md Fauzi[2,3], Roslina Omar[1]
*[1]Department of Pathology, Hospital Ampang, Selangor, Malaysia; [2]Department of Haematology, Hospital Ampang, Selangor, Malaysia; [3]Department of Medical Sciences II, Faculty of Medicine and Health Sciences, Universiti Sains Islam Malaysia, Negeri Sembilan, Malaysia*

*Introduction:* Capillary electrophoresis (CE) provides an accurate assessment of HbA1c in the presence of haemoglobin (Hb) variants, owing to its ability to distinctly separate Hb fractions, provided that both HbA1c and HbA0 peaks are present. However, rare Hb variants may still interfere with the accurate interpretation of results. *Case report:* We report a case of unreportable HbA1c due to the absence of its peak. A 64-year-old Malay man with no known underlying medical conditions was admitted for suspected multiple metastatic brain lesions. HbA1c testing using CE revealed the absence of an HbA1c peak, despite the presence of a measurable HbA0 peak of 50%; additionally, an HbE peak was detected at 45.2%. Repeat analysis yielded consistent results. Hb analysis, however, revealed the absence of HbA, with 46.7% HbF and 46.8% HbE. His full blood count showed an Hb level of 13.8 g/dL, microcytic hypochromic indices, elevated RBC count ($6.79 \times 10^6/\mu L$), and raised RDW (19.9%). *Discussion:* The absence of HbA, confirmed by Hb analysis, indicates that the patient lacks HbA and consequently HbA1c, making HbA1c testing impossible. In this case, the apparent HbA0 detected during HbA1c testing was likely a variant Hb that had shifted into the HbA0 region. Other variants, such as Hb Malay and Hb Phnom Penh, are also known to co-migrate with HbA0. Glycated HbE may also co-migrate into the HbA0 region, although its contribution is usually negligible. Although rare, abnormal Hb phenotypes can significantly challenge accurate interpretation of HbA1c results, highlighting the need for careful evaluation.

**CP33: Feasibility of browser-based refineR application for paediatric indirect reference interval estimation using alkaline phosphatase as an analyte model**

Nasuruddin DN [1,2], Sarker MR[2], M.S.M. Zabri Tan[4], Ali A[3], Salwana E[2]
*[1]Department of Pathology, Hospital Canselor Tuanku Muhriz, Universiti Kebangsaan Malaysia; [2]Institute of Visual Informatics, Universiti Kebangsaan Malaysia; [3]Department of Paediatrics, Hospital Canselor Tuanku Muhriz, Universiti Kebangsaan Malaysia; [4]Department of Information System, Faculty of Computer Science and Information Technology, Universiti Malaya*

*Introduction:* Indirect methods for establishing paediatric reference intervals (RIs) using routine laboratory data are increasingly adopted due to their cost-efficiency and real-world applicability. The refineR algorithm, a data-driven method to estimate RI from mixed populations, has shown promise but is traditionally confined to R-based desktop environments. This may limit usability and reproducibility in low-resource or non-technical environments. *Materials & Methods:* This study evaluated a web-based implementation of refineR for estimating age- and sex-specific RIs in a multi-ethnic Malaysian paediatric population. Alkaline Phosphatase (ALP) results (n = 28,880) from individuals aged 0–18 years were extracted from a university hospital laboratory information system (2011–2021), de-identified, and partitioned by age and sex. Each subset was analysed using the refineR web tool (https://kc.uol.de/rifindr/#). Distribution fit was visually assessed using the generated violin plots and reference interval plots. The results were benchmarked against established RI modelling approaches. *Results:* The tool successfully generated biologically plausible RIs across most partitions, with adolescent males showing the highest ALP peaks and greater variability observed in infancy. Outputs were visually consistent with physiological patterns. The interface enabled rapid analysis via simple copy-paste input without storing data, thus supporting data privacy and ease of use. *Discussion:* The browser-based refineR tool is practical for indirect RI estimation and facilitates harmonised RI workflows without requiring R coding expertise. However, confidence intervals are not yet available via this platform, limiting statistical uncertainty around the estimates. Verification against published data or local CLSI-guided validation remains essential. Future work should extend this approach to other analytes to test broader applicability.

**CP34: Mapping the global landscape of indirect reference intervals: A bibliometric analysis with a Malaysian perspective**

Nasuruddin DN [1,2], Sarker MR[2], M.S.M. Zabri Tan[4], Ali A[3], Salwana E[2]
*[1]Department of Pathology, Hospital Canselor Tuanku Muhriz, Universiti Kebangsaan Malaysia; [2]Institute of Visual Informatics, Universiti Kebangsaan Malaysia, [3]Department of Paediatrics, Hospital Canselor Tuanku Muhriz, Universiti Kebangsaan Malaysia [4]Department of Information System, Faculty of Computer Science and Information Technology, Universiti Malaya*

*Introduction:* Indirect methods for establishing reference intervals (RIs) are gaining traction as ethical and practical alternatives to direct sampling. However, the global research landscape remains underexplored. This study maps current trends, key contributors, and thematic developments in the field over the past three decades, highlighting emerging methodologies, Collaboration networks, and research gaps, particularly the need for multi-ethnic studies in underrepresented regions like Southeast Asia. *Materials & Methods:* A total of 11,133 publications (1994–2024) were retrieved from the Web of Science Core Collection using a refined search strategy targeting indirect or retrospective RI estimation methods. After applying eligibility filters and topic-based exclusions, 331 articles were retained for final analysis. Records were cleaned using OpenRefine and analysed via Biblioshiny and VOSviewer across descriptive, conceptual, intellectual, and social dimensions. *Results:* Results show a sharp rise in publications since 2015, with foundational contributions from Katayev, Zierk, and Jones. Thematic mapping highlights dominant clusters around "paediatric reference intervals" and "clinical chemistry," alongside growing interest in public health and endocrine-related topics. Co-citation and document coupling confirm a strong foundation in both statistical methods and clinical applications. Collaboration networks remain regionally siloed, with limited Southeast Asian involvement. *Discussion:* Indirect RI research especially in the paediatric population is expanding and gaining global interest. While analytical tools have improved, consistent implementation remains a challenge. We recommend that Malaysia undertake comprehensive indirect RI studies in both adult and paediatric populations, tailored to its multi-ethnic composition, to fill existing gaps in global ethnicity-stratified research and to strengthen regional scientific visibility.

**CP35: Serum phoenixin as a potential emerging laboratory biomarker in reproductive conditions: A systematic review**

Siti Nadirah Ab Rahim[1], Khairul Anwar Zarkasi[2], Siti Hajar Adam[2], Tuan Salwani Tuan Ismail[3]
*[1]Pathology unit, Faculty of Medicine and Defence Health, Universiti Pertahanan Nasional Malaysia, Kuala Lumpur, Malaysia; [2]Pre-clinical department, Faculty of Medicine and Defence Health, Universiti Pertahanan Nasional Malaysia, Kem Perdana Sungai Besi 57000 Kuala Lumpur, Malaysia; [3]Department of Chemical Pathology, School of Medical Sciences, Universiti Sains Malaysia, Kota Bharu, Kelantan, Malaysia*

*Introduction:* Phoenixin (PNX) is a neuropeptide existing in two bioactive forms, PNX-14 and PNX-20. It binds to the G protein-coupled receptor (GPR173) to exert biological effects. While preclinical studies in rodents and cell cultures have demonstrated phoenixin's biomarker role in reproductive function, evidence in humans remains limited. This systematic review aims to investigate the association of serum phoenixin levels in human reproductive conditions. *Materials & Methods:* A systematic search of SCOPUS and PubMed was conducted using the terms "phoenixin AND human study" for studies published between January 2013 and June 2024. Inclusion criteria were human studies assessing serum or plasma phoenixin in reproductive health, original case-control studies, and English-language articles. Exclusion criteria included animal studies, narrative reviews, and those without control groups. Data extraction was conducted by four authors, and quality assessment was made using the Newcastle-Ottawa Scale. *Results:* Five studies met the inclusion criteria. Most were of moderate to high quality. Findings indicate that serum PNX-14 levels are significantly higher in pregnant women following ovarian stimulation ($p<0.001$), in women with polycystic ovary syndrome (PCOS) ($p=0.001$), and in pregnant women with hyperemesis gravidarum (HG) ($p<0.05$). A positive correlation with BMI was also observed in PCOS cases ($p=0.000$). Conversely, PNX-14 levels were significantly lower in women with endometriosis ($p<0.001$). *Discussion:* Current evidence suggests that serum PNX-14 levels vary with reproductive conditions, indicating potential as a biomarker. However, condition-specific patterns highlight the need for further research to establish its diagnostic and therapeutic relevance in reproductive medicine.

**CP36: Precision evaluation of lipoprotein (a) assay on Roche Cobas 6000 analyzer: The particle-enhanced turbidimetric method**

Nani Nordin[1], Siti Nadirah Ab Rahim[1], Ahmad Zakuan Kamarudin[2], Mohamad Syazwan Zahari[3]
*[1]Pathology Unit, Faculty of Medicine and Defence Health, National Defence University of Malaysia, Kuala Lumpur, Malaysia; [2]Pathology Department, Hospital Angkatan Tentera Tuanku Mizan, Kuala Lumpur, Malaysia; [3]BP Clinical Laboratory Sdn Bhd., Selangor, Malaysia*

*Introduction:* Lipoprotein(a) [Lp(a)] is an independent marker for cardiovascular risk factors, and its accurate quantification is essential for risk stratification and management. Analytical precision of Lp(a) assays must meet stringent standards due to their clinical relevance and variability across populations. A method verification study is mandatory to evaluate the performance of any new assay in a laboratory. As part of the method verification component, this study aimed to assess the imprecision of a newly introduced Lp (a) assay in our laboratory using the Roche Cobas 6000 platform. *Materials & Methods:* A precision study protocol based on the Clinical and Laboratory Standards Institute (CLSI) EP9 guideline was utilised. Aliquots of low-level (~42 nmol/L) and high-level (~105 nmol/L) quality control materials were run on the Roche Cobas 6000 analyzer, adopting the particle-enhanced turbidimetric method. Samples were run in 5 replicates daily for 5 consecutive days. Within-run imprecision and total imprecision were calculated using Microsoft Excel and compared with the imprecision claimed by the manufacturer and the European Federation of Clinical Chemistry and Laboratory Medicine (EFLM) desirable analytical imprecision (CVa) goal. *Results:* The within-run coefficient variation (CV) and total CV for the low-level control are 2.5% and 3.8%, respectively, whereas those of the high-level control are 1.7% and 2.5%, respectively. All values fall within the CVs claimed by the manufacturer (within-run CV of 4.00 % and total CV of 6%) and within the EFLM CVa goal of ≤ 5.1%. *Conclusion:* The Roche Cobas 6000 particle-enhanced turbidimetric Lp(a) assay meets the required analytical standards for precision to be considered for routine use. Further studies assessing accuracy would complement these findings to conclude the method verification.

**FORENSIC (FP)**

**FP1: Primary Versus Secondary Head Injuries- The Importance in Forensic Pathology Practice: A case report**

Kay Ly Chng[1], Umul Khairil Fatimah Mohd Mussadik, Hafizatul Solehah Zaki, Husna Syaza Hasim, Khairul Anuar Zainun[2]
*[1]Forensic Unit, Pathology and Laboratory Medicine Department, Sultan Ahmad Shah Medical Centre @IIUM, Pahang, Malaysia; [2]Department of Forensic Pathology, Hospital Sultan Idris Shah, Serdang, Malaysia*

*Introduction:* Cases of traumatic brain injury (TBI) with periods of survival are not uncommon in forensic pathology practice. Autopsy in this cohort plays a crucial role as it provides vast information from multiple points of view. *Case report:* The deceased, an adult male, was allegedly hit on the head during an altercation, succumbed to death after being treated conservatively for one and a half days. He had sustained primary and secondary head injuries. The primary head injuries had led to increased intracranial pressure, hence causing herniation and subsequently post-traumatic cerebral infarction. No significant natural disease contributed to death. *Discussion:* Differentiating primary from secondary injuries is very crucial in coming into best expert opinion for cases of TBI with period of survival. It is of paramount importance to extricate this information as not to mistake these secondary changes as contusions, as it will imply that the number of impacts and overall, the mechanisms are different.

**FP2: Unravelling Mystery: Renal Tubular Acidosis in a Teen with Southeast Asian Ovalocytosis – A case report**

Umul Khairil Fatimah Mohd Mussadik[1], Hafizatul Solehah Zaki[1], Husna Syaza Hasim[1], Asmah Hanim Hamdan[2], Kay Ly Chng[1]
*[1]Forensic Unit, Department of Pathology and Laboratory Medicine, Sultan Ahmad Shah Medical Centre @IIUM, [2]Histopathology Unit, Department of Pathology and Laboratory Medicine, Sultan Ahmad Shah Medical Centre @IIUM*

*Introduction:* Hypokalaemia paralysis is a rare but fatal condition caused by severe potassium depletion, leading to muscle weakness and potential respiratory failure. Renal tubular acidosis (RTA), which has been associated with Southeast Asian Ovalocytosis (SAO), exacerbates potassium loss, increasing the risk of severe electrolyte imbalances and hypokalaemia. We present a forensic case of a 15-year-old girl with no known medical history, who experienced progressive weight loss and weakness but did not seek further medical attention. A week before her death, she developed bilateral lower limb paralysis and loss of appetite before being found deceased at home. *Case Report:* Autopsy revealed a cachexic, pale individual with poor hygiene and no external injuries. Internally, both lungs showed pulmonary infarctions, the kidneys appeared pale, and the heart was grossly unremarkable. Histopathology, confirmed with special stains, revealed pulmonary infarction with antemortem microthrombi, renal changes consistent with RTA, and cardiomyocyte wasting. A full blood picture indicated mild anaemia of inflammation with underlying SAO. Additionally, nucleated red blood cells suggesting a hypoxic response. Postmortem potassium levels remained low at 3.9 mmol/L. The cause of death was determined as hypokalaemia paralysis, with RTA and underlying SAO as contributing factors. *Conclusion:* This case underscores the fatal risk of chronic hypokalaemia in SAO patients with renal dysfunction. The link between SAO and RTA highlights the need for early recognition, electrolyte monitoring, and timely intervention. Forensic pathology plays a key role in uncovering overlooked metabolic disorders, emphasising the importance of a multidisciplinary approach and greater awareness to prevent avoidable deaths.

**FP3: Sudden Death from Peritonitis: An Autopsy Case Report of Duodenal Ulcer Perforation by Helicobacter pylori**

Hazimin Syahir Jamil[1], Bashirah Mohd Nor[1], Shahirah Azman[1], Wan Ajeerah Wan Mustaffa[1], Woo Tay Cheong[1], Asyraff Mohd Najib[1], Faridah Mohd Nor[1,2]
*[1]Forensic Unit, Department of Pathology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia, [2]Department of Clinical Medicine and Surgery, Sir Jeffrey Cheah Sunway Medical School, Faculty of Life and Medical Sciences, Sunway University, Sunway City, Malaysia*

*Introduction: Helicobacter pylori* is a well-established cause of peptic ulcer disease globally. While often presenting as a chronic condition, it can lead to severe complications such as duodenal ulceration and gastrointestinal perforation. Perforation of the gastrointestinal tract may result in peritonitis, a life-threatening condition that can lead to sudden and unexpected death. In such cases, autopsy plays a crucial role in identifying underlying or previously undiagnosed causes. *Case report:* We present the case of a 24-year-old male who had experienced abdominal discomfort for five days before being found unresponsive at home. He had previously consulted a general practitioner and was treated for acute gastroenteritis. Autopsy revealed generalized peritonitis and a 0.5x0.5 cm perforated ulcer on the anterior wall of the duodenum. Histological examination showed chronic inflammation with mucosal ulceration, and special staining confirmed the presence of *H. pylori* within the affected area. *Discussion:* This case underscores the potentially fatal consequences of *H. pylori*-associated peptic ulcers. In the absence of clear clinical signs, such complications may only be discovered postmortem. Recognising *H. pylori* as a contributing factor in sudden deaths due to ulcer perforation highlights the importance of early diagnosis and treatment of peptic ulcer disease to prevent life-threatening outcomes.

**FP4: Anaphylaxis at Autopsy: Unveiling the Lethal Cascade**

Shahirah Azman[1], Woo Tay Cheong[2], Bashirah Mohd Nor[2], Hazimin Syahir Jamil[2], Wan Ajeerah Wan Mustaffa[2], Asyraff Mohd Najib[2], Faridah Mohd Nor[2], Mohamed Swarhib Shafie[3]
*[1]Forensic Unit, Department of Laboratory and Diagnostic Services, Hospital Canselor Tuanku Muhriz UKM, Kuala Lumpur, Malaysia; [2]Forensic Unit, Department of Pathology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia; [3]Department of Forensic Medicine, Faculty of Medicine, Universiti Sultan Zainal Abidin, Terengganu, Malaysia*

Anaphylaxis is a severe, acute, and potentially fatal hypersensitivity reaction that manifests as a rapidly progressing, multisystem allergic response. Clinical presentations vary from mild symptoms such as cutaneous flushing and pruritus to life-threatening respiratory compromise. Diagnosing anaphylaxis post-mortem poses a significant challenge due to the often-non-specific nature

of its findings. Therefore, confirmation requires a comprehensive evaluation encompassing clinical history, autopsy findings, and laboratory investigations. *Case Report:* A 48-year-old male with a documented allergy to beer was found unresponsive following complaints of generalized pruritus. Prior to the event, he had consumed a chicken burger and a soft drink. He was declared dead at the scene. Autopsy examination revealed multiple excoriation marks over the extremities and back, significant laryngeal oedema, and congestion in various organs. Histological analysis demonstrated mast cell degranulation in the larynx and prominent capillary congestion in the pulmonary tissues. Biochemical analysis of post-mortem blood samples revealed elevated levels of serum tryptase and total IgE, supporting a diagnosis of fatal anaphylaxis. *Discussion:* Post-mortem diagnosis of anaphylaxis requires a multidisciplinary approach, as classical signs may be minimal or absent. While findings such as laryngeal oedema and pulmonary congestion are frequently observed, they are not pathognomonic. Histopathological evidence and biochemical markers, especially elevated serum tryptase and total IgE, are pivotal in confirming the diagnosis. This case underscores the importance of thorough autopsy procedures and maintaining a high index of suspicion in instances of sudden unexplained death with potential allergen exposure.

**FP5: FORENSICVAULT: Transforming Forensic Evidence Management Online**

Nadiawati Abdul Razak[1], Abdullah Azam Mohd Abrary[2], Mohd Fahmi bin Mohamad[2]
*[1]Unit of Forensic Medicine, Faculty of Medicine and Defence Health, National Defence University of Malaysia, Kuala Lumpur, Malaysia; [2]Department of Computer Sciences, Faculty of Science and Defence Technology, National Defence University of Malaysia, Kuala Lumpur, Malaysia.*

*Introduction:* The chain of custody is documented evidence of the forensic specimen handling from collection to the final disposition. ForensicVault is an innovative web-based system designed to track the movement of test specimens efficiently for forensic settings and criminal investigations. The chain of custody should be constantly maintained; thus, the system provides greater protection against specimen loss or damage by improving the forensic experts' capacity to securely store specimen data and monitor the movement of evidence between departments and the police. *Method:* The ForensicVault system was developed using PHP as the programming language and MySQL as the database system and using a user-centred approach, with the data collected from interviews. The system aims to create a protected and intuitive web-based system developed for law enforcement and forensic experts. *Discussion:* The ForensicVault provides a powerful solution for the secure data storage and systematic tracking of forensic test specimens, thereby reducing the risks of loss or contamination of the evidence. The system enables efficient monitoring and documentation of the chain of custody so that only authorised persons can access and manage the specimens. This ensures that evidence can be presented in court with integrity. *Conclusion:* The development of ForensicVault represents a remarkable milestone and a reliable system that minimises the risks of tampered evidence in forensic evidence management. This technological innovation reinforces compliance with chain-of-custody protocols, trust in forensic practices, and judicial outcomes.

**FP6: AI-Driven Classification of Blunt and Sharp Force Injuries using Image Processing: A Conceptual Framework**

Nadiawati Abdul Razak[1], Saifouridzal Jamil[2], Mohd Fahmi bin Mohamad[2], Muhammad Fairuz Abd Rauf[2], Nurul Kharmila bintiAbdullah[3], Wan Hassan Basri bin Wan lsmail[4]
*[1]Unit of Forensic Medicine, Faculty of Medicine and Defence Health, National Defence University of Malaysia, Kuala Lumpur, Malaysia, [2]Department of Computer Sciences, Faculty of Science and Defence Technology, National Defence University of Malaysia, Kuala Lumpur, Malaysia, [3]Faculty of Medicine and Health Sciences, Universiti Sains Islam Malaysia, [4]Faculty of Computer Science and Information Technology, Management and Science University*

*Introduction:* The application of artificial intelligence (AI) in forensic practices offers a transformative method for injury identification and categorisation. The system's conceptual framework for an AI-based image processing tool focuses on injury classification to enhance forensic investigations. The system uses advanced deep learning models, including both convolutional neural networks (CNNs) and recurrent neural networks (RNNs), to automate digital image analysis for injury detection and classification of either blunt or sharp trauma. *Method:* The project encompasses creating a comprehensive annotated dataset of forensic injury images while applying image preprocessing techniques to enhance visual clarity and conducting extensive model validation through cross-validation methods and independent test sets. The project will develop algorithms tailored to identify both blunt force trauma and sharp force injuries. *Discussion:* This research produced a user-friendly software tool which incorporates AI models to support the practical use of legal authorities such as forensic doctors, police or lawyers in their work. Forensic experts will conduct pilot testing to verify real-world practical applications and help refine the system through iterative improvements. Evaluation of system performance will involve metrics including precision, recall, F1-score and the area under the ROC curve. *Conclusion:* The conceptual framework supports AI integration into forensic practices while promoting interdisciplinary team Collaboration. The main objective involves creating a standardised and consistent forensic injury detection system that will enhance both criminal investigation procedures and legal outcomes.

**FP7: Forensic evaluation of a suspected infanticide: autopsy and medico-legal consideration**

Lii Jye Tan[1], Shazuan Amir Enuan[1], Ain Nurfarahana Hamdan[1], Mohammad Shafie Othman[1]
*[1]Department of Forensic Medicine, Hospital Raja Permaisuri Bainun, Perak Darul Ridzuan, Malaysia.*

*Introduction:* The investigation of suspicious neonatal deaths presents significant forensic complexities, particularly determining foetal maturity, viability and differentiating live birth from stillbirth. Accurate interpretation of these findings is essential for medico-legal certification, especially in cases where criminal acts such as concealment of birth or infanticide are suspected. *Case report:* We present a case involving a male neonate, reportedly delivered by a young, single mother with autism spectrum disorder. The infant was discovered by a grandparent inside a plastic bag and subsequently brought to a hospital, where resuscitative efforts were initiated. Forensic autopsy revealed inconclusive evidence to definitively establish live birth or stillbirth. No significant injuries

were identified that could independently account for the circumstances surrounding the death. *Discussion:* Comprehensive forensic assessment in suspected infanticide cases is vital to evaluate key parameters including gestational maturity, viability, presence of live birth indicators, and potential cause of death. Integration of autopsy findings, scene investigation, and maternal history is necessary to arrive at an accurate medico-legal conclusion. In cases where evidence of live birth is equivocal or non-reproducible, it is ethically and legally sound to certify the case as an undetermined or stillbirth. This cautious approach upholds the legal principle of *in dubio pro reo*—"when in doubt, rule in favor of the accused"—thereby maintaining the integrity of criminal responsibility by adhering to the standard of proof beyond a reasonable doubt.

**FP8: Histopathological Changes in Post-COVID Autopsy Cases**

Pei Yen Dong[1], Sheue Feng Siew[2], Zhao Peng Koo[3], Poh Soon Lai[2]
*[1]Department of Forensic Medicine, Hospital Sultan Idris Shah, Selangor, Malaysia; [2]Department of Forensic Medicine, Hospital Kuala Lumpur; [3]Department of Forensic Pathology, University of Malaya Medical Centre.*

*Introduction:* Since the emergence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), there have been growing concerns regarding possible sequelae in those who have recovered from the acute disease. These groups of persistent symptoms are commonly known as 'long COVID' or 'post-COVID syndrome'. *Materials & Methods:* This study is a retrospective cross-sectional analysis comparing the prevalence of histopathological pulmonary changes in post-COVID forensic autopsies to a series of controls. Cases were selected from a stipulated time period of 1st January 2022 to 31st December 2022, based on inclusion and exclusion criteria. The post-COVID group included 38 cases with a history of a positive COVID-19 swab at least 4 weeks prior to death. 30 controls from the same stipulated time period with no known history of COVID-19 were also randomly selected for comparison. Demographic details, relevant investigations, and pulmonary histology slides of each case were reviewed and analysed. *Results:* This study showed a significant difference in the prevalence of fibrin microthrombi in post-COVID autopsy cases compared to control. Other abnormal findings, such as thromboemboli, pulmonary fibrosis and diffuse alveolar damage were also increased in post-COVID cases. *Discussion:* Although their long-term clinical significance may not be clear at this point in time, the findings of this study may provide data for further prospective studies with larger sample sizes in order to discern the true effects of post-COVID pulmonary disease. The study was carried out in compliance with the relevant laws and ethical guidelines. (NMRR ID-23-01997-RH)

**FP9: Subinvolution of the placental site presenting as puerperal sepsis: A rare diagnostic challenge**

Song Yang Low[1], Jessie Hiu[1], Nurul Atiqah Abu Sahmah[2], Suria Hayati Pauzi[2], Faridah Mohd Nor[3]
*[1]Department of Forensic Medicine, Hospital Queen Elizabeth, Sabah, Malaysia; [2]Department of Pathology, Hospital Canselor Tuanku Muhriz, Wilayah Persekutuan Kuala Lumpur, Malaysia; [3]Department of Forensic Medicine, Hospital Canselor Tuanku Muhriz, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* Subinvolution of the placental site *(SPS)* is a rare but potentially life-threatening cause of postpartum haemorrhage. Diagnosis may be delayed, particularly in cases presenting atypically without active bleeding. *Case report:* We describe the case of a 38-year-old undocumented Suluk immigrant who was found deceased seven days following an unassisted home delivery. A visit to a local health clinic one day prior noted only complaints of shortness of breath. At autopsy, findings included generalized oedema, bilateral pleural effusions, ascites, and a foul-smelling discharge on her sarong and perineum—initially pointing toward puerperal sepsis. The uterus appeared bulky and contained a red-grey mass firmly attached to the posterior uterine wall, resembling a retained placenta. Although placenta accreta was initially suspected, histological examination revealed numerous dilated, subinvoluted vessels at the implantation site. The mass itself was composed entirely of organized blood clots and necrotic debris, with no residual placental tissue on immunohistochemistry. The presence of extravillous trophoblasts within the vessels confirmed the location as the placental implantation site. Microbial cultures isolated *Enterobacter cloacae* and *Escherichia coli. Discussion: SPS* is marked by the persistence of dilated, low-resistance spiral arteries at the placental implantation site due to inadequate post-delivery involution. These vessels are highly susceptible to haemorrhage. In this case, haemorrhage was masked by the presence of clots, allowing infection to supervene and dominate the clinical picture. Recognising *SPS* requires a high index of suspicion, especially when clinical features mimic puerperal sepsis or retained products of conception without obvious bleeding.

**FP10: When The Brain Turns Against Itself: Death Due To Limbic Encephalitis with Positive Anti-NMDA**

Khairunnisa Kosnin[1], Nur Ayutimasery Abdullah[1], Gan Soon Ching[2], Wong Kum Thong[3]
*[1]Department of Forensic Medicine, Hospital Tengku Ampuan Rahimah, Klang, Malaysia; [2]Department of Pathology Hospital Tengku Ampuan Rahimah, Klang, Malaysia; [3]Department of Pathology, University Malaya, Wilayah Persekutuan, Kuala Lumpur, Malaysia*

*Introduction:* Limbic encephalitis is a rare disease and its definitive diagnosis through biopsy or autopsy represents a significant hurdle to understanding and managing the disease. *Case report:* We report a case of a 30-year-old woman who presented with a brief history of headache, altered mental status and seizure. She was hospitalized for only a week and sought for AOR discharge. Unfortunately, she died the following day at home. During autopsy, there was no remarkable finding on the external body. The brain weight was 1200 gm, and was not atrophied with no focal lesions. Microscopic examination of the brain revealed perivascular cuffing and oedema along with loss of neurons and pyramidal cells within the hippocampus. The tissue was further sent for immunohistochemistry, where it was positive for mature T-lymphocytes (CD3, CD4, CD8) and mature B-lymphocytes (CD20), with the former being predominant. Other ancillary investigations taken during autopsy yielded negative results. Following a more in-depth inquiry at the hospital where she was admitted, no abnormalities were detected in the blood investigation. The sole positive finding in the cerebrospinal fluid was the presence of anti-NMDAR antibodies. CECT and CT scan of the brain demonstrated unremarkable findings. *Discussion:* Forensic pathologists are often confronted with challenging situations and should be aware of NMDAR- or other autoimmune encephalitis as a possible cause of unclear encephalitis. This report highlights the critical value of antemortem investigations in such cases, as exclusive dependence on postmortem findings might have led to a missed conclusive diagnosis.

**FP11: Unforeseen obstruction: Pulmonary tumour thromboembolism in a young man with metastatic testicular germ cell tumour**

Oi Chia Yap[1,2], Norafifah Mohd Yusoff[3], Faridah Mohd Nor[1], Mohd Swarhib Shafee[4]
*[1]Unit of Forensic Medicine, Department of Pathology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Kuala Lumpur; [2]Department of Forensic Medicine, Hospital Tengku Ampuan Afzan, Pahang, Malaysia; [3]Department of Pathology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Kuala Lumpur; [4]Department of Forensic Medicine, Faculty of Medicine, University Sultan Zainal Abidin, Terengganu, Malaysia*

*Introduction:* Pulmonary thromboembolism (PTE) is relatively uncommon in young males. This case highlights a rare and catastrophic presentation of metastatic testicular germ cell tumour (GCT). *Case report:* 22-year-old man with a recent hospital admission for pneumonia presented with a 5-week history of intermittent cough, fever, and shortness of breath before collapsing at a petrol station. Post-mortem examination showed tumour thromboemboli in the pulmonary trunk, both lungs, and the inferior vena cava. Thromboemboli were observed in the right atrium and left renal vein. Tumours were identified in the left testis, measuring 14 x 9 x 6 cm, both lungs, liver, soft tissues of left adrenal gland/kidney, and retroperitoneal para-aortic lymph nodes. Histology of tumours demonstrated metastatic mixed GCT of the left testis, predominantly embryonal carcinoma with a choriocarcinoma component. Elevated serum tumour markers supported the diagnosis. His death was attributed to pulmonary tumour thromboembolism due to metastatic testicular germ cell tumour. *Discussion:* The pulmonary thromboembolism in this case was likely predisposed by tumour metastasis and the hypercoagulable state induced by the tumour. Non-seminomatous GCTs exhibit a propensity for early and frequent haematogenous metastasis and carry a poorer prognosis compared to their seminomatous counterparts. Young men should be aware of the potential danger of a unilateral solid testicular mass and seek early medical attention to prevent an untimely demise.

**FP12: An Infant of Cardiac Rhabdomyoma (CR): The Autopsy**

Ain Nurfarahana Hamdan, Mohammad Shafie Othman@Osman, Tan Lii Jye
*Department of Forensic Medicine, Hospital Raja Permaisuri Bainun, Perak, Malaysia*

*Introduction:* Primary cardiac tumours are extremely rare, occurring 0.2% of children. CR is a benign tumour arising from striated muscle and may result in sudden cardiac death (SCD). *Case report:* This 2-month-old boy, born at 34-weeks' gestation via scheduled caesarean section due to symmetrical intrauterine growth restriction with high resistance umbilical artery detected by Doppler ultrasound. He was admitted until 5 weeks of age for respiratory distress syndrome, anaemia in prematurity and a small atrial septal defect/patent foramen ovale (ASD/PFO). He was well upon discharge; however, at 2-month-old, he was found death in supine position while sleeping. Postmortem examination of the heart revealed PFO and multiple pale nodules on the ventricular myocardium. Histological examination of the heart demonstrated multiple well-circumscribed nodules composed of vacuolated myocytes and presence of spider cells. The vacuolated myocytes were positive for myoglobin and desmin stains, and were negative for actin, periodic-acid-schiff and CD68 stains. *Discussion:* CR is the most common cardiac tumour in children for approximately 45% of cases, with a uniform distribution between sexes. It primarily manifests clinically within the first year of life. Most of the cases are asymptomatic. However, the affected child may manifest as congestive heart failure, arrhythmia (such as bradycardia, ventricular or atrial tachycardia), obstruction of the ventricular inflow/outflow tract, and SCD. Diagnosis is made by imaging and histology examination. Although echocardiography is effective, CR can be missed, particularly when the tumour is small, located intramurally, situated in an atypical area such as the atria, or due to technical limitations.

**FP13: The Autopsy of Paradoxical Amniotic Fluid Embolism (PDAFE)**

Ain Nurfarahana Hamdan, Mohammad Shafie Othman@Osman, Tan Lii Jye, Nur Aida Zainuddin, Nurul Sofea Nor Hishamuddin
*Department of Forensic Medicine, Hospital Raja Permaisuri Bainun, Perak, Malaysia*

*Introduction:* Paradoxical Embolism (PDE) occurs when embolic material (blood clot, fat particle, air, amniotic fluid, or tumour) from venous circulation bypasses the pulmonary filtration system- typically via an intracardiac shunt- and enters the systemic arterial circulation. *Case report:* A 30-year-old woman underwent induction of labour at 38-weeks' gestation due to reduced foetal movement. Nine-hours following rupture of membranes, she became unresponsive warrants resuscitation, followed by an emergency caesarean section. A CT scan of the brain performed on Day-1 postpartum demonstrated generalized cerebral oedema with evidence of coning and multiple cerebral infarcts. Postmortem examination conducted on Day-8 postpartum revealed evidence of amniotic fluid embolism with multiorgan failure. Notably, she had atrial septal defect (ASD) comprising both ostium secundum defect and vestibular atrial septal defect. Histological examination demonstrated the presence of foetal squames within pulmonary, cerebral, and uterine vasculature. *Discussion:* Emboli can vary in size and origin, with cerebrovascular events being the most common clinical manifestation in PDE. The diagnosis of PDE is based on three-criteria: (1) identification of venous source of embolism, (2) the presence of intracardiac defect (such as patent foramen ovale or ASD) or pulmonary arteriovenous malformation, and (3) evidence of systemic arterial embolization. However, clinical diagnosis remains challenging, and the true incidence of PDE is likely underestimated. Among ASDs, **ostium secundum defects** are the most common subtype (approximately 75% of cases). In the presence of elevated right-sided cardiac pressures seen in pulmonary embolism or pulmonary hypertension—the risk of right-to-left shunting and thus PDE is increased.

**FP14: An Unusual Autopsy Finding: Bilateral Common Iliac Artery Aneurysms with Rupture and Dissection**

Wan Ajeerah Wan Mustaffa[1], Hazimin Syahir Jamil[1], Bashirah Mohd Nor[1], Shahirah Azman[1], Woo Tay Cheong[1], Asyraff Mohd Najib[1], Faridah Mohd Nor[1]
*[1]Forensic Unit, Department of Pathology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia*

*Introduction:* Atherosclerosis, a prevalent vascular disorder, can lead to aneurysm formation, carrying significant risks of dissection

and rupture, which may result in fatal haemorrhage. Aortic aneurysms are often asymptomatic for long periods, enabling some individuals to live into advanced age without diagnosis or treatment. *Case report:* We present a rare case of bilateral common iliac artery aneurysms in a 74-year-old man with a history of poorly controlled hypertension but no prior symptoms. Postmortem examination revealed a ruptured aneurysm of the left common iliac artery associated with a 700 ml haemoperitoneum. Additionally, a dissecting aneurysm with an organized thrombus was identified in the right common iliac artery. *Discussion:* Although ruptured dissecting aortic aneurysms are relatively common, their isolated occurrence in the common iliac arteries, particularly involving bilateral aneurysms, is exceedingly rare. The underlying cause was attributed to severe atherosclerosis, compounded by chronic hypertension. The remainder of the aorta also demonstrated advanced atherosclerotic changes.

**FP15: Unusual Site of Intracranial Tuberculoma in Disseminated Tuberculosis: An Autopsy Case Report**

Nur Amirah Mohd Azam[1], Nor'amirah Ahmad[1], Nurul Liyana Karis[1]
*[1]Department of Forensic Medicine, Hospital Sultan Idris Shah Serdang, Selangor, Malaysia*

*Introduction:* Tuberculosis (TB) rarely involves the central nervous system (CNS), accounting for 1–2% of all tuberculosis cases. CNS TB typically manifests as these three conditions: tuberculous meningitis, spinal arachnoiditis and intracranial tuberculoma. Intracranial tuberculoma commonly located in the cerebrum, followed by the cerebellum and the brain stem. Herein, we present a case of tuberculoma unusually located at the lateral ventricular wall causing ventricular obstruction. *Case report:* A 22-year-old gentleman with history of headache and generalised body weakness, collapsed and died at the airport. Autopsy examination revealed generalised cerebral oedema with bilateral dilation of the lateral and third ventricles. Sectioning exposed a nodular lesion attached to the left lateral ventricle wall, filled with green, gelatinous material within a thin, tan capsule. The histology revealed caseous necrosis, which was surrounded by epithelioid cells, rim of lymphocytes and numerous Langhans giant cells. Tiny caseating granuloma with lymphocytic infiltrations were seen in the Virchow Robin spaces. The tuberculosis culture tested positive for *Mycobacterium tuberculosis* complex. Nodular lesions were observed in all lung lobes and the right kidney, with dense pericardial adhesions and enlarged mesenteric lymph nodes of which histologically showed presence of caseating granulomas. *Discussion:* Due to the vague clinical history obtained, the initial diagnosis of cerebral oedema suggested neoplastic lesions or intracranial haemorrhage. However, in TB-endemic regions, CNS TB warrants consideration when neurological symptoms are present. It can occur as a manifestation of disseminated TB or as early presentation before the primary site is clinically evident. Therefore, appropriate samples for tuberculosis cultures should be sent for confirmation via laboratory diagnosis.

**FP16: "Tracing the red: hydrogen peroxide as a presumptive tool for blood detection on human bones"**

Muhammad Izzul Jamaludin[1], Asrul Fahmi Abdul Mutalib[2], Rosaniza Kamarudin[2], Mohamad Aznool Haidy Ahsorori[2]
*[1]Department of Forensic Medicine, Hospital Enche' Besar Hajjah Khalsom, Johor, Malaysia; [2]Department of Forensic Medicine, Hospital Sultanah Aminah, Johor, Malaysia*

*Introduction:* Identifying postmortem changes and reconstructing the depositional history of human remains are key aspects of forensic anthropology. Detecting blood stains on bones can be challenging due to decomposition and environmental effects. This study aims to evaluate whether hydrogen peroxide is a reliable method for identifying blood-related staining on bone surfaces in forensic contexts. *Materials & Methods:* Two human rib bones were firstly cleaned by using detergent and rinsed with hot water to remove any soft tissue attached. One of the bones was soaked partly in a compartment which contained human blood, whereas the other bone which was soaked in tap water used as a control. Over the period of 9 months, the appearance and progression of the bones stained were observed documented and finally tested with 39% hydrogen peroxide solution. *Results:* Bloodstained discolouration on the bones showed bubbles reaction when tested with hydrogen peroxide. *Discussion:* Hydrogen peroxide was used as a presumptive test for blood due to its availability and reliance of heme's peroxidase-like activity, which produces visible oxygen bubbles. Bubbling was observed within 5 seconds of application on suspected blood stains, even after cleaning and on samples aged up to nine months, suggesting the test's reliability despite degradation over time. However, further research is warranted to validate its effectiveness across varied environmental condition and to compare its performance with other established presumptive tests (example: Phenolphthalein, Leucomalachite green, Luminol, Tetramethylbenzidine, Leucorystal violet, and o-toluidine) for blood detection.

**FP17: Vessels that wouldn't close: The silent bleed in birth**

Wong P.M.[1], Nurfarrah b.a.[1].
*[1]Department of Forensic Medicine, Hospital Sultan Ismail, Johor*

*Introduction:* Subinvolution of the placental site is a rare but significant cause of secondary postpartum haemorrhage, typically occurring days to weeks after delivery. It is important and yet often clinically underdiagnosed or unidentified, thereafter presented during autopsy in cases of unexplained postpartum death. Placenta site subinvolution is resulting from the failure of the uterine spiral arteries at the placental site to undergo normal involution, leading to prolonged bleeding and which in this case, maternal mortality. *Case report:* A 28 years old postpartum 13 days lady was found unresponsive in her house and subsequently brought in dead to hospital. On gross examination, the uterus appeared enlarged, soft, and boggy, with a placental site that appears congested. Histopathology examination revealed dilated, thrombosed subinvolution spiral arteries and involuted arteries with persistent trophoblasts, indicating incomplete vascular regression. There was area of endometritis seen. Immunohistochemical cytokeratin showed positive of trophoblast. *Discussion:* Subinvolution is believed to result from a combination of hormonal, vascular, and possibly immunological factors. The persistence of trophoblastic cells and lack of proper arterial remodelling prevent adequate closure of maternal vessels, predisposing to delayed haemorrhage. Risk factors include multiparity, infection, retained placental tissue, and uterine atony. Clinically, diagnosis is challenging, and it often mimics other causes of postpartum bleeding. Awareness of this condition is essential for obstetricians and forensic pathologists alike. Early recognition can enable timely intervention,

whereas failure to diagnose may result in fatal outcomes. Postmortem identification is critical in maternal mortality investigations and can provide valuable insights into preventive strategies.

**FP18: Beyond Imaging: The Role of Autopsy in Distinguishing Accessory Sutures from Skull Fractures in Children**

Wan Mohammad Hafiz Wan Razali[1], Rashed Shatnawi[2], Mohamad Helmee Mohd Nor[3], Mohamad Azaini Ibrahim[4], Faridah Mohd Nor[5]

*[1]Department of Forensic Pathology, Faculty of Medicine, Sungai Buloh Campus, Universiti Teknologi MARA, Selangor, Malaysia; [2]Department of Forensic Medicine and Toxicology, School of Medicine, Yarmouk University, Irbid, Jordan; [3]Department of Radiology, Hospital Kuala Lumpur, Kuala Lumpur, Malaysia; [4]Department of Forensic Medicine, Hospital Kuala Lumpur, Kuala Lumpur, Malaysia; [5]Forensic Unit, Department of Pathology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia.*

*Introduction:* Computed tomography scans are widely employed in the evaluation of suspected head trauma, especially in paediatric patients. However, it is crucial to understand their limitations, particularly in differentiating anatomical variants, such as accessory sutures, from actual skull fractures. Misinterpretations may result in incorrect assumptions regarding the presence of trauma, the manner of death, and ultimately, the cause of death. *Case report:* We report the case of a previously healthy 2-month-old infant, who was initially admitted for meningitis. A cranial ultrasound during this admission showed no evidence of intracranial haemorrhage. Following two weeks of treatment, the infant was discharged, only to collapse at home less than 12 hours later. He was brought to a different hospital, where resuscitation successfully restored spontaneous circulation. Despite intensive medical intervention, the child succumbed to his illness four days later. A computed tomography scan obtained during the second hospitalisation showed a parietal bone fracture and intracranial bleeding, leading to the suspicion of traumatic injury. However, post-mortem examination revealed that the supposed fracture was in fact an accessory suture. *Conclusion:* This case underscores the critical role of autopsy in forensic evaluations, particularly when imaging findings may be ambiguous or misleading. Without a thorough post-mortem examination, there is an increased risk of diagnostic error and potential legal misjudgement. Accurate differentiation between anatomical variations and true trauma is essential to support just and evidence-based forensic outcomes.

**FP19: Liver and Kidney Vacuolation in Paediatric Sepsis: Insights from Two Autopsy Cases**

Nuraida Khalid[1], Nur Syuhada Othman[1], Norazwa Khairina Amatkhri[1], Mohamad Aznool Haidy Ahsorori[1]

*[1]Department of Forensic Medicine, Hospital Sultanah Aminah, Johor, Malaysia*

*Introduction:* Cytoplasmic vacuolation in the kidneys and liver often signifies underlying pathological processes and can aid in determining the cause of death. While vacuolation may arise from different mechanisms in each organ, its concurrent presence in both organs may help narrow differential cause of death. This case report presents two paediatric sepsis-related deaths with similar histological findings but differed in metabolic profiles, as evidenced by the presence and absence of ketones. *Case report:* A 5-month-old Rohingya infant and a 2-year-old Orang Asli toddler both presented with gastrointestinal symptoms prior to death. On postmortem examination, both exhibited an enlarged, pale yellow liver and kidneys with pale cortices and congested medullae. Histology revealed periodic acid-Schiff (PAS)-negative cytoplasmic vacuolation in both organs. The Rohingya infant had *Escherichia coli* sepsis with ketonuria, while the Orang Asli toddler had *Campylobacter jejuni gastroenteritis* complicated by *Klebsiella pneumoniae* sepsis, without ketonuria. Vitreous glucose levels and inborn error of metabolism screening were of a non-diagnostic profile in both cases. *Discussion:* These findings underscore the variable metabolic responses in paediatric sepsis. The presence or absence of ketonuria may reflect different underlying metabolic stress pathways, which could have important implications for pathological interpretation and understanding the metabolic derangements associated with severe illness and death in paediatric populations.

**FP20: Artificial Intelligence in Forensic Pathology: A Systematic Review of Global Advances, Challenges, and Legal Implications with Insights from Malaysia**

Anaiki Zaini[1], Noor Asyikin Suaidi[1]

*[1]Department of Forensic Medicine, Hospital Umum Sarawak, Kuching, Sarawak, Malaysia*

*Introduction:* Artificial intelligence (AI) is increasingly being integrated into forensic pathology, offering transformative potential in autopsy diagnostics, postmortem imaging, and histological interpretation. AI's ability to process complex datasets can enhance diagnostic accuracy and efficiency, but its application varies globally, especially in developing contexts like Malaysia. This review systematically evaluates global advancements in AI for forensic pathology, identifies implementation challenges, and explores legal implications with a focus on Malaysia. *Materials and Methods:* A systematic literature search was conducted in four databases: PubMed, Scopus, Web of Science, and Google Scholar; covering publications from January 2010 to April 2025. Search terms included combinations of "artificial intelligence," "forensic pathology," "postmortem," "machine learning," and "legal." Articles were screened according to PRISMA guidelines. Inclusion criteria were English-language peer-reviewed publications addressing AI applications in forensic pathology with clinical or legal relevance. *Results:* Key AI applications include postmortem computed tomography (PMCT) interpretation, trauma pattern classification, time-since-death estimation, facial reconstruction, and increasingly, AI-assisted histological image analysis. Challenges identified include limited annotated datasets, algorithmic transparency, ethical concerns, and legal admissibility. Malaysia-specific barriers include infrastructural constraints, lack of digital pathology integration, and unclear regulatory frameworks. *Discussion:* While global trends support AI's transformative potential, its application in Malaysia requires cautious and context-specific integration. Regulatory frameworks, training, and interdisciplinary Collaboration are essential for ethical adoption and legal compliance in forensic settings.

## GENETIC PATHOLOGY (GP)

**GP1: Disorders of sex development (DSD) prevalence among local population in University Malaya Medical Centre (UMMC) – A single centre study.**

Mardziah Mohamad, Hana Shafinaz Jamaluddin, Mohammad Zarizi Abd Ghani, Wan Nor Saliana Wan Ali, Juwariah Abu Bakar, Santhini Sankaran Kutti, Mohd Fouzan M Ibrahim, Nur Syuhadah Ramat

*Cytogenetic Unit, Division of Laboratory Medicine, University Malaya Medical Centre, Wilayah Persekutuan Kuala Lumpur, Malaysia.*

*Introduction:* Disorders of sex development (DSD) refers to a group of congenital conditions in which the development of sex characteristics such as chromosomes, external genitalia and gonads deviates from the typical male or female patterns. DSD are generally Categorised into three main groups: sex chromosome DSD, 46,XY DSD and 46,XX DSD. Given the limited data on DSD in local population, this study aims to assess the prevalence of DSD among the patients referred to UMMC. *Materials & Methods:* A retrospective study was conducted in the Cytogenetic unit, UMMC on all patients diagnosed with DSD between January 2014 and December 2024. Data were analysed with regard to clinical presentation, phenotypic features, sex-assignment and laboratory diagnosis based on G-banding chromosome analysis. *Results:* A total of seventy-two DSD patients were identified. Of the three major categories, sex chromosome DSD recorded the highest prevalence of 72% (52/72) mostly presented with short stature and infertility. The majority of the cases were mosaic Turner syndrome(15/72) and variant Turner syndrome (14/72). 20% (14/72) of cases had 46,XY DSD and 4% (3/72) had 46,XX DSD. We identified three rare cases of ovotesticular DSD presented with mixed gonadal dysgenesis, in which corrective surgeries were performed on two of the patients. *Discussion:* This study offers valuable insights into the prevalence of DSD in the local population. It also highlights the need for ongoing research to further enhance and improve early diagnosis as well as the management of DSD.

**GP3: Optimising banding patterns in blood karyotyping: Early strategies for a new cytogenetics laboratory**

Sri Wahyuni Giarto Gatot[1], Siti Roziana Romali[1], Maizurani Japri[1], Rose Adzrianee Adnan[1,2], Ruzi Hamimi Razali[1,2]

*[1]Department of Clinical Diagnostic Laboratories, Hospital Al-Sultan Abdullah UiTM, Bandar Puncak Alam, Selangor; [2]Department of Pathology, Faculty of Medicine, Universiti Teknologi MARA, Sungai Buloh Campus, Selangor*

*Introduction:* Accurate chromosome identification in blood karyotyping relies heavily on the quality of banding patterns. Giemsa-banding (G-banding) is the standard technique employed to generate distinct light and dark bands that facilitate the identification of individual chromosomes. In a newly established cytogenetics laboratory, achieving consistent high-quality G-banded metaphase spreads is essential to detect chromosomal abnormalities. Hence, ensuring reproducibility of high-quality banding patterns across samples is critical for diagnostic accuracy and laboratory credibility. *Materials & Methods:* This study focuses on optimising metaphase spread and banding contrast through adjustments in the technique for dropping fixed cells, banding of chromosomes, staining duration, and slide preparation for microscopic analysis. Parameters including hypotonic treatment conditions, slide aging, trypsin digestion time, and staining intensity were evaluated to enhance the quality of metaphase chromosomes. *Results:* This preliminary study provides insights for new cytogenetics laboratories working towards optimising blood karyotyping techniques. Optimised hypotonic treatment and controlled trypsinization yielded clearer metaphase spreads and more distinct banding patterns. *Discussion:* Early observations highlight common challenges, including banding inconsistencies and chromosome clustering, which impact karyotype interpretation. These issues may hinder the identification of chromosomal abnormalities. By refining staining protocols and systematically addressing common technical errors, we aim to enhance the reliability and consistency of chromosome analysis in our laboratory.

**GP4: From Sunlight to SNPs: Exploring Vitamin D Status and VDR Gene Variants in a Paediatric Malaysian Cohort**

Rose Adzrianee Adnan[1], Nur Faten Hafizah Rosli[2], Siti Hamimah Sheikh Abdul Kadir[2,4,5], Noor Shafina Mohd Nor[2,3,4]

*[1]Department of Pathology, Faculty of Medicine, Universiti Teknologi MARA (UiTM), Cawangan Selangor, Kampus Sungai Buloh, Malaysia; [2]Institute of Medical Molecular Biotechnology (IMMB), Faculty of Medicine, Universiti Teknologi MARA(UiTM), Cawangan Selangor, Kampus Sungai Buloh, Malaysia;[3]Department of Paediatrics, Faculty of Medicine, Universiti Teknologi MARA (UiTM), Cawangan Selangor, Kampus Sungai Buloh, Malaysia; [4]Institute for Pathology, Laboratory and Forensic Medicine (IPPerForM),Universiti Teknologi MARA (UiTM), Cawangan Selangor, Kampus Sungai Buloh, Malaysia; [5]Department of Biochemistry and Molecular Medicine, Faculty of Medicine, Universiti Teknologi MARA (UiTM), Cawangan Selangor, Kampus Sungai Buloh, Malaysia*

*Introduction:* Vitamin D deficiency is a widespread global health issue, particularly among the youth. In Malaysia, studies have reported high prevalence rates, influenced by factors such as gender, ethnicity, and urban lifestyles. Additionally, polymorphisms in the vitamin D receptor (VDR) gene specifically *FokI, BsmI,* and *TaqI* polymorphisms which affect vitamin D metabolism and levels. This study investigated the prevalence of vitamin D deficiency and its potential association with these VDR gene polymorphisms in a Malaysian paediatric cohort. *Materials & Methods:* Fifty-four participants aged 7 to 17 years were recruited from Hospital Al-Sultan Abdullah, UiTM, Selangor. Serum 25-hydroxyvitamin D [25(OH)D] levels were measured using the electrochemiluminescence immunoassay. Genotyping of the VDR polymorphisms was performed using standard molecular techniques. Data analysis was conducted using SPSS. Results: The average participant age was 9.56 years, and vitamin D deficiency was observed in 59.3% (n=32) of the samples. The most common genotypes among deficient participants were TC for *TaqI* (n=27), GG for *BsmI* (n=25), and TC for *FokI* (n=18). However, statistical analysis found no significant association between these VDR polymorphisms and vitamin D status. *Discussion:* The study highlights a high prevalence of vitamin D deficiency among Malaysian children and adolescents, aligning with previous national findings. While certain VDR genotypes were more common among those with deficiency, no significant association were found between the polymorphisms and vitamin D levels. This suggests that while genetic factors may

play a role in vitamin D metabolism, other factors e.g. environmental exposure, dietary intake, and lifestyle may influence vitamin D levels in this population. Further research with larger sample sizes and consideration of additional genetic and environmental factors is warranted to elucidate the complex factors influencing vitamin D status in Malaysian youth.

**GP5: A case of t(X;13) : Revealing hidden mechanisms of recurrent pregnancy loss**

Wan Nur Amalina Zakaria[1], Aziati Azwari Annuar[1], Nazihah Mohd Yunus[1], Siti Mariam Ismail[1], Norhidayah Ramli[1], Nurul Alia Mohd Nawi[1], Nik Mohd Zulfikri Mat Zin[1], Zulaikha Abu Bakar[1], Fatin Syahirah Rasudin[1]

*[1]Human Genome Centre, School of Medical Sciences, Health Campus, Universiti Sains Malaysia, Kelantan, Malaysia; [2]Hospital Pakar Universiti Sains Malaysia, Kelantan, Malaysia*

*Introduction:* Recurrent pregnancy loss, defined as two or more consecutive miscarriages, affects up to 1-2% of women of reproductive age. Among the various potential causes, chromosomal abnormalities, particularly balanced translocations in one of the partners, are well-recognised factors of recurrent miscarriage. Although rare, X-autosome translocations are of particular clinical significance due to their potential impact on fertility and pregnancy outcomes. *Case report:* We present a rare case of a young woman with five consecutive first-trimester miscarriages. Physical examination was unremarkable, and laboratory screening for antiphospholipid antibody was negative, excluding antiphospholipid syndrome as a contributing factor. Due to the absence of other identifiable causes, cytogenetic analysis of her peripheral blood was undertaken. Karyotyping and FISH analysis confirmed an X;13 chromosomal translocation, described cytogenetically as 46,X,t(X;13)(p11.2;q22).ish t(X;13)(p11.1;q22)(pcpXp-,wcp13+;wcp13+,pcpXp+). *Discussion:* X-autosome translocations are rare cytogenetic events that, although may not result in phenotypic abnormalities in female carriers, can lead to significant fertility issues. Clinical outcomes vary depending on factors such as the location of the breakpoint, the genes involved, and the pattern of X-chromosome inactivation. A significant segment of the X chromosome involved in this translocation is associated with an increased risk of offspring with sex chromosome abnormalities. Imbalance of 13q22qter from partial monosomy or trisomy increases miscarriage risk or severe anomalies at birth, as chromosome 13 carries genes vital for embryonic development. While X-chromosome inactivation can mitigate gene imbalance in unbalanced conceptions, aberrant inactivation in balanced X-autosome translocations can paradoxically cause functional imbalance. This possibility should be carefully considered when evaluating reproductive risks in female carriers.

**GP6: Multi-omics insights reveal molecular signatures of metabolic alterations associated with breast cancer-related lymphoedema**

Khairunnisa' Md Yusof[1,2,3*], Sabrina Ambok Malek[1], Kelly A. Avery-Kiejda[3], Benjamin Lau Yii Ching[4], Hamizah Shahirah Hamezah[5], Shafinah Ahmad Suhaimi[2,6], and Rozita Rosli[2]

*[1]International Medical School, Management and Science University, Selangor, Malaysia; [2]UPM-MAKNA Cancer Research Laboratory, Institute of Bioscience, Universiti Putra Malaysia, Selangor, Malaysia; [3]College of Medicine, Health and Wellbeing, The University of Newcastle, New South Wales, Australia; [4]Malaysian Palm Oil Board, Selangor, Malaysia; [5]Institute of Systems Biology, Universiti Kebangsaan Malaysia, Selangor, Malaysia; [6]Advanced Medical and Dental Institute, Universiti Sains Malaysia, Pulau Pinang, Malaysia*

*Introduction:* Breast cancer-related lymphoedema (BCRL) is defined as abnormal fluid retention resulting from obstructive lymphatic vessels due to cancer treatment or obesity. The present study aimed to identify molecular signatures associated with BCRL to gain further insight into its pathophysiology. *Materials & Methods:* Blood serum samples were obtained from 46 breast cancer survivors with (BCRL) and without lymphoedema (non-BCRL). MiRNA-sequencing was performed on 14 samples (BCRL *n*=7 vs non-BCRL, *n*=7) to characterise regulated miRNAs while protein profiling using liquid chromatography-mass spectrometry approach was employed on all 46 samples (BCRL, *n*=23 vs non-BCRL, *n*=23) to identify differentially expressed proteins in both groups. Bioinformatics analyses were performed to identify miRNAs, target genes, proteins, functional enrichment, and regulated pathways. *Results:* The transcriptomic and proteomic analyses revealed 16 miRNAs (i.e *hsa-miR-144-5p, hsa-miR-3199, hsa-miR-7-5p, hsa-miR-3733, hsa-miR-151a-3p, hsa-miR-199b-3p*) and four proteins (*PLG, SERPING1, APOC2, and APOH*) were significantly and differentially expressed in BCRL group. Analysis of miRNAs showed that target genes (i.e *HIF-1, IGF1, HGF, ARF1*, and *MAPK1*) were enriched in inflammation and metabolic-associated pathways such as HIF-1 signalling, ErbB, MAPK, and insulin signalling pathways. Protein analysis indicated cholesterol metabolism, blood coagulation and complement cascade, as well as PPAR signalling pathway were regulated in BCRL group. *Discussion:* Metabolic pathways (mainly carbohydrate and lipid) and blood coagulation cascade have been previously identified to be dysregulated in secondary lymphoedema. In line with the reported studies, the findings of the current investigation may help to support and further elucidate the underlying molecular mechanisms and circulating biomarkers involved in BCRL.

**GP7: Molecular classification of endometrial carcinoma: A single-centre study - Subang Jaya Medical Centre (SJMC) retrospective data**

Che Zairieha Che Zainudin[1], Bee Suan Tay[1], Qing Min Ng[1], Nurul Syahirah Mazhar[1], Ning Yi Yap[1], Yoke Kqueen Cheah[2,3], Pathmanathan Rajadurai[1,4]

*[1]Molecular Diagnostic Services, Laboratory, Subang Jaya Medical Centre, Selangor, Malaysia, [2]Department of Biomedical Sciences, Faculty of Medicine and Health Sciences, University Putra Malaysia, Selangor, Malaysia, [3]UPM-MAKNA Cancer Research Laboratory, Institute of Bioscience, Universiti Putra Malaysia, Serdang, Selangor, Malaysia, [4]Jeffrey Cheah School of Medicine & Health Sciences, Monash University, Bandar Sunway, Selangor, Malaysia*

*Introduction:* Current international guidelines recommend that molecular classification of endometrial carcinoma (EC) be incorporated with histopathological assessment. However, molecular profiling of EC is not yet widely implemented in Malaysia, and local data is limited. This study aims to characterise the molecular subtypes of EC within the SJMC cohort. *Materials &*

*Methods:* We retrospectively analysed 88 EC cases diagnosed between November 2021 and April 2025, assessing for polymerase epsilon exonuclease (*POLE*) mutations, tumour protein P53 (*TP53*) alterations and mismatch repair (MMR) deficiency. This study received institutional ethics approval (Ref No.: 202504.4). *Results:* Endometrioid carcinoma was the predominant histological subtype (93.2%). *POLE* mutations were identified in 8.0% (7/88) of cases with the most prevalent hotspot mutations, P286R and V411L, were detected in three cases each. *TP53* alterations were found in 22.7% (20/88), and MMR deficiency was observed in 18.2% (16/88) of cases. No Specific Molecular Profile (NSMP) was noted in 47.7 % (42/88) while 3.4% (3/88) of cases exhibited multiple classifiers. *Discussion: POLE*-mutant tumours, which are associated with a favourable prognosis, accounted for 8.0% of the cohort. MMR deficient and NSMP subtypes were associated with intermediate prognosis (65.9%), while *TP53*-altered tumours (22.7%) conferred poor prognosis. Integrating molecular classification into routine endometrial cancer management can significantly enhance prognostic assessment and therapeutic decision-making. This study, conducted in a private Malaysian healthcare setting, establishes foundational molecular data for endometrial cancer in Malaysia, and underscores the need for wider adoption of molecular diagnostics.

**GP8: Effects of kaempferol on glycosaminoglycan synthesis: insights into substrate reduction therapy on primary fibroblast for mucopolysaccharidosis type II**

Fatimah Diana Amin Nordin[1], Siti Aishah Mohd Erham[1], Affandi Omar[1], Julaina Abdul Jalil[1]
*[1]IEM & Genetics Unit, Nutrition, Metabolism & Cardiovascular Research Centre, Institute for Medical Research, National Institutes of Health, Ministry of Health Malaysia, Selangor, Malaysia*

*Introduction:* Mucopolysaccharidosis type II (MPS II) is a rare genetic disorder caused by a deficiency of iduronate-2-sulphatase; resulting in the accumulation of glycosaminoglycans (GAGs). Flavonoids such as kaempferol have demonstrated promising therapeutic potential in substrate reduction therapy (SRT). The objective of this study is to investigate the effects of kaempferol on glycosaminoglycan synthesis in MPS II patient fibroblasts. *Materials & Methods:* Fibroblasts from eight MPS II patients were seeded into 96-well cell culture plate at a density of $3x10^4$ cells/well. After 24 hours of incubation, the medium was replaced with fresh medium supplemented with kaempferol at concentrations of 5 µM, 30 µM, and 60 µM, and incubated for another 96 hours. GAGs measurement was assessed using 1,9-dimethylmethylene blue (DMB) assay. Total GAGs were quantified and normalised to total protein content, and expressed as µg GAGs per mg of protein. *Results:* Kaempferol treatment led to a reduction in GAGs accumulation in fibroblasts derived from MPS II patients. Notably, two out of eight patients exhibited significant reduction in GAGs levels at kaempferol concentrations of 30 µM ($p < 0.001$) and 60 µM ($p < 0.01$). However, the overall effect across all patient samples was not statistically significant ($p > 0.05$). *Discussion:* Significant reductions in GAGs accumulation were observed in two patients, both of whom carrying c.1079T>G gene mutation. The non-significant result across all patients suggests a potential influence of patient-specific variability in treatment response. These findings indicate that kaempferol may serve as a potential SRT agent for MPS II patients with c.1079T>G gene mutation.

**GP9: When extra makes a difference: A case of tetrasomy 9p**

Wan Norizzati WMZ[1], Sarimah S[1], Nor Balqish Faranija S[1], Hashima H[1], Huey Yin Leong [2],Loi Khim Chin[1]
*[1]Department of Pathology, Hospital Tunku Azizah, Ministry of Health Malaysia, Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia; [2]Genetics Department, Hospital Kuala Lumpur, Ministry of Health Malaysia, Wilayah Persekutuan Kuala Lumpur, Malaysia.*

*Introduction:* Tetrasomy 9p which was first reported in 1973 by Ghymers et al. is a rare chromosomal abnormality, resulting from an isochromosome derived from the short arms of chromosome 9. It is associated with a broad phenotypic spectrum including developmental delay, craniofacial dysmorphism, and congenital anomalies. *Case report:* We report a case of a 9-month-old boy referred for evaluation of dysmorphic features, laryngomalacia, communicating hydrocephalus, and failure to thrive. He is the first child of a non-consanguineous couple with no family history of genetic disorders. Cytogenetic analysis of peripheral blood revealed a non-mosaic isochromosome 9p in all metaphases examined, with a karyotype of 47,XY,+i(9)(p10)dn. Whole chromosome painting for chromosome 9 confirmed the aberration. Parental karyotypes were normal, consistent with a de novo origin. *Discussion:* Isochromosome 9p may encompass the entire short arm and, in some cases, heterochromatic or euchromatic segments of the long arm. Clinical phenotypes are variable and may include growth restriction, psychomotor and intellectual delays, craniofacial abnormalities, skeletal anomalies, and cardiac defects. The chromosomal rearrangement likely arises from maternal meiosis II nondisjunction followed by centromeric misdivision, resulting in the duplication of the short arm and loss of the long arm of chromosome 9. Although this aberration appears non-mosaic in peripheral blood, tissue mosaicism cannot be excluded and may influence clinical severity. Early diagnosis is essential for clinical management, prognostic assessment, and genetic counselling.

**GP10: From balanced to unbalanced: Consequences of a cryptic parental translocation in a child with 22q13 deletion and 20q13 duplication**

Wan Norizzati WMZ[1], Rui Yuan Kuah[1], Emynurshiela A[1], Nor Balqish Faranija S[1], Hashima H[1], Huey Yin Leong[2], Loi Khim Chin[1]
*[1]Department of Pathology, Hospital Tunku Azizah, Ministry of Health Malaysia, Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia;[2]Genetics Department, Hospital Kuala Lumpur, Ministry of Health Malaysia, Wilayah Persekutuan Kuala Lumpur, Malaysia.*

*Introduction:* Rare neurodevelopmental disorder Phelan-McDermid syndrome (PMS), also known as 22q13.3 deletion syndrome, is caused by the loss of chromosome 22's distal long arm. Common manifestations are global developmental delay (GDD), neonatal hypotonia, autistic traits, and craniofacial dysmorphism. The SHANK3 gene, often deleted in PMS, plays a key role in synaptic development and function. *Case Report:* 1-year-old girl who presented with GDD, axial hypotonia, limb hypertonia, dystonia, hepatomegaly, and dysmorphic features such as frontal bossing and a bulbous nasal tip. Brain MRI showed corpus callosum

dysgenesis and ventriculomegaly. Whole Exome Sequencing (WES) detected a heterozygous distal deletion on chromosome 22q13 and a duplication on chromosome 20q13. Parental cytogenetic and FISH analyses were performed to investigate the origin of these findings. The results revealed that the father carried a balanced translocation involving the long arms of chromosomes 20 and 22, suggesting that the child's unbalanced rearrangement likely arose from this cryptic parental translocation. This probably caused the child's unbalanced rearrangement to happen. *Discussion:* The co-occurrence of a 22q13 deletion and a 20q13 duplication is rare and may explain the patient's complex phenotype. SHANK3 and potentially ARSA contribute in the 22q13 deletion, which correlates to lysosomal function. Though its impact is less acknowledged, the 20q13 duplication may add further effects. This case highlights the importance of comprehensive genomic testing and parental chromosomal analysis in children with unexplained neurodevelopmental disorders and adds to the expanding clinical spectrum of PMS.

**GP11: Artificial intelligence (AI) and molecular dynamics simulation (MD)-based predictions of PDHA1 variants in Malaysian patients**

Ernie Zuraida Ali[1], Tengku Hanis Nuha Tuan Zaimi[1], Mohd Khairul Nizam Mohd Khalid[1], Julaina Abdul Jalil[1], Nur Amira Hidayah Ahmad[1], Yusnita Yakob[2], Nor Azimah Abdul Azize[3], Ngu Lock Hock[3]

*[1]Inborn Error of Metabolism and Genetic Unit, Institute for Medical Research, Ministry of Health Malaysia, Selangor, Malaysia; [2]Molecular Diagnostics Unit, Institute for Medical Research, Ministry of Health Malaysia, Wilayah Persekutuan Kuala Lumpur; [3]Department of Genetics, Hospital Kuala Lumpur, Ministry of Health Malaysia, Wilayah Persekutuan Kuala Lumpur.*

*Introduction:* Pyruvate dehydrogenase Complex (PDHc) has a vital role in cellular energy production in mitochondria. However, mutation at pyruvate dehydrogenase E1 α subunit (PDHA1) has been linked to a genetic disease, PDHA1 deficiency that alters its function in converting pyruvate into acetyl-coA. Functional studies on the effects of mutations in the PDHA1 gene are limited. Therefore, this study aims to investigate the effects of PDHA1 gene mutations in patients using artificial intelligence (AI) approach and computational methods. *Materials & Methods:* 12 mutations were initially evaluated using computational tools and tested using AI tools such as Evolutionary Model of Variant Effect (EVE), Evolutionary Scale Modeling (ESM-fold) and AlphaMissense (AM). PDHA1 protein models were generated based on the PDHc structure (PDB ID: 3EXE) using MODELLER 10.5 and subsequently validated using SAVES v6.1. Molecular dynamics simulations were performed using GROMACS 2020.6 to inspect conformational changes, with visualisation carried out using PyMOL and ChimeraX. *Results:* Nine novel mutations were discovered whereas another 3 mutations have been reported in the literature. Seven out of eight missense mutations predicted using AI were classified as pathogenic. In addition, computational analysis indicated that all missense mutations induced conformational changes compared to wild-type protein. Structural analysis also revealed that a frameshift mutation resulted in an elongated protein structure, while two other mutations produced truncated proteins. *Conclusion:* In conclusion, the combination of AI and MD-based methods provided comprehensive prediction on the effect of *PDHA1* mutations in Malaysian patients. Both methods proved to be reliable predictors of pathogenicity, particularly missense variants. These approaches improve understanding of mutation-specific effects and enable to provide earlier diagnosis in clinical settings. However, large-scale validation is required before these tools can be integrated into standard variant interpretation frameworks. Nevertheless, these preliminary findings are promising.

**GP13: Rare de novo partial trisomy 8 mosaicism in a dysmorphic newborn: A case report**

Nurul Diyanah Kamarudin, Aziati Azwari Annuar, Wan Nur Amalina Zakaria, Hidayati Husainy Hasbullah, Nazihah Mohd Yunus, Siti Mariam Ismail, Norhidayah Ramli, Nik Mohd Zulfikri Mat Zin

*Human Genome Centre, School of Medical Sciences, Health Campus, Universiti Sains Malaysia, Kubang Kerian, Kelantan, Malaysia; Hospital Pakar Universiti Sains Malaysia, Kubang Kerian, Kelantan, Malaysia*

*Introduction:* Trisomy 8 mosaicism is a rare chromosomal abnormality, occurring in approximately 1 in 50,000 births, with partial trisomy 8 mosaicism being even rarer. Here, we present the first reported case of partial trisomy 8 mosaicism with a terminal deletion of 8p21. *Case Report:* A term newborn of a healthy 34-year-old mother exhibited multiple dysmorphic features, including craniofacial anomalies (scaphocephaly, prominent forehead, gingival hypertrophy, high-arched palate, receding chin), limb abnormalities (overlapping fingers, camptodactyly, a deep palmar crease), and a significant cardiac defect (large dysplastic heart). Ultrasound findings revealed no corpus callosum agenesis and no genitourinary system anomalies. No history of consanguinity or genetic disorders were reported. Karyotyping and FISH analysis confirmed a rare mosaic karyotype: 47,XX,+del(8)(p21)[8]/46,XX[24]. ish +del(8)(wcp8+). Parental karyotyping were normal. *Discussion:* Patients with trisomy 8 mosaicism have variable clinical presentation ranging from early death to being nearly normal. Common features include a prominent forehead, deep-set eyes, hypertelorism, thick everted lips, camptodactyly, and deep palmar or/and plantar creases, which are distinctive of trisomy 8 mosaicism. Intellectual disability and renal anomalies are frequently reported, with congenital heart defects affecting 25% of cases. Increased risk of leukaemia and myelodysplastic syndrome was also observed. Some of our patient's features overlap with known mosaic trisomy 8 phenotypes, thus reinforcing its place in the spectrum of mosaic full trisomy 8 syndrome. Cytogenetics combined with molecular cytogenetics remain key in detection of full or partial trisomy 8 mosaicism syndrome due to its extremely variable clinical presentation.

**GP14: Cytogenetic signatures of gene amplification in acute myeloid leukaemia: A case series**

Durar Aqilah Zamri[1], Wan Norizzati WMZ[1], Noor Ayutika Ahmad[1], Nur Amirah Liyana Razeman[1], Nur Ashikin Azemi[1], Yi-Ting Cheng[2], Loi Khim Chin[1]

*[1]Genetics Laboratory, Department of Pathology, Hospital Tunku Azizah, Ministry of Health Malaysia, Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia; [2]Department of Pathology, Hospital Balik Pulau, Ministry of Health Malaysia, Pulau Pinang, Malaysia*

*Introduction:* Gene amplification is a key oncogenic mechanism that drives the overexpression of otherwise normal cellular proteins.

In neoplasia, it is cytogenetically detectable as extrachromosomal double minutes (dmin), intrachromosomal homogeneously staining regions (hsr), or ring chromosomes (r). While these features are frequently observed in solid tumours, they are rare in leukaemia, occurring in fewer than 1% of acute myeloid leukaemia (AML) cases with abnormal karyotypes. In haematological malignancies, gene amplification most commonly involves *MYC* (8q24.21) or *KMT2A* (11q23). *Case report:* We describe a series of four AML cases diagnosed between 2022 and 2024, each showing cytogenetic evidence of gene amplification involving either *MYC* or *KMT2A*. Case 1 was a 61-year-old female with a complex karyotype which include 5q deletion, isochromosome 17q, and gain of the X chromosome, demonstrated dmin carrying *KMT2A* amplification confirmed by fluorescence in situ hybridisation (FISH) with a break-apart probe. Cases 2 and 3 were a 76-year-old male and a 69-year-old female, respectively, where both exhibited dmin as the sole cytogenetic abnormality involving *MYC* amplification. Case 4 was an 81-year-old male with a complex karyotype and showed dmin, hsr, and two ring chromosomes, all involving *MYC* amplification. *Discussion:* Gene amplification in AML is typically associated with older age, complex karyotypes, and poor prognosis. Notably, in two of our cases, dmin was the sole cytogenetic abnormality, suggesting that amplification alone may be sufficient for leukaemogenesis in certain cases. This series supports the role of *MYC* and *KMT2A* amplification as oncogenic hallmarks in AML and highlights the importance of recognising these rare cytogenetic features during diagnostic evaluation.

**GP15: Complex chromosomal rearrangement in a newborn arising from biparental translocations: A rare cytogenetic finding in a family with recurrent pregnancy loss**

Sarimah Samulong[1], Farah Amalina Mohd Zulkufli[1], Ariff Shah Haris[1], Hafidzshuhada Yahya[1], Hashima Hashim[1], Loi Khim Chin[1]
*[1]Department of Pathology, Hospital Tunku Azizah, Ministry of Health Malaysia, Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* Complex chromosomal rearrangements (CCRs) are structural abnormalities involving three or more chromosomal breakpoints and the exchange of genetic material between at least two chromosomes. These rearrangements can result in partial trisomy or monosomy, often associated with dysmorphic features and congenital anomalies. *Case report:* We report a rare familial case of a live-born female with a derivative chromosome 4 and a translocation t(3;11). She is the only viable offspring in a family with a history of four miscarriages. The proband presented with severe intrauterine growth restriction (IUGR), low-set ears, bilateral microphthalmia, hypertelorism, cleft palate, clinodactyly, trisomic finger, short sternum, microstomia, and micrognathia—features suggestive of an underlying unbalanced chromosomal abnormality. Conventional cytogenetic analysis was performed on peripheral blood lymphocytes of the proband and her parents using standard culture and harvesting protocols. GTG banding at 400–550 band resolution was applied, and 20 metaphases were analysed. Karyotyping was interpreted following ISCN 2024 guidelines. *Discussion:* The proband demonstrated a karyotype of 46,XX,t(3;11)(q13.1;q13.2)mat,der(4)t(4;10)(q35;q24)dpat. The father carried a balanced translocation t(4;10), and the mother carried a balanced translocation t(3;11). Consequently, the proband inherited a paternally derived unbalanced derivative chromosome 4 and a maternally derived balanced translocation 3;11, resulting in a complex chromosomal rearrangement involving both parental contributions. *Discussion:* This case highlights how dual parental rearrangements can increase the risk of unbalanced gametes and recurrent pregnancy loss. Genetic counselling is essential for reproductive risk assessment and consideration of prenatal or preimplantation genetic testing.

**GP16: Tissue-specific upregulation of mir-34a in cervical squamous cell carcinoma**

Ahmad Shahir Mohamad Nazri[1], Nazihah Mohd Yunus[1], Aziati Azwari Annuar[1], Ahmad Aizat Abdul Aziz[1], Mohd Pazudin Ismail[2], Nur Asyilla Che Jalil[3], Daniel Roza Duski[4]
*[1]Human Genome Centre, School of Medical Sciences, Health Campus, Universiti Sains Malaysia, Kelantan; [2]Department of Obstetrics and Gynaecology, School of Medical Sciences, Health Campus, Universiti Sains Malaysia, Kelantan; [3]Department of Pathology, School of Medical Sciences, Health Campus, Universiti Sains Malaysia, Kelantan; [4]Department of Obstetrics and Gynaecology, Hospital Sultan Ismail, Ministry of Health Malaysia, Johor Bahru*

*Introduction:* MicroRNAs (miRNAs) play a pivotal role in cervical cancer pathogenesis. This study aimed to evaluate the expression patterns of miR-34a and miR-451a in cervical cancer tissue compared to adjacent normal tissue, and among different histological subtypes. *Materials & Methods:* Forty-eight paired cervical cancer and adjacent normal tissues were analysed for expression levels of miR-34a and miR-451a using reverse-transcription quantitative polymerase chain reaction (RT-qPCR). Relative expression was calculated via the Livak method ($2^{-\Delta Ct}$ and $2^{-\Delta\Delta Ct}$). The Wilcoxon signed-rank test was used for paired comparisons, and the Kruskal-Wallis test for between-group analysis. *Results:* The 48 paired cervical cancer samples consisted of squamous cell carcinoma (SCC, n=29), adenocarcinoma (n=11), and neuroendocrine carcinoma (NEC, n=8). Overall, no significant difference was observed in miR-34a (p=0.136) or miR-451a (p=0.454) expression between tumour and adjacent normal tissue. However, subgroup analysis revealed that miR-34a was significantly upregulated in SCC tissue compared to its matched normal tissue (median: 0.072 vs 0.051; p=0.030), while no significant differences were found in adenocarcinoma or NEC subtypes. miR-451a showed no significant paired differences in any subtype. Comparison of tumour tissues across histological subtypes showed no statistically significant differences in expression of either miR-34a (p=0.110) or miR-451a (p=0.591). *Discussion:* Despite being known as a tumour-suppressor miRNA, the significant upregulation of miR-34a in SCC may suggest a subtype-specific regulation and role of miR-34a in cervical cancer. miR-451a expression however did not differ significantly. Limitations of this study include small sample size, unequal distribution among groups, tissue heterogeneity and potential external factors that may influence miRNA expression.

**GP17: Intersecting genomic anomalies: A case of ectrodactyly and ocular dysgenesis with 16p11.2 duplication and balanced t(2;7)(q32;q21) translocation**

Rose Adzrianee Adnan[1], Ruzi Hamimi Razali[1], Fatimah Azman[2], Nur Amirah Liyana[2], Eva Foong[2], Roshaidie Abdul Rashid[2], Hashima Hashim[2], Loi Khim Chin[2]

*[1]Department of Pathology, Faculty of Medicine, Universiti Teknologi MARA, Sungai Buloh, Selangor, Malaysia; [2]Genetic Laboratory, Department of Pathology, Hospital Tunku Azizah, Ministry of Health Malaysia, Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia.*

*Introduction:* Chromosomal microarray analysis has emerged as a pivotal tool in diagnosing congenital dysmorphisms and neurodevelopmental disorders, often revealing pathogenic copy number variations (CNVs) that may not be detected through conventional cytogenetic methods. *Case report:* We present a unique case of a 4-year-old boy with ectrodactyly, hearing loss, corneal opacities, anterior segment dysgenesis and developmental delay. Conventional karyotyping revealed that he was a balanced translocation carrier of t(2;7)(q32;q21). Concurrently, microarray analysis uncovered a pathogenic 16p11.2 duplication variant and three variants of uncertain significance on chromosome 1p, 9q and 17p, respectively. Both parents have normal karyotypes. *Discussion:* As far as we are aware, there have been no reported cases of t(2;7)(q32;q21) in the literature. Duplication of 16p11.2 as found in this patient has been documented in the literature and it is associated with a spectrum of neurodevelopmental impairments including intellectual disability which explains the developmental delay in this patient. Reported cases of 7q21 microdeletion have shown that it is associated with split-hand/foot malformation but copy number anomalies were not detected at the 7q21 region in this patient through microarray analysis. The patient would benefit from further molecular study, such as next-generation sequencing, to evaluate the possibility of having DNA sequence mutation. This case underscores the complexity of interpreting multiple genomic alterations and highlights the necessity for integrated genetic analyses to confirm diagnosis and to guide management strategies in paediatric cases with dysmorphism and neurodevelopmental disorders.

**GP18: Distinguishing pathogenic deletions from variants: Genotype-phenotype analysis of a chromosome 9q13-q21 deletion**

Syaedzatul Syazwani Ridzuan[1], Emynursheila Anuar[1], Hashima Hashim[1], Loi Khim Chin[1]

*[1]Department of Pathology, Hospital Tunku Azizah, Ministry of Health Malaysia, Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur.*

*Introduction:* The chromosome 9 pericentric region has a complex genomic architecture. It includes diverse heterochromatic and euchromatic polymorphic variants. *Case report:* A 3-year-old girl presented with down-slanting palpebral fissures, a smooth philtrum, a wide nasal tip, flared lateral eyebrows, and square-shaped fingers. Peripheral blood samples were obtained for lymphocyte culture. G-banding was then performed on the child and her parents. Cytogenetic analysis revealed a 9q13–q21 deletion in both the girl and her father. These findings raise important questions regarding the clinical relevance, penetrance, and pathogenicity of this chromosomal abnormality. *Discussion:* Literature review reveals that the 9q13-q21 region contains both benign polymorphisms and pathogenic microdeletions. Willatt et al. (2007) noted that certain euchromatic variants in this region are benign polymorphisms with no phenotypic effect. However, research by De Falco et al. (2023) has described a 9q21.13 microdeletion syndrome characterised by dysmorphic features, including low anterior hairline, hypertelorism, long philtrum, high palate, thin upper lip vermilion, and upslanted palpebral fissures, with candidate genes such as RORB and TRPM6 implicated in the phenotype. The proximity of the deletion breakpoints to these critical genes suggests potential pathogenicity, yet the absence of phenotypic features in the father indicates possible variable expressivity or that the deletion may be a benign polymorphism in this family. Cytogenetic methods have limitations that restrict the interpretation of chromosomal abnormalities. Therefore, advanced molecular cytogenetic techniques with C-banding and BAC-FISH are recommended for accurate characterisation of deletions, ultimately supporting informed genetic counselling and clinical management.

**GP19: Optimising treatment in early-stage breast cancer: Chemotherapy or de-escalation?**

Azlah Kamilah Azhari, Nenny NS, Lokzhashininimisha P, Nur Izzlyana I, Usha NG, Nur Aina NY, Fatin HM, Sayyidi Hamzi AR, Sharifah Noor Akmal SH, Mohd Hareeff M

*Cytogenetics and Molecular Diagnostics Lab, Reference Specialized Laboratory, Premier Integrated Labs Sdn. Bhd., Pantai Hospital Kuala Lumpur, Bangsar, Kuala Lumpur.*

*Introduction:* Breast cancer remains the most prevalent cancer among Malaysian women, accounting for 46.1% of all female cancer cases and 19.3% of cancer-related mortality. While incidence is rising, mortality is declining due to earlier diagnosis and therapeutic advances. The NCCN Guidelines (v4.2025) recommend the Prosigna® PAM50 assay for node-negative, hormone receptor-positive (HR+)/HER2-negative early-stage breast cancer (eBC) to assess the Risk of Recurrence (ROR) and guide adjuvant chemotherapy decisions. This study evaluates the clinical utility of the Prosigna in stratifying recurrence risk and supporting personalised treatment strategies. *Materials & Methods:* Thirty formalin-fixed paraffin-embedded (FFPE) tissue samples from HR+/HER2- eBC patients (July2024 - April 2025) were analysed using the Veracyte FFPE RNA Extraction Kit and Nanostring nCounter ® DX System. *Results:* The median patient age was 54 years (range 32-71). Most cases were invasive ductal carcinoma (76.7%), grade 2 (36.7%), and T1-N0 stage (66.7%). PAM50 subtyping revealed 76.7% Luminal A (LumA), primarily low-risk T1-N0 tumours. In contrast, 20% were Luminal B (LumB), including several high-risk T1-N0 and N1-3 cases. One basal-like high-risk case was identified in N1-3. LumA cases exhibited a favourable prognosis and responsiveness to endocrine therapy, while LumB and basal-like subtypes indicated poorer outcomes and higher recurrence risk. *Discussion:* Transitioning from outsourced testing in the UK to in-house analysis reduced turnaround time from 14 to 5 working days, enhancing clinical efficiency and timely decision-making. This study affirms the Prosigna assay's value in optimising risk-adapted therapy and advancing precision oncology in the Malaysian context.

**GP20: Enhancing variant detection in whole exome sequencing: Integrating artificial intelligence (AI) in a clinical genomics workflow in Premier Integrated Lab**

Fatin HM, Nenny NS, Lokzhashininimisha P, Azlah KA, Sayyidi-Hamzi AR, Roziana A, Hareeff M
*Cytogenetics and Molecular Diagnostics Lab, Reference Specialized Laboratory, Premier Integrated Labs Sdn. Bhd., Pantai Hospital Kuala Lumpur, Kuala Lumpur.*

*Introduction:* Whole-exome sequencing (WES) has become a pivotal diagnostic tool in clinical genetics by focusing on protein-coding regions where disease-causing mutations are most prevalent. This study highlights the application of explainable artificial intelligence (XAI) through EMEDGENE software in the analysis of WES data from 42 clinical cases processed at Premier Integrated Labs between 2024 and April 2025. *Materials & Methods:* Samples were obtained from formalin-fixed paraffin-embedded (FFPE) tissue and peripheral blood (EDTA) across a diverse age range (21 weeks' gestation to 71 years). Clinical indications included forensic (23.8%), prenatal (26.2%), and hereditary screening (50%) for rare disorders such as Duchenne muscular dystrophy, haemophilia, and Marfan syndrome. DNA extraction was performed using the Illumina DNA Prep with Exome 2.5 Enrichment panel (minimum coverage 50x), followed by library preparation and sequencing on the Illumina NextSeq 550 platform. Bioinformatics analysis utilised the DRAGEN v4 pipeline, with tertiary analysis powered by EMEDGENE's XAI-driven variant prioritisation. *Results:* The system effectively identified clinically relevant variants in genes including *RYR1, PKP2, MYBPC3* (forensic); *GATA4, KCNH2, FANCC* (prenatal); and *DMD, ENG, GATA2* (hereditary), using curated collective scientific evidence. This integration of AI-driven interpretation improved variant classification and clinical correlation based on phenotypic data provided by referring physicians. *Discussion:* Our findings support the utility of WES in providing timely and accurate molecular diagnoses across varied clinical settings. The use of explainable AI enhances diagnostic confidence and advances the application of precision medicine, enabling earlier intervention and improved patient outcomes.

**GP21: Cytogenetic profiling in clinically diagnosed Turner syndrome: A cross-sectional study**

Noor Ayutika Ahmad[1], Loi Khim Chin[1], Hashima Hashim[1], Eva Foong[1], Wan Norizzati WMZ[1]
*[1]Department of Pathology, Hospital Tunku Azizah, Ministry of Health Malaysia, Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* Turner syndrome is commonly associated with underlying X chromosome abnormalities. Cytogenetic analysis plays a vital role in confirming diagnoses and guiding clinical management. This study aims to characterise the chromosomal patterns in patients clinically diagnosed with Turner syndrome. *Materials & Methods:* Conventional G-banding analysis was performed on blood samples from 185 Turner syndrome patients received at our centre in 2024. Fluorescence *in situ* hybridisation (FISH) was used to confirm X or Y chromosome material in cases with ring, marker, Y, and isodicentric Y chromosomes. Results: Among 185 patients, 136 (73.5%) exhibited a normal 46,XX karyotype, while 49 cases (26.5%) demonstrated chromosomal abnormalities. Among these, 20 cases (40.8%) presented with the classical 45,X monosomy. Single cases of 46,XY and 47,XXX karyotypes were also identified. Additionally, three cases revealed structural abnormalities involving autosomes. The remaining 24 cases consisted of Turner syndrome variants, including 4 cases with isochromosome Xq and 1 case with a derivative X chromosome. Nineteen cases demonstrated mosaicism involving 45,X in combination with other cell lines such as 46,XX, 46,XY, 47,XXX, isochromosome Xq, ring X, derivative X and isodicentric Y chromosomes. *Discussion:* This study highlights the cytogenetic heterogeneity of Turner syndrome, reflecting a wide range of clinical phenotypes. Differential diagnoses should be considered in cases with autosomal structural abnormalities or normal chromosome results. Low-level mosaicism may also be missed, underscoring the importance of advanced genetic testing to ensure accurate diagnosis and effective clinical management.

**GP22: Mapping epidermal growth factor receptor mutations (EGFR) in Malaysian non-small cell lung cancer (NSCLC): A cornerstone of precision oncology**

Siti Syahirah Mat, Nor Khatijah Mohd Aris, Muhammad Ehsan Fitri Rusli, Mohd Harris Ibrahim Samsudin, Fatimah Azman, Loi Khim Chin
*Molecular Genetics Laboratory, Department of Pathology, Hospital Tunku Azizah, Ministry of Health Malaysia, Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction: EGFR* mutations are key oncogenic drivers in NSCLC, with higher prevalence in Asian populations. However, Malaysian data are limited despite its ethnic diversity. Local prevalence studies are essential to guide biomarker-driven treatment, ensure access to targeted therapies, and inform national lung cancer guidelines. *Materials & Methods:* This retrospective study analysed 10,611 NSCLC patients referred to the Molecular Genetics Laboratory at Hospital Tunku Azizah from January 2015 to May 2025. DNA was extracted from formalin-fixed paraffin-embedded tissue (FFPET) using the *cobas® DNA Sample Preparation Kit*, and *EGFR* mutation testing was performed with the *cobas® EGFR Mutation Test v2*, targeting 42 mutations in exons 18–21. *Results:* Among the patients included in the analysis, 36.6% tested positive for *EGFR* mutations, 57.7% were negative, and 5.1% yielded unsatisfactory results. The most prevalent mutation was the exon 19 deletion, observed in 57.8% (n = 2248) of positive cases, followed by the exon 21 L858R point mutation at 29.3% (n = 1139). A total of 202 patients harboured double *EGFR* mutations, comprising either dual sensitizing mutations or a combination of sensitizing and resistance mutations. Female patients demonstrated a slightly higher frequency of *EGFR* mutations (55.5%) compared to males. By ethnicity, the highest mutation frequency was observed among Malay patients, followed by Chinese and Indian populations. *Discussion:* The high prevalence of *EGFR* mutations supports routine molecular testing at diagnosis to identify candidates for first-line *EGFR* TKIs. Expanding access to broader multi-gene testing is also justified to guide targeted therapy in *EGFR*-negative patients lacking actionable drivers.

**GP23: Cytogenetic analysis of balanced and unbalanced chromosomal rearrangements in three unrelated families: Implications for clinical phenotype and genetic counselling**

Nor Hidayah JAN[1], Raja Teh Sophia RH[1], Siti Zaharah Farah Dura AB[1], Emynurshiela A[1], Farah Amalina MZ[1], Kamalru Azman D[1], Noor Ayutika A[1], Wan Norizzati WMZ[1], Aminah M[1], Hashima H[1], Loi Khim Chin[1]

*[1]Department of Pathology, Hospital Tunku Azizah, Ministry of Health Malaysia, Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* Balanced chromosomal rearrangements, such as reciprocal translocations and insertions, remain silent in carriers. However, they pose a considerable reproductive risk due to the possibility of producing gametes with unbalanced genetic materials, which may result in miscarriages, congenital anomalies, or developmental disorders in offspring. High-resolution G-banded karyotyping remains essential for characterising these anomalies and ultimately facilitating reproductive and genetic counselling. *Case report:* Chromosome analysis of three unrelated families was performed. In the first family, a proband who died at three months old and her cousin, both of whom had syndromic features, were found to have an unbalanced der(7) resulting from translocation 7;11. The abnormality was inherited from their respective fathers, in which both siblings carried balanced t(7;11)(q35;p15) chromosomes. In the second family, a proband exhibited dysmorphic features, and chromosomal analysis revealed a recombinant chromosome 7 with a partial deletion of chromosome 7q. His sibling, who had learning difficulties, carried a recombinant chromosome 9 with a partial duplication involving the same region. Both rearrangements resulted from a paternal balanced ins(9;7)(p23;q31.3q31.1) chromosomes. In the third family, a female with a history of recurrent first-trimester miscarriages had a balanced t(11;18)(q21;p11.2). The similar aberration was also identified in three clinically asymptomatic siblings. *Discussion:* These findings illustrate the diverse phenotypic consequences associated with unbalanced chromosomal segregation in offspring of balanced carriers. Cytogenetic analysis remains essential for detecting large chromosomal rearrangements, providing critical insights into inherited structural abnormalities and serving as a cornerstone for familial screening and genetic counselling.

**GP24: Combined use of cytogenetic and molecular methods in the diagnosis of azoospermia factor region microdeletion in men: Hospital Tunku Azizah experience**

Ahmad Akmal Azman[1], Syazwani Ridzuan[1], Ashikin Azemi[1], Amirah L. Razeman[1], Fatimah Azman[1], Hashima Hashim[1], Loi Khim Chin[1]

*[1]Department of Pathology, Hospital Tunku Azizah, Ministry of Health Malaysia, Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia.*

*Introduction:* Azoospermia factor region (AZF) located on the long arm of the chromosome Y (Yq11), is involved in male fertility. Deletions within this region can cause spermatogenic failure and azoospermia, leading to infertility. *Case report:* We present three rare cases of male infertility diagnosed using a combination of multiplex ligation-dependent probe amplification (MLPA) and conventional cytogenetics methods. The three patients- Patient A, Patient P and Patient Q - presented with azoospermia. All three patients were detected to have deletions in the AZFbc region by MLPA; however, the ratios were irregular and inconsistent. Patient A has an irregular partial deletion ranging from probe Yp11.31 (SRY gene probe) to Yq11.221 (NLGN4Y gene probe). Conventional cytogenetic analysis revealed that this patient had mosaic Turner syndrome with 45,X[18]/46,XY[12] karyotype. For patients P and Q, both exhibited partial duplication of probe Yp11.31 to Yq11.222 and probe Yp11.31. to Yp.221 respectively. Conventional cytogenetics and FISH using SRY/ CEPX and CEP Y probes identified isodicentric Y chromosome in both patients. These chromosomal numerical and structural abnormalities explained the irregular ratio seen in their MLPA testing results. All the above conditions are associated male infertility and azoospermia. *Discussion:* Molecular technique such as MLPA is a fast and robust technique often used to detect microdeletions and duplications in AZF region of the Y-chromosome. However, MLPA has its own limitations. A combined approach involving molecular techniques and conventional cytogenetic analysis is essential in the diagnosis of male infertility.

**GP25: Divergent Genomic Profiles in Monozygotic Twins with chILD: A Comparative AI-Driven and In-House Bioinformatics Analysis**

Sasi Devi Saminathan[1], Ahmad Akmal Azman[1], Sarimah Samulong[1], Fatimah Azman[1], Tan Lu Ping[3], Lui Sze Chiang[2], Maria Kamal[2], Fafwati Faridatul Akmar Mohammad[2], Adi Ratna Mat Ripen[2], Asiah Kassim[2], Roziana Ariffin[1]

*[1]Molecular Genetics Laboratory, Genetics Laboratory, Department of Pathology, Hospital Tunku Azizah, Ministry of Health Malaysia, Kuala Lumpur, Malaysia; [2]Child Respiratory Unit, Peadiatric Department, Hospital Tunku Azizah, Ministry of Health Malaysia, Kuala Lumpur, Malaysia; [3]Institute for Medical Research, National Institutes of Health, Ministry of Health Malaysia, Jalan Setia Murni U13/52, Bandar Setia Alam, 40170 Shah Alam, Selangor, Malaysia.*

*Introduction:* Childhood interstitial lung disease (chILD) comprises a spectrum of rare, genetically heterogeneous disorders that impair pulmonary function in children. Monozygotic twins provide a unique model to investigate both shared and divergent genetic contributors to disease expression, allowing for insights into genotype–phenotype correlations, post-zygotic mosaicism, and gene–environment interactions. This study aims to analyse and compare whole exome sequencing (WES) data from monozygotic twins diagnosed with chILD using both an AI-assisted platform (SOPHiA DDM™) and an in-house bioinformatics pipeline to identify clinically relevant variants, characterise concordant and discordant genomic profiles, and explore potential immunological contributors to disease pathogenesis. *Materials and Methods:* WES was performed on both twins and analysed via SOPHiA DDM™, an AI-enhanced cloud-based genomic analysis platform. Variant calls were compared with results from an in-house pipeline. Shared and unique variants were cross-referenced against ClinVar, OMIM, and literature for clinical significance and disease association. *Results:* Numerous shared variants were detected, including a variant in *PTEN*, a regulator of *PI3K/Akt* signalling with known involvement in pulmonary fibrosis. Notably, Twin 1 (CH01) harboured a unique INDEL in *TRNT1*, a gene implicated

in mitochondrial dysfunction and interstitial lung pathology. Twin 2 (CH34) exhibited a unique SNP in NLRP3, a gene associated with inflammasome-mediated inflammation. Shared variants in *KMT2D, PLCG2, C12orf57*, and *TBX1* were identified across both pipelines, suggesting contributions to immune or developmental components of the disease. *Conclusion:* Despite identical germline origins, rare post-zygotic and mosaic variants may contribute to phenotypic divergence in monozygotic twins with chILD. The integration of AI-guided analysis and traditional bioinformatics highlights complementary strengths in capturing disease-relevant variants and supports multi-layered interpretation strategies in rare disease genomics.

**GP26: A 10-year retrospective study on prenatal cytogenetic analysis**

Tay Chiew Hong, Mangaleswary A/P Kuppusamy, Vivek Prasad, Sharvin Manickam, Roziana binti Ariffin, Saira Bahnu Binti Mohamed Yousoof, Sayyidi Hamzi bin Abdul Raub, Mohd Hareeff bin Muhammed

*Cytogenetics and Molecular Diagnostics Lab, Reference Specialized Laboratory, Premier Integrated Labs Sdn. Bhd., Pantai Hospital Kuala Lumpur, Bangsar, 59100 Kuala Lumpur.*

*Introduction:* Prenatal diagnosis of chromosomal abnormalities has been practiced since the mid-1960s, with G-banded karyotyping remaining the gold standard for detecting numerical and structural abnormalities, often due to nondisjunction or chromosomal breakage. Diagnostic yield varies by indication: approximately 6% for advanced maternal age, 3% for positive biochemical screening, and significantly higher for foetuses with structural anomalies (49% in the first trimester and 17% in the second trimester). This study aims to retrospectively review a 10-year experience in prenatal foetal karyotype analysis. *Material & Methods:* Between 2014 and 2024, 6,996 prenatal cases were analysed in our laboratory using amniotic fluid, chorionic villus samples (CVS), cordocentesis, and products of conception (POC). *Results:* The average maternal age at diagnosis was 31.1 ± 4.2 years. Chromosomal abnormalities were detected in 1,494 of 6,996 cases (21%), with 52% showing foetal malformations on ultrasound and 29% identified as high-risk by NIPT. The most common abnormalities were Trisomy 18 (34%) and Trisomy 21 (32%). Other findings included Trisomy 13, Turner, Klinefelter, Jacobs, and Triple X syndromes, structural rearrangements like translocations, deletions, inversions, additions, ring chromosomes, mosaicisms. Abnormal karyotypes were significantly more frequent (59%) in women aged ≥35 years. *Discussion:* Foetuses with indications for amniocentesis have a significant risk of chromosomal abnormalities, making prenatal cytogenetic analysis essential for diagnosing birth defects, guiding genetic counselling, informing pregnancy decisions, and planning postnatal care. It is recommended for pregnancies with high-risk NIPT results or abnormal ultrasound findings.

**GP27: Characterisation of clinically actionable mutations in non-small cell lung cancer using targeted next-generation sequencing in a private healthcare setting**

Ho Keat Yie[1], Ervina Raja Api Wirjaya[1], Nur Syamimi Aqilah Hudri[1], Fatin Nadiah Mustaffa[1], Khoo Jo Lynn[1], Norziha Zainul Abidin[1], Yap Peak Shean[2], Teoh Kean Hooi[2,3], Wan Muhaizan Wan Mustaffa[2], Roziana Ariffin[1]

*[1]Genetic & Molecular Diagnostic Laboratory, Sunway Medical Centre, Selangor, Malaysia; [2]Anatomical Pathology Laboratory, Sunway Medical Centre, Selangor, Malaysia; [3]Department of Clinical Medicine and Surgery, School of Medical and Life Sciences, Sunway University*

*Introduction:* Lung cancer remains a leading cause of cancer-related mortality worldwide. Precision oncology has become essential in guiding targeted therapy, particularly in the management of non-small cell lung cancer (NSCLC). This study aimed to characterise the mutation profile in NSCLC patients using a targeted next-generation sequencing (NGS) panel for diagnostic, prognostic, and therapeutic purposes. *Materials & Methods:* NGS was performed on DNA and RNA extracted from FFPE samples of 27 NSCLC patients (aged 34-82 years; median: 61), with equal gender distribution. Sequencing analysis was conducted with a minimum read depth of 1000× and variants were reported using a ≥5% variant allele frequency (VAF) threshold. *Results & Discussion:* Clinically relevant mutations were detected in 96% (26/27, 95% CI: 81.7-99.3) of cases, with VAF ranging from 2.7% to 82.2%. Co-mutations observed in 52% (14/27, 95% CI:33.9-69.3). The most frequent alteration was EGFR, 48% (13/27, 95% CI: 30.7-66.0), including exon 19 deletions, L858R, G719A, T790M and EGFR amplification. Other notable mutations included TP53, 30% (8/27, 95% CI: 15.9-48.5), while ERBB2 and KRAS each showed 11% (4/27 95% CI: 5.92-32.5), and less commonly, ALK (5%), ROS1, BRAF, RET (3% each). Rare mutations were also found in CTNNB1 (5%) and PIK3CA (3%). Co-occurrence of TP53 mutations with other oncogenic drivers (EGFR, KRAS, BRAF, ERBB2) was observed in eight cases. High-VAF somatic mutations (VAF range: 41–83%) were observed in EGFR exon 19 deletion and L858R, ERBB2 non-frameshift insertion, TP53 Y220H, KRAS G12D and G12V, and PIK3CA G106R. These findings may suggest a possible germline origin, though confirmation would require matched normal tissue or blood testing. Clinically actionable mutations such as EGFR and ALK predict response to tyrosine kinase inhibitors (TKIs), while mutations in TP53 and PIK3CA, may inform prognosis and risk stratification. *Conclusion:* This study demonstrates the value of targeted NGS in identifying diverse and clinically relevant mutations in NSCLC. The findings reinforce the integration of precision oncology in private healthcare, enabling personalised treatment, improving diagnostic accuracy, and informing prognosis for lung cancer patients.

**GP28: Clinical application of a targeted next-generation sequencing (NGS) panel in colorectal cancer: Mutation detection and molecular insights**

Ervina Raja Api Wirjaya[1], Ho Keat Yie[1], Nur Syamimi Aqilah Hudri[1], Fatin Nadiah Mustaffa[1], Khoo Jo Lynn[1], Norziha Zainul Abidin[1], Yap Peak Shean[2], Teoh Kean Hooi[2,3], Wan Muhaizan Wan Mustaffa[2], Roziana Ariffin[1]

*[1]Genetic & Molecular Diagnostic Laboratory, Sunway Medical Centre, Selangor, Malaysia; [2]Anatomical Pathology Laboratory, Sunway Medical Centre, Selangor, Malaysia; [3]Department of Clinical Medicine and Surgery, School of Medical and Life Sciences, Sunway University*

*Introduction:* Next-generation sequencing (NGS) is a vital tool in precision oncology, allowing comprehensive detection of tumour-specific genetic alterations. In colorectal cancer (CRC), identification of actionable mutations, especially when integrated with

microsatellite instability (MSI) status supports personalised therapy. This study evaluates the utility and precision of a targeted NGS panel for detecting clinically relevant mutations in CRC, with correlation to MSI status. *Materials & Methods:* Thirteen FFPE tissue samples from CRC patients were retrospectively analysed using a targeted NGS panel covering 46 actionable genes. DNA and RNA were extracted, quantified, and sequenced per manufacturer protocols. Variant calling and annotation were conducted using validated bioinformatics pipelines. MSI status was available for 8 cases, in which 6 were microsatellite stable (MSS), 1 MSI-high (MSI-H) and 1 low probability MSI-H; while the other 5 cases remained undetermined. The cohort included patients aged 38–76 years (median 61), with a male predominance (62%). *Results & Discussion:* Somatic mutations were found in 92% (12/13, 95% CI: 66.7-98.6) of cases. The most frequently mutated gene was TP53; 77% (10/13, 95% CI:49.7-91.8), followed by PIK3CA; 31% (4/13, 95% CI: 12.6-57.6) and KRAS; 23% (3/13, 95% CI: 8.2-50.3). BRAF mutations were found in 15.4% (2/13, 95% CI: 4.3-42.2) while CTNNB1 mutation and gene amplifications in EGFR and ERBB2 were each detected in 8% of the cohort. Three mutations with high variant allele frequencies (VAF) of ≥40%; TP53 R273C and R282W and CTNNBB1 T41A, suggested potential clonal dominance or germline origin, however, further analysis would be needed to distinguish between somatic and germline events. In the MSI-H case, co-occurring activating mutations in KRAS and PIK3CA were observed, indicating a complex molecular profile with potential therapeutic implications. Most mutations were linked to key oncogenic pathways including MAPK and PI3K-AKT. *Conclusion:* This study highlights the practical utility of targeted NGS for identifying actionable mutations in CRC, supporting its integration into routine molecular workflows. Even in a small cohort, combining NGS with MSI profiling provided clinically relevant insights that may inform individualised treatment decisions. Larger studies are warranted to validate associations between MSI status and mutation burden.

## HAEMATOLOGY (HM)

**HM1: Adult orbital chloroma: A rare presentation of relapsed Acute Myeloid Leukaemia**

Geetha Nallappan, Siti Rafikka Rahem, Wan Hayati Mohd Yaakob, Siti Zubaidah Mustapha
*Department of Pathology, Hospital Tengku Ampuan Rahimah, Selangor, Malaysia*

*Introduction:* Myeloid sarcoma (MS), also known as chloroma, is a malignant extramedullary tumour composed of immature myeloid cells that replace normal tissue architecture. It may present de novo, concurrently with other myeloid neoplasms, or as a manifestation of disease relapse. While the orbital region is a common site of involvement in children, we highlight a rare case of unilateral periorbital MS in an adult, presenting as a relapse of acute myeloid leukaemia (AML) without bone marrow involvement. *Case report:* A 24-year-old male was diagnosed with AML in late May 2022, with 40% myeloblasts expressing CD19 aberration. He successfully completed a full course of chemotherapy and achieved complete remission by June 2022, with plans for a stem cell transplant. However, six months later, while preparing for the transplant, he developed right periorbital swelling. A CECT of the brain and orbit revealed a permeative bony lesion at the right zygoma with associated periorbital soft tissue involvement. An incisional biopsy was performed, and immunohistochemistry confirmed myeloid sarcoma. Interestingly, a concurrent bone marrow aspirate and biopsy showed no excess blasts. *Discussion:* MS occurs due to alterations in homing signals on leukaemic blast cells, disrupting their normal localisation in the bone marrow. It can indicate leukaemia progression or relapse, though relapse without bone marrow involvement is rare. Therefore, early recognition of MS, including rare infiltration sites, is crucial for timely, individualised treatment, given its high mortality risk and poor prognosis.

**HM2: Point-of-care diagnostic test for thalassaemia**

Noor Aini Anuwar[1], Nur Aqilah Tajul Lile[1], Siti Nurrazan Zulkifli[1], Saidatul Akmal Amir[2], Anisah Musa[2], Noor Farisah A Razak[2], Azrena Anee[2], Arthi Dhanabalan[3], Maslina Erdawaty Minhad[3], Raja Zahratul Azma Raja Sabudin[1]
*[1]Department of Pathology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia; [2]Department of Laboratory Diagnostic Services Hospital Canselor Tuanku Muhriz, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia; [3]Active Scientific Sdn. Bhd., Kuala Lumpur, Malaysia*

*Introduction:* To date, more than 8000 symptomatic thalassaemia patients in Malaysia and most of them required regular blood transfusion and chelation therapy to prevent complications. Availability of highly sensitive equipment in the screening for thalassaemia carriers will be greatly advantageous in high prevalence countries like Malaysia. Here, we present Gazelle Hb Variant, a paper-based microchip electrophoresis platform that enables the point-of-care diagnostic test for *β*-thalassemia using a whole blood sample. *Materials and Methods:* We evaluated the accuracy of Gazelle for the β-thalassaemia screening among 100 volunteer subjects at Haematology laboratory, Department of Laboratory Diagnostic Services, Hospital Chancellor Tuanku Mukhriz, UKM, Cheras. A total of 20 µL blood samples were mixed with dye and then applied onto cellulose acetate of the test cartridge. The results were then compared with Capillary 3 Octa by Sebia (France). Results: A total of 16 β-thalassaemic blood samples were found positive with Gazelle and the remaining were negative for β-thalassemia disease and trait. Gazelle quantifies Hb A, Hb F, and Hb A2/C/E, demonstrated high levels of correlation with the results reported through capillary electrophoresis by SEBIA (CE), yielding a Pearson correlation coefficient of 0.95 ($p<0.001$). *Discussion:* Gazelle is a portable, miniaturized version of the gold standard haemoglobin electrophoresis test method, user-friendly which able to interpret results in 8 minutes by providing accurate Hb A, Hb F, Hb S and Hb A2/C/E without requirement for extensive laborious infrastructure, making it more accessible, faster, and cost-effective, especially in low-resource or remote settings which beneficial for a large-scale screening and diagnosis of β-thalassemia.

**HM3: A rare case of acute megakaryoblastic leukaemia with RAM immunophenotype and CBFA2T3::GLIS2 fusion**

Woon Lee Yong[1], Khai Nee Koo[1], Alia Suzana Asri[1], Farah Azima Abdul Muttlib[1], Hafiza Alauddin[2], Raja Z. Azma[2], Mohd Fikri Mustapa[2], Sie Chong Doris Lau[3], C-Khai Loh[3], Nur Alyaa Afifah Md Shahri[4], A Rahman A Jamal[4]

*[1]Department of Diagnostic Laboratory, Hospital Tuanku Ampuan Besar Tunku Aishah Rohani, Universiti Kebangsaan Malaysia, Wilayah Persekutuan Kuala Lumpur, Malaysia; [2]Department of Pathology, Hospital Canselor Tunku Mukhriz, Universiti Kebangsaan Malaysia, Wilayah Persekutuan Kuala Lumpur, Malaysia; [3]Department of Pediatric, Universiti Kebangsaan Malaysia, Wilayah Persekutuan Kuala Lumpur, Malaysia; [4]UKM Medical Molecular Biology Institute, Universiti Kebangsaan Malaysia, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* The CBFA2T3::GLIS2 fusion gene is a rare oncogenic alteration linked to paediatrics non-Down Syndrome Acute Megakaryoblastic Leukaemia (non-DS AMKL), accounting for 3-10% of childhood AML. It is frequently associated with the RAM immunophenotype, characterised by bright CD56 with lacking expression of CD45, CD38 and HLA-DR. This is associated with grim clinical outcomes and forthcoming treatment challenges. *Case report:* We report a case of a one-year-old girl with partial sacral agenesis type II who presented with fever and lethargy. A full blood picture revealed severe anaemia (Hb:5.9g/dL), marked leucocytosis (WBC:79.8x$10^9$/L), severe thrombocytopenia (Platelets:13x$10^9$/L) with 23% of blasts. Bone marrow aspiration morphology and immunophenotyping findings confirmed the diagnosis of AMKL, as the blast was CD45 negative and expressed CD34, CD117, CD33, CD13, cyCD42a and cyCD61. As CD56 was not included in the initial panel, RAM immunophenotype was unrecognised at diagnosis. Karyotyping revealed complex karyotypes (47,XX,t(4;9)(q11;q34),del(16)(q24),+21) which are commonly associated with AMKL. Despite two courses of induction chemotherapy, lack of remission prompted subsequent targeted sequencing, which identified CBFA2T3::GLIS2 fusion. Her treatment was intensified to FLA-Ida regimen followed by an early haematopoietic stem cells transplant (HSCT). Unfortunately, the patient experienced disease relapse with 55% blasts, along with identification of RAM immunophenotype three months post-HSCT. She succumbed nine months following the initial diagnosis. *Discussion:* This case underscores the significant challenges in managing CBFA2T3::GLIS2 fusion AMKL, emphasising early genomic tests and future exploration of targeted therapies. The RAM immunophenotype serves as a rapid predictive marker for poor prognosis. Its incorporation into diagnostic immunophenotype is recommended to enable timely identification and effective intervention.

**HM4: Digital PCR vs RT-qPCR: A New Era in CML Monitoring**

Ramlah Mohamed Ibrahim[1], Raja Zahratul Azma Raja Sabudin[1], Azlin Ithnin[1], Mohd Fikri bin Mustapa[2], Siti Hawa Abu Amis[2], Nor Hidayati Sardi[2], Nor Rafeah Tumian[3]

*[1]Department of Pathology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia; [2]Department of Medicine, Laboratory Diagnostic Services, Hospital Canselor Tuanku Muhriz, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia; [3]Department of Laboratory Diagnostic Services, Hospital Canselor Tuanku Muhriz, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia*

*Introduction:* Chronic myeloid leukaemia (CML) is characterised by the *BCR::ABL1* fusion gene, resulting from the Philadelphia chromosome translocation. Accurate quantification of *BCR::ABL1* transcripts is essential for monitoring treatment response, detecting minimal residual disease (MRD), and determining eligibility for treatment-free remission (TFR). This study compares the performance of real-time quantitative PCR (RT-qPCR) and digital PCR (dPCR) in quantifying *BCR::ABL1* transcripts. *Materials & Methods:* Blood samples from 20 CML patients with confirmed *BCR::ABL1* fusion were collected at Hospital Canselor Tuanku Muhriz (HCTM), Kuala Lumpur. RNA was extracted and analysed using RT-qPCR (EntroGen BCR-ABL P210 One-Step Detection Kit) and dPCR (Dr. PCR™ BCR-ABL1 Major IS Detection Kit). Statistical analysis was performed to assess the correlation and accuracy between the two methods. *Results:* A moderate correlation ($R^2 = 0.769$) was observed between RT-qPCR and dPCR. RT-qPCR consistently overestimated *BCR::ABL1* levels in samples with high transcript expression. The Mann-Whitney U test revealed significant differences ($p < 0.05$), with dPCR providing more accurate and precise quantification. *Conclusion:* Although both methods can detect *BCR::ABL1* transcripts, dPCR offers superior sensitivity and precision, especially at lower transcript levels, making it a valuable tool for MRD assessment and TFR decision-making in CML management. Further research with larger cohorts is needed to validate these findings.

**HM5: A retrospective cross-sectional study on the causes and investigations of adults' patients with autoimmune haemolytic anaemia**

Agila Ganasagaran, Nurul Shahirah Mohd Shafiai, Koshila Kumari, Siti A'ini Syazrah, Nor Ashikin Azizan, Azura Abdul Hamid

*Department of Pathology, Hospital Tengku Permaisuri Norashikin, Selangor, Malaysia*

*Introduction:* Autoimmune haemolytic anaemia (AIHA) is a haematological disorder caused by autoantibodies, (can be divided into cold, warm and mixed AIHA, depending on the temperature reactivity of the autoantibodies) leading to acute haemolysis. This study aims to determine the causes and specific investigations for AIHA. *Materials & Methods:* A retrospective cross-sectional study was conducted from January to December 2024. All Full blood pictures (FBP) with acute haemolysis as listed in the FBP test list sheet (HKJG/JP/HEMA/ PK-07-01) were reviewed. Patients with AIHA were identified, and study data was extracted from medical records and Laboratory Information System (LIS). *Results:* Eleven patients, aged 39- 84 years old (45% female and 55% male) were identified. Presenting symptoms were symptomatic anaemia (50%), jaundice (30%) and, cough with shortness of breath (20%). The causes of AIHA were haematological malignancy (36.5%), infection (36.5%), autoimmune (9%), and undetermined due to lack of information (18%). The investigations included Full blood count (FBC), FBP, lactate dehydrogenase (LDH), bilirubin, direct antiglobulin test (DAT), reticulocyte count, antibody screening, anti-nuclear antibody titre, complement, cold agglutinin titre, serum and urine electrophoresis. The frequency, mean and range were calculated. *Discussion:* Haematological malignancy (lymphoproliferative disease) and infections (cellulitis, dengue) were the most common causes of AIHA. Basic laboratory

investigations (FBC, FBP, LDH, reticulocyte count, bilirubin and DAT) were performed in almost all patients. Other tests were conducted for some patients, depending on their clinical presentation. In essence, an individualised approach to investigation is crucial for appropriate treatment of this disorder.

**HM6: Essential Thrombocythaemia (ET) transformed to Acute Myeloid Leukaemia (AML) with recurrent cytogenetic abnormality RUNX1::RUNX1T1 : A Case Report**

[1]Nur Aisyah Shaiful Azman, [1]Lailatul Hadziyah Mohd Pauzy, [1]Mohd Fikri Mustapha, [1]Nur Farahin Hashnor, [2]Nor Rafeah Tumian, [2]Tshering Pem

*[1]Department of Pathology, Laboratory Diagnostic Services, Hospital Canselor Tuanku Muhriz, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia. [2]Department of Internal Medicine, Hospital Canselor Tuanku Muhriz, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia.*

*Introduction:* A notable cytogenetic abnormality in de novo AML is the t(8;21)(q22;q22.1) translocation, resulting in *RUNX1::RUNX1T1* fusion gene. This is frequently observed in de novo AML but is rarely encountered in secondary AML arising from Myeloproliferative Neoplasm (MPNs). *Case report:* We report the case of a 58-year-old lady with *JAK2*-positive Essential Thrombocythemia diagnosed in 2011, managed with Hydroxyurea. Disease progressed to early fibrosis in 2016, and subsequent monitoring showed worsening anaemia with increasing blasts. Bone marrow aspirate and trephine biopsy done in November 2024 showed 10-15% blasts, while immunophenotyping (IPT) confirmed 8.9% myeloblasts. Cytogenetic analysis showed t(8:21) translocation, indicating the presence of *RUNX1::RUNX1T1* fusion gene. *Discussion:* Leukaemic transformation in MPNs is influenced by several factors, including MPN subtype, treatment history, and genetic mutations. Additional genetic alterations involved in epigenetic regulation, signalling pathways and RNA splicing can cooperate with *JAK2, CALR,* or *MPL* mutations to drive the transformation of ET to AML. Unlike primary AML, secondary AML from ET often lacks favourable mutations (e.g, *NPM1*) and commonly exhibits p53 mutations or complex karyotypes. Transformation of *JAK2*-positive ET to AML with *RUNX1::RUNX1T1* fusion has only been reported once in a Japanese patient in 2024 with a favourable outcome following combination chemotherapy with hypomethylating agents. Identifying high-risk patients more effectively remains crucial, and both clinical and genetic factors contribute to disease progression in essential thrombocythemia (ET). Therefore, advancements in genetic profiling help in establishing a better understanding of MPN progression, allowing for improvement in patient risk assessment and treatment strategies.

**HM7: Genotypes Diversity of Beta Thalassemia Among Sabah Population: A Retrospective Review**

Nur Aisyah Shaiful Azman[1], Raja Zahratul Azma Raja Sabudin[1], Alia Suzana Asri[1], Qhasmira Abu Hazir[1], Raja Muhammad Zul Hatta[2], Noorhana Sofia[2], Ahmad Nasirudin Mustafa[2], Nizmah Mahani[2], Noraesah M[3], Norafiza Mohd Yasin[4], Ezalia Esa[4]

*[1]Department of Pathology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia, [2]Departments of Pathology, Hospital Queen Elizabeth, Sabah, Malaysia, [3]Departments of Pathology, Hospital Kuala Lumpur, Kuala Lumpur, Malaysia, [4]Institute of Medical Research (IMR), National Institutes of Health (NIH), Selangor, Malaysia.*

*Introduction:* β-thalassemia is characterised by reduced (β+) or absent (β°) synthesis of the β-globin chains due to mutations in the β-globin gene on chromosome 11. Spectrum of β-thalassemia mutations is heterogeneous and significantly different in certain regions and ethnics. These mutations affect gene expression at multiple levels. In Malaysia, Sabah records the highest number of thalassemia cases (22.72%) certain regions led molecular characterisation of thalassemia among those populations is limited. Our study emphasises the molecular diversity of β-thalassemia among indigenous populations in Sabah, which remains underexplored. *Materials & Methods:* A retrospective analysis of 11,000 thalassemia cases was conducted at Hospital Queen Elizabeth from January 1 to December 31, 2021. Haemoglobin analysis and genotyping were performed using Sebia Capillary Electrophoresis, Bio-Rad HPLC, and molecular tools including Multiplex GAP, ARMS-PCR, MLPA and Sanger sequencing. *Results:* 2,735 positive samples selected from Hb analysis for molecular analysis showed heterogenous pattern of mutations. $\beta^{+}$ mutations identified include IVS 2-654, PolyA [AATAAA>AATAGA], and Cap+1 5'UTR (A>C). Heterozygous $\beta^{0}$ revealed Filipino 45kb deletion and a rare Hb Khon Kaen CD123-125 (-ACCCCACC). The common β-variant, Codon 26 [GAG>AAG] Hb E, was prevalent among Malays. Homozygous $\beta^{0}$, especially $\beta^{0}$-Filipino 45kb deletion, was associated with β-thalassemia major, predominant among Dusun. Compound $\beta^{0}/\beta^{+}$ mutations included $\beta^{0}$-Filipino with -28(A>G) and SEA deletion with IVS 2-654. Compound $\beta^{0}/\beta^{0}$ cases featured $\beta^{0}$-Filipino with Codon 41/42[-TTCT]. Complex heterogeneity was observed with Hb E co-inherited with Hb Malay, Hb L'Aquila, or Hb Khon Kaen variants. *Discussion:* This study provides valuable reference for better diagnostic strategies, targeted screening and appropriate healthcare interventions.

**HM8: Spotting leukaemia in the cradle: a case series of congenital leukaemia from two centres**

Siti Shahrum Muhamed. Said[1], Siti Aisyah Abdullah[1], Nurimatussolehah Sarijan[1], Fatin Adlia Arifin[1], Suzana Zainol[1], Norazlina Azman[1], Shenaz Banu Said Khan[1], Azly Sumanty Ab Ghani[2], Wan Amal Hayati Wan Hassan[2], Wan Zuhairah W. Embong[2], Nor Ainiza Mansor[2], Wee Nee Tan[3], Mimi Azura Aziz[1]

*[1]Department of Pathology, Hospital Tunku Azizah, Kuala Lumpur, Malaysia; [2]Department of Pathology, Hospital Sultanah Nur Zahirah, Kuala Terengganu, Malaysia; [3]Department of Paediatric, Hospital Tunku Azizah, Kuala Lumpur, Malaysia*

*Introduction:* Congenital leukaemia (CL) is a rare haematological malignancy manifested within the first month of life, with an incidence of 1–5 per million live births. It accounts for <1% of all childhood leukaemia. Unlike typical childhood leukaemia patterns, approximately two-thirds of CL cases are acute myeloid leukaemia (AML). *Case series:* We reviewed seven (7) CL cases diagnosed at Hospital Tunku Azizah, Kuala Lumpur and Hospital Sultanah Nur Zahirah, Kuala Terengganu between 2019 and 2024. Clinical, haematological, and molecular data were analysed. Patients presented between Day 0 and Day 30 of life; five (71.4%) were male. Leucocytosis was seen in six patients (85.7%), and four (57.1%) had hyperleukocytosis (>$100\times10^{9}$/L). All had

extramedullary involvement: hepatomegaly (n=6), splenomegaly (n=5), and cutaneous infiltrates (n=5). Five cases (71.4%) were AML and two (28.6%) were B-acute lymphoblastic leukaemia. *KMT2A* rearrangements were identified in five patients (71.4%). Three patients (42.8%) succumbed to the disease, one was discharged against medical advice, one achieved spontaneous remission, and two underwent chemotherapy. *Discussion:* Congenital leukaemia presents significant diagnostic challenges due to its rarity and clinical overlap with neonatal sepsis. The prognosis remains poor, with reported mortality rates of 68%–74% within the first two years of life, primarily due to chemoresistance and treatment-related complications. Nonetheless, spontaneous remission has been documented. The presence of *KMT2A* rearrangements is associated with an adverse outcome. Early recognition and a comprehensive diagnostic approach encompassing morphology, immunophenotyping, cytogenetic, and molecular analyses are critical for accurate diagnosis and optimal management in this vulnerable population.

**HM9: The immature platelet fraction in patients hospitalised in a tertiary healthcare institution**

Fatmawati Kamal[1], Nur Amalina Adhwa Najibollah[1], Zalizah Khalid[1]
*[1]Department of Pathology, Faculty of Medicine, Universiti Teknologi MARA, Sungai Buloh, Selangor, Malaysia*

*Introduction:* Immature platelet fraction (IPF) is an extended parameter offered by most automated haematology analysers to estimate the number of reticulated platelets. An IPF greater than 7% is considered to have been raised and indicates active thrombopoiesis. In this study, we intend to document the level of IPF in hospitalised patients, regardless of their platelet counts. *Materials & Methods:* One hundred and ten IPF results were analysed from inpatients between June 2024 and December 2024. IPF was generated whenever our haematology analyser used the reticulocyte channel. The other blood cell parameters, such as mean platelet volume (MPV) and platelet distribution width (PDW), were also analysed. *Results:* The mean IPF value was 7.7% (min: 1.2, max: 46.1). The mean IPF in males was significantly higher than in females, p= 0.02. The mean MPV and PDW were significantly raised when IPF was more than 7%, $p<0.001$ and $p = 0.015$, respectively. The mean platelet count was significantly lower when IPF was >7% (mean: 168.6x109/L, $p<0.001$). *Discussion:* IPF was shown to be slightly increased in inpatients. Since this study used random sampling, the causes of illness were variable. Thus, raised IPF may be caused by active thrombopoiesis due to peripheral destruction like immune thrombocytopenia, bleeding or recovering from an infection. Inpatients may have a slightly higher IPF regardless of the platelet count. The mean MPV and PDW did not exceed the normal range and were generally regarded as inferior to IPF in predicting the rate of thrombopoiesis.

**HM10: 5-Azacytidine Induces Transcriptomic Dysregulation and Prognostic Biomarker Identification in MM1.S Multiple Myeloma Cell Line**

Nor Hayati Ismail[1,2], Shafini Mohamed Yusoff[1], Azlan Husin[3], Muhammad Farid Johan[1]
*[1]Department of Haematology, School of Medical Sciences, Universiti Sains Malaysia, Kelantan, Malaysia; [2]Hospital Sultan Ismail Petra, Kelantan, Malaysia; [3]Department of Internal Medicine, School of Medical Sciences, Universiti Sains Malaysia, Kelantan, Malaysia*

*Introduction:* Multiple myeloma (MM) is a haematological malignancy marked by the clonal proliferation of plasma cells in the bone marrow. Epigenetic alterations significantly contribute to MM pathogenesis, positioning agents like 5-azacytidine (5-AZA) as potential therapeutic options. This study examines the effects of 5-AZA on the MM1.S cell line, focusing on transcriptomic changes and prognostic biomarker identification. *Materials & Methods:* MM1.S cells were treated with varying concentrations of 5-AZA. Cell proliferation, cell cycle and apoptosis were evaluated. RNA sequencing identified differentially expressed genes (DEGs), followed by gene ontology and KEGG pathway analyses. Protein-protein interaction networks were constructed using STRING and analysed with Cytoscape's MCODE plugin. Kaplan–Meier survival analyses evaluated the prognostic significance of core genes. *Results:* 5-AZA inhibited MM1.S cell proliferation in a dose-dependent manner, with an $IC_{50}$ of $23.41 \pm 5.2$ μM. Treatment induced significant G0/G1 phase arrest ($76.77\% \pm 0.82$, $p \leq 0.01$) and increased late apoptosis ($31.89\% \pm 1.67$, $p \leq 0.01$). RNA sequencing revealed DEGs enriched in pathways related to cell adhesion molecules ($q = 2.6\times10^{-4}$), microRNAs ($q = 2.46\times10^{-3}$), and cancer pathways ($q = 2.8\times10^{-3}$). Notably, several core histone genes were downregulated post-treatment. Fifty-six core genes were identified, with key genes such as *NUSAP1, CENPE, KIF20A, AURKA, TPX2, CDC20, KIF4A, CDCA8,* and *PLK1* showing strong associations with improved survival outcomes (log-rank $p = 1.4\times10^{-16}$). *Discussion:* 5-AZA exerts significant anti-proliferative effects on MM1.S cells by inducing cell cycle arrest and apoptosis, accompanied by transcriptomic dysregulation, including downregulation of histone genes. The identification of core genes associated with favorable survival outcomes underscores the therapeutic potential of 5-AZA in MM treatment and highlights novel prognostic biomarkers.

**HM11: Renal anaemia masking Myelodysplastic Syndrome with Fibrosis: A Case Report**

Zubaidah Ahmad
*Department of Pathology, Hospital Shah Alam, Selangor, Malaysia*

*Introduction:* Anaemia in CKD caused by bone marrow dysfunction is rarely considered as the primary issue, thus it is often overlooked. Myelodysplastic Syndrome with fibrosis (MDS-F) is a distinct subtype under WHO haematolymphoid tumour classification. Frequent red blood cell transfusion was associated with a higher incidence of MDS. *Case report:* A 78-year-old with underlying CKD stage IV and diabetes was noted to have anaemia and fluctuating platelet count, which was initially thought to be attributed to renal disease. His anaemia was not corrected by monthly red cell transfusions, s/c Mircera and iv venofer. FBP done in November 2023 showed leucoerythroblastic pictures. BMAT revealed hypercellular marrow with grade 2 fibrosis and foci of dense reticulin fibres and significant dysplastic megakaryocytes. Cytogenetics showed an abnormal male karyotype with trisomy 8. JAK2/ MPL/ CAL-R were negative. He was then required 2 weekly PC transfusions. Thalidomide was commenced in mid-August 2024. Two weeks later, he presented with abdominal distension with leucocytosis. FBP showed 6% blasts raising suspicion of transformation to acute leukaemia. He succumbed in early September 2024 from shock due to intra-abdominal sepsis.

*Discussion:* Regular blood transfusion in advanced renal patients and secondary hyperparathyroidism are associated with MDS incidence due to the effect of certain cytokines. Abnormal cytogenetic findings have been reported in MDS-F, which increased the likelihood of transformation to acute leukaemia. The lack of JAK2 and CALR mutation in this case helps to rule out primary myelofibrosis as a cause of fibrotic marrow.

**HM12: Evaluation Study of Sebia Capillarys 3 Octa Analysers in Selayang Hospital**

Nor Hafiza Saad, Nurmatul Shida Noor Mohamed, Sharifah Mai Sarah Syed Azim, Hasliza Husin
*Department of Pathology, Hospital Selayang, Selangor, Malaysia*

*Introduction:* The Capillarys 3 Octa instrument is an automated analyser which performs a complete haemoglobin profile for quantitative analysis of the normal haemoglobin fractions and for the detection of major haemoglobin variants. This study was carried out to evaluate performance of this analyser including correlation and normal range verification between Capillarys 3 Octa and current in-use Capillarys 2 Flex Piercing. *Materials & Methods*: The study used Capi 3 Haemoglobin Kit, normal control HbA2, pathological control HbA2 and 80 random patients' sample. Evaluation includes precision study, linearity, carry over, correlation and normal range verification. *Results:* The precision results for both HbA2 Normal and Pathological Control were good. The relationship between low HbF and high HbF showed good linearity with $r^2 = 0.970$ and the relationship between low HbA2 and high HbA2 also showed good linearity with $r^2= 0.975$. There was no carry over detected for both HbA2 and HbE. The correlation for HbA2, HbE and HBF between Capillarys 3 Octa and Capillarys 2 Flex Piercing were good with $r^2 > 0.975$ and correlation coefficient $r\approx1$. Normal range for HbA, HbA2 and HbF were acceptable and within the expected range of reference value by manufacturers. *Discussion:* The overall performance of Capillarys 3 Octa was excellent in terms of precision, linearity, and correlation with current in-use analyser with no carry over detected. Thus, this analyser is satisfied to be used as automated analyser comparative to another principle of analyser for diagnosis of thalassemia and haemoglobinopathies.

**HM13: Hb Tanah Merah: A Novel β-Globin Variant Identified Among Malays in the Malaysian Population**

Suguna Somasundram[1], Faidatul Syazlin Abdul Hamid[1], Syahzuwan Hassan[1] Aisyah Aziz[1], Ezalia Esa[1], Ezzanie Suffya Zulkefli[1], Nik Fatma Fairuz Nik Mohd Hasan[2], Azian Naila Md Nor[1], Ermi Neiza Mohd Sahid[1], Yuslina Mat Yusoff[1], Norafiza Mohd Yasin[1]
*[1]Haematology Unit, Cancer Research Centre, Institute for Medical Research, Shah Alam, Selangor; Department of Pathology, Hospital Selayang, Selangor, Malaysia; [2]Pathology Department, Hospital Raja Perempuan Zainab II, Kelantan*

*Introduction:* We report a novel haemoglobin (Hb) variant, Hb Tanah Merah, identified exclusively among Malays in Malaysia. This variant results from a β-globin chain amino acid substitution at codon 122 (TTC>TGC)(HBB:c.368T>G). To date, this variant has not been reported in any public database. *Materials & Methods*: This retrospective cross-sectional study describes the haematological, phenotypic, and genotypic characteristics of 18 individuals with *Hb Tanah Merah*, collected over an eight-year period. *Results:* All *Hb Tanah Merah* cases were of Malay ethnicity, with the majority (15/23) originating from Tanah Merah, Kelantan, Malaysia. Eighteen out of the twenty-three cases were analysed. The mean (±2SD) haematological parameters for the 18 individuals were: Hb: 14.37 ± 3.00 g/dL; RBC: 5.65 ± 0.92 × $10^{12}$/L; MCV: 76.44 ± 8.94 fL; MCH: 25.48 ± 3.48 pg; RDW: 14.65 ± 3.24%; Hb A: 96.42 ± 0.56%; Hb $A_2$: 3.50 ± 0.38%. All individuals were heterozygous for the variant and clinically asymptomatic. Using bioinformatics software, Alamut® predicted the variant to be of uncertain significance. The affected nucleotide is highly conserved (phyloP: 8.38), and multiple computational tools support a deleterious effect. However, all individuals demonstrated borderline elevated Hb $A_2$ levels (range: 3.3–3.9%) and hypochromic microcytic indices, features consistent with a thalassaemia trait phenotype. *Discussion:* We report a novel *HBB* gene variant associated with borderline elevated Hb $A_2$ levels and thalassaemia-like red cell indices. Based on the available phenotypic, genotypic, and computational evidence, we propose classifying this variant as likely pathogenic. Accurate classification is essential for appropriate risk assessment and management in affected families.

**HM 14: Rare Autoantibodies Mimicking Rhesus (Rh) Alloantibodies: A Case Series from a Tertiary Care Hospital**

Nur Afifah Suhemi[1], Rabeya Yousuf[1], Kaalpana Jayakumar[1], Nor Fadzliana Abdullah Thalith[1], Mohd Asmawi Che Omar[1], Qhasmira Abu Hazir[1],
*[1]Department of Diagnostic Laboratory Services, Hospital Canselor Tuanku Muhriz, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia*

*Introduction:* Mimicking autoantibodies lose specificity after alloadsorption with red blood cells (RBCs) that do not express the corresponding antigen, whereas true alloantibodies maintain their specificity during alloadsorption. We reported a case series of rare autoantibodies mimicking Rh specificities. *Case Series:* Case-1 involves a 26-year-old lady with osteoarthritis and no history of transfusion. Her blood group was O Rh D positive, with a CDe/CDe phenotype and positive DAT for anti-IgG, with an eluate showing panagglutination. Antibody identification revealed anti-e, positive autocontrol, suspecting autoanti-e. Further testing using alloadsorbed plasma and CDe/CDe and cDE/cDE cells revealed removal of anti-e reactivity, confirming the presence of mimicking antibodies. Case-2 describes a 56-year-old man with multiple transfusions due to variceal bleeding. His blood group was B Rh D positive, with CDe/cDE phenotype and positive DAT for anti-IgG, accompanied by positive autocontrol. Antibody identification and elution study detected both anti-C and anti-e, suspected to be autoantibodies. Alloadsorption using CDe/CDe and cDE/cDE removed the reactivity of both anti-C and anti-e, confirming the presence of mimicking alloantibodies. Case-3 features a 73-year-old woman, transfusion-dependent beta-thalassemia. Her blood group was A RhD positive with CDe/cDE phenotype, positive DAT for anti-IgG and a panagglutinating eluate. Antibody identification revealed anti-C and anti-e. Alloadsorption with cDE/cDE cells resulted in loss of reactivity. Genotyping confirmed the Rh antigen, guiding the transfusion process. *Discussion:* This series highlights the diagnostic difficulties posed by mimicking autoantibodies emphasising the importance of advanced diagnostic techniques. Clinical correlation is essential for safe transfusion management.

**HM15: A case of Homozygous Southeast Asian Ovalocytosis (SAO) associated with Distal Renal Tubular Acidosis (dRTA) in a Live-born Neonate in Sabah Women and Child Hospital (SWACH)**

Noor Hayati S[1], Asma B[1], Roihan AI[1], Kimberly FJ[1], Hafizuddin MF[2], Nor Hafiza S[3]
*[1]Pathology And Transfusion Medicine Department, Sabah Women and Child Hospital, Sabah, Malaysia; [2]Advance Diagnostic Laboratory, Institut Perubatan dan Pergigian Termaju, Universiti Sains Malaysia, Kelantan, Malaysia; [3]Molecular Haematology Laboratory, Haematology Unit, Pathology Department, Hospital Kuala Lumpur, Malaysia.*

*Introduction:* Southeast Asian Ovalocytosis (SAO) is an autosomal dominant red blood cell membrane disorder caused by a small deletion in the SLC4A1 gene, which encodes the erythrocyte band 3 anion exchanger (AE1) protein, leading to membrane rigidity. The AE1 protein is also present in α-intercalated renal cells, where it is essential for acid secretion in urine. Loss of AE1 activity in the kidneys results in distal renal tubular acidosis (dRTA). Here, we report a case of homozygous SAO associated with dRTA in a live-born neonate at SWACH. *Case presentation:* A premature baby girl was born at 33 weeks via emergency caesarean due to foetal distress. At birth, she had anaemia, hyperbilirubinemia, and hepatosplenomegaly. Initial investigations confirmed acute haemolysis with alpha zero thalassemia trait (αα/--SEA), requiring biweekly blood transfusions. Further testing identified red cell changes in both parents consistent with Southeast Asian Ovalocytosis (SAO), and her molecular analysis confirmed homozygous SAO due to a band 3 gene deletion. At one month, she was diagnosed with distal renal tubular acidosis (dRTA) and succumbed at nine months due to sepsis. *Discussion:* SAO is prevalent in Southeast Asia and typically presents with ovalocytes and stomatocytes on blood films. While heterozygous SAO is often asymptomatic, homozygous SAO is usually considered lethal in utero. In this exceptional case, the child survived birth but developed complications including dRTA, likely due to complete AE1 dysfunction in both red blood cells and renal intercalated cells. This highlights the critical role of AE1 in both haematologic and renal physiology.

**HM16: Unexpected Moderate Haemophilia A in Siblings with Double Mutations: A Case Report**

Azian Naila Md Nor, Nursaedah Abdullah Aziz, Ermi Neiza Mohd Sahid, Norafiza Mohd Yasin, Ezalia Esa, Suguna Somasundram, Lam Kah Yuen, Siti Nor Assyuhada Mat Ghani, Nur Hakimah Mohamad Fadilah, Izzatul Nabila Lukman, Yuslina Mat Yusoff
*Haematology Unit, Cancer Research Centre, Institute for Medical Research, National Institutes of Health, Selangor, Malaysia*

*Introduction:* Haemophilia A is an inherited bleeding disorder caused by mutations in the Factor VIII (F8) gene, resulting in reduced activity or dysfunction of clotting factor VIII. The clinical severity varies from mild to severe and often correlates with the nature and location of the underlying mutation. While most cases involve a single pathogenic variant, the occurrence of multiple mutations in the same individual is rare and can complicate diagnosis and phenotype prediction. *Case report:* We report two brothers with double mutations in the F8 gene. The elder sibling, aged 13, presented with intermittent gum bleeding, whereas the younger, aged 7, developed swelling of the right elbow joint and bruising. Coagulation studies showed prolonged activated partial thromboplastin time (APTT) with correction in mixing studies. Factor VIII activity levels were moderately reduced at 2.4% and 3%, respectively. Genetic analysis using polymerase chain reaction (PCR) and Sanger sequencing identified two-point mutations: p.Ile192Thr in exon 4 and p.Glu340Lys in exon 8 of the F8 gene. Further testing of their mother revealed similar mutations. *Discussion:* This case underscores the diagnostic and clinical significance of double F8 mutations, which, although individually associated with mild haemophilia A, resulted in a moderate phenotype in both siblings. It highlights the complexity of genotype-phenotype relationships and the potential additive or interactive effects of multiple mutations on factor VIII structure and function. Comprehensive molecular and clinical assessment is essential for accurate diagnosis, prognosis, and individualised management in such atypical presentations of haemophilia A.

**HM17: Haemoglobin Utrecht in Malaysia: The Role of Genetic Sequencing in Identifying Rare Variants**

Ulfatul Khusna Samuri[1], Ermi Neiza Mohd Sahid[1], Azian Naila Md Nor[1], Suguna Somasundram[1], Ezalia Esa[1], Syahzuwan Hassan[1], Aisyah Aziz[1], Norsafina Zainal[2], Norafiza Mohd Yasin[1], Yuslina Mat Yusoff[1]
*[1]Haematology Unit, Cancer Research Centre (CaRC), Institute for Medical Research (IMR), National Institute for Health (NIH) Setia Alam, Selangor, Malaysia; [2]Department of Pathology, Hospital Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* Haemoglobin α2 codon 129 CTG>CCG, also known as Hb Utrecht, is a rare alpha-globin variant first identified in a Dutch family with very few cases documented globally. The mutation was recently identified in a Malaysian teenager through National Thalassemia Screening Program, marking the first reported case in the region. *Case report:* A 16-year-old Malay boy was found to have mild hypochromic microcytic anaemia, despite no clinical abnormalities or family history. Laboratory evaluation showed a haemoglobin level of 13.6 g/dL, with a mean corpuscular volume (MCV) of 70.3 fL, mean corpuscular haemoglobin (MCH) of 22.8 pg, and red cell distribution width (RDW) of 12.4%. Capillary electrophoresis revealed no abnormal haemoglobin bands, with HbA accounting for 97.4% and HbA2 for 2.6%. Molecular testing using multiplex Gap-PCR and ARMS-PCR did not detect common deletions or point mutations. However, subsequent alpha-globin gene sequencing identified heterozygosity for a mutation at α2 codon 129 (CTG>CCG), consistent with Hb Utrecht. *Discussion:* Hb Utrecht is a non-deletional $\alpha^+$-thalassaemia variant caused by a leucine-to-proline substitution that disrupts the alpha-globin chain's structure, impairing synthesis and resulting in an $\alpha^+$thalassaemic phenotype. Its identification is clinically significant in regions like Malaysia, where alpha-globin deletions are common, increasing the risk of compound heterozygosity and more severe outcomes such as non-deletional Hb H disease. This case emphasises the limitations of standard haematological and molecular tests in detecting rare variants, highlighting the importance of advanced genetic sequencing for accurate diagnosis, effective clinical management, and informed genetic counselling.

**HM18: Learn Haematology: A Digital Platform for Case Studies and Morphology Learning**

Sumaiyah Adzahar[1], Adibah Daud[1], Mohammad Hudzaifah Nordin[2], Muhammad Aizuddin Ahmad[2], Razan Hayati Zulkeflee[3]
*[1]Department of Pathology and Medical Laboratory, Faculty of Medicine, Universiti Sultan Zainal Abidin, Terengganu, Malaysia, [2]Department of Ophthalmology, Faculty of Medicine, Universiti Sultan Zainal Abidin, Terengganu, Malaysia, [3]Department of Haematology, School of Medical Sciences, Universiti Sains Malaysia, Health Campus, Kelantan, Malaysia*

*Introduction:* Haematology education is vital in developing diagnostic skills among medical and biomedical students, yet traditional methods such as textbooks and slide-based lectures often lack interactivity, limiting student engagement. To address these challenges, we introduce *Learn Haematology*, an innovative digital platform designed to enhance haematology education through interactive case studies and morphology-based learning. *Materials & Methods: Learn Haematology* offers an accessible online environment where students can explore real-world cases, analyse microscopic findings, and reinforce their diagnostic skills in a structured, engaging manner. The platform features a comprehensive repository of haematology case studies covering red cell disorders, white cell abnormalities, platelet disorders, and other haematological conditions. A digital morphology library with high-resolution blood smear images and interactive annotations supports recognition of key morphological features. Self-assessment tools, including quizzes and case-based exercises, are incorporated to test knowledge and reinforce learning. Content is updated regularly to ensure the platform remains current with advancements in haematology. *Results:* Feedback from 65 students showed that over 90% found the platform helpful in improving diagnostic skills, understanding morphology, and enhancing overall learning engagement. Students praised the case-based approach and interactive features as superior to traditional learning methods. *Discussion:* By incorporating digital innovation, *Learn Haematology* bridges the gap between theoretical knowledge and practical application. The platform fosters self-directed learning, enhances pattern recognition, and improves knowledge retention through real-world clinical correlations. This initiative has the potential to revolutionise haematology education by providing an effective, scalable, and impactful learning experience that strengthens diagnostic competency and deepens understanding of haematology.

**HM19: Silent Risk: Unmasking Hereditary Protein S Deficiency Through Family History**

Sumaiyah Adzahar[1], Nurul Izza Yunus[2], Adibah Daud[1]
*[1]Department of Pathology and Medical Laboratory, Faculty of Medicine, Universiti Sultan Zainal Abidin, Terengganu, Malaysia, [2]Department of Family Medicine, Faculty of Medicine, Universiti Sultan Zainal Abidin, Terengganu, Malaysia*

*Introduction:* Hereditary Protein S deficiency is a rare but significant thrombophilia disorder that increases the risk of both venous and arterial thrombotic events. *Case report:* We present the case of a 31-year-old woman who underwent further evaluation due to a strong family history of premature cerebrovascular accidents. Both her father and mother had died of major strokes in their mid-50s, raising concerns about an inherited prothrombotic condition. A comprehensive thrombophilia workup revealed persistently low Protein S levels—initially measured at 48% and later confirmed at 27%, leading to a diagnosis of hereditary Protein S deficiency. Subsequent family screening identified Protein S deficiency in two of her siblings. *Discussion:* This case highlights the critical importance of incorporating detailed family history into cardiovascular risk assessments, especially when conventional risk factors are absent or minimal. Early identification of hereditary thrombophilia facilitates timely intervention, appropriate lifestyle modifications, and targeted prophylaxis during high-risk periods, such as surgery or pregnancy. Additionally, cascade screening of family members allows for early diagnosis and preventive management. A multidisciplinary approach involving primary care physicians, haematologists, and genetic counsellors is essential to ensure optimal outcomes. This case illustrates that even asymptomatic individuals with low conventional risk scores may have inherited conditions that predispose them to significant thrombotic events, reinforcing the need for increased clinical vigilance when family history suggests such risks.

**HM20: A Rare Case Of Compound Codon 26 [GAG>AAG] ($B^E$) Hb E And Codon 26 [GAG>TAG] ($B^0$) Identified Using Beta Sanger Sequencing In Malaysia**

Nurul Hidayah Musa[1], Faidatul Syazlin Abdul Hamid[1], Munirah Abdul Razak[2], Syahzuwan Hassan[1], Ezzanie Suffya Zulkifle[1], Aisyah Aziz[1], Sharifah Suhana Syed Abd Rahman[1], Ermi Neiza Mohd Sahid[1], Azian Naila Md Nor[1], Suguna Somasundram[1], Ezalia Esa[1], Norafiza Mohd Yasin[1], Yuslina Mat Yusoff[1]
*[1]Haematology Unit, Cancer Research Centre (CaRC), Institute for Medical Research (IMR), National Institute of Health (NIH), Setia Alam, Selangor, Malaysia; [2]Department of Pathology, Hospital Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia.*

*Introduction:* Codon 26 [GAG>AAG] or Hb E, is the most prevalent variant in Southeast Asia. In contrast, a [GAG>TAG] substitution at the same codon, which creates a premature stop codon, leads to rare beta-zero thalassemia mutation. *Case report:* A 32-year-old Malay female presented with severe anaemia requiring monthly blood transfusions. She had hepatomegaly and splenectomy done. Her Hb was 6.6 g/dL, with RBC 2.95 × $10^6$/µL, MCV 73.0 fL, MCH 22.4 pg, and reticulocyte count 25.26%. Post-transfusion Hb analysis showed elevated Hb E zone (24.9%), Hb $A_2$ (4.4%), Hb F (3.4%), and Zone 12 (1.4%). Initial molecular analysis using reverse dot blot (RDB) flow-through hybridization revealed homozygous Hb E mutation. However, due to the severe phenotype, further testing with Sanger sequencing was performed to exclude the presence of other beta mutations. This confirmed compound heterozygosity at codon 26, with one allele carrying the Hb E mutation [GAG>AAG] and the other carrying a nonsense mutation [GAG>TAG], a rare beta-zero-thalassaemia mutation affecting the same codon. *Discussion:* Typically, compound Hb E/beta-zero thalassemia presents as thalassemia intermedia with variable severity, whereas homozygous Hb E is usually asymptomatic. In this case, mismatched hybridization between the target DNA carrying the nonsense mutation at codon 26 and the mutant probe in the RDB kit led to homozygous Hb E mutation pattern. Therefore, accurate diagnosis of this rare compound mutation requires careful correlation of the patient's phenotype, Hb analysis results, and the knowledge of various molecular methods. Additional comprehensive molecular testing is necessary to achieve a definitive diagnosis.

**HM21: Recognising the Uncommon: Paediatric Chronic Myeloid Leukaemia Case Series**

Nur Farahin Hashnor[1], Ramlah Mohamed Ibrahim[1], Yong Woon Lee[2], Farah Azima Abdul Muttlib[2], Suria Abdul Aziz[1], Hafiza Alauddin[1]

*[1]Department of Pathology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia. [2]Department of Pathology, Laboratory Diagnostic Services, Hospital Tuanku Ampuan Besar Tuanku Aishah Rohani, Children Specialist Hospital, National University of Malaysia, Kuala Lumpur, Malaysia.*

*Introduction:* Chronic Myeloid Leukaemia (CML) is a rare paediatric malignancy, comprising less than 5% of childhood leukaemias, characterised by clonal myeloid proliferation driven by the Philadelphia chromosome. This case series presents two paediatric CML cases, outlining clinical features, diagnostic findings and management. *Case report:* Case 1 involved a 7-year-old girl with a one-month history of abdominal distension, low-grade fever, and weight loss. Examination revealed marked hepatosplenomegaly. Laboratory studies demonstrated anaemia (Hb 7.6 g/dL), hyperleukocytosis (WBC 664.92 x $10^9$/L) and thrombocytosis (Platelet: 775 × $10^9$/L). Peripheral smear and bone marrow aspiration were suggestive of CML, confirmed by Philadelphia chromosome and major BCR::ABL1 transcript. She was initiated on Imatinib with supportive care, showing early clinical improvement. Case 2 featured an 11-year-old boy presented with a four-month history of progressive weight loss without appetite loss or gastrointestinal symptoms. Examination revealed mild pallor and marked hepatosplenomegaly. Laboratory investigations revealed hyperleukocytosis (WBC: 474.16 x $10^9$/L), anaemia (Hb: 7.7g/dL) and thrombocytosis (Platelet: 602 x $10^9$/L). Peripheral smear and bone marrow aspiration suggested CML, confirmed by detection of major BCR::ABL1 transcript. He was started on Imatinib and tolerated therapy without early complications. *Discussion:* Both cases illustrated classic clinical manifestations of paediatric CML, notably unexplained weight loss and hepatosplenomegaly. Although presenting with similar clinical features, the diagnostic courses differed; Case 1 exhibited an acute onset necessitating prompt diagnostic evaluation, whereas Case 2 demonstrated a more insidious progression. Early initiation of tyrosine kinase inhibitor therapy, coupled with supportive measures, was effective in achieving disease stabilisation and preventing early complications.

**HM22: Unmasking Sarcoidosis in A Myeloma Workup: A Case Report**

Nor Syazana Jamali[1], Nurul Afiqah Nadzari[1], Asmawiza Awang[2], Jason Tan Seng Hong[3], Navin Kumar A/L Santha Moorthy[4]

*[1]Department of Pathology; [2]Department of Pathology, Hospital Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia; [3]Department of Medicine and [4]Department of Radiology, Hospital Banting, Selangor, Malaysia*

*Introduction:* Sarcoidosis is a multi-organ disease of unknown aetiology characterised by non-caseating granulomas. We report a case of a patient who was initially investigated for plasma cell myeloma (PCM). *Case report:* A 57-year-old lady with multiple co-morbid illnesses presented with prolonged fever and constitutional symptoms. The physical examination was unremarkable. She was noted to be hypercalcaemic (serum calcium 2.81-3.41mmol/L) with progressively deteriorating renal function. Further investigations showed anaemia (haemoglobin 9.7g/dL) with short rouleaux formation on peripheral blood film, low serum parathyroid hormone (0.93pmol/L) and negative tumour markers. Serum and urine electrophoresis showing IgG lambda paraprotein (5.1g/L) with no immunoparesis and no light chain detected. Bone marrow examination was done to rule out PCM in view of persistent hypercalcemia with the presence of monoclonal gammopathy. Bone marrow smears were not suggestive of PCM. Trephine biopsy showed dense collections of non-caseating granuloma with no findings of PCM or other neoplasm. Further stains were negative for *Mycobacterium tuberculosis (MTB)* and fungi. No *MTB* were detected by culture and molecular. Skeletal survey shows no lytic lesions. High-resolution computed tomography shows extensive symmetrical perilymphatic nodularity, suggestive of pulmonary sarcoidosis. Consequently, the patient's hypercalcaemia was attributed to sarcoidosis, with possible concurrent monoclonal gammopathy of unknown significance (MGUS). *Discussion:* This case highlights the diagnostic challenges of sarcoidosis especially with concurrent presence of monoclonal gammopathy. Patients with sarcoidosis and MGUS or multiple myeloma have been reported, however true association requires larger prospective studies. Bone marrow infiltration is a rare finding as bone marrow biopsy is not a standard workup in sarcoidosis.

**HM23: Clonal Cytopenia of Undetermined Significance with Inv(3)(q21.3q26.2): A Case Report of Thrombocytopenia in a Patient with Hepatocellular Carcinoma**

Hana Shafinaz Jamaluddin

*Laboratory Medicine Department, University Malaya Medical Centre*

*Introduction:* This case report describes a 70-year-old male patient with a history of Hepatocellular carcinoma (HCC), who experienced persistent thrombocytopenia.

*Case Report:* The patient was treated with Lenvatinib for HCC, after which thrombocytopenia developed and persists. This was initially attributed to the drug. However, platelet counts did not improve following cessation of Lenvatinib. As part of the investigations for unexplained thrombocytopenia, a bone marrow examination was performed and demonstrated hypercellularity with isolated suppression of megakaryocytopoiesis, suggestive of acquired amegakaryocytic thrombocytopenia (AAMT). Bone marrow karyotyping showed male karyotype with inv(3)(q21.3q26.2) in all 20 metaphases. At 6 months after the initial bone marrow examination, routine full blood count noted worsening thrombocytopenia with presence of blasts. A repeat bone marrow examination revealed significant dysplasia in at least two cell lineages with increased blasts. *Discussion:* The patient was diagnosed with clonal cytopenia of undetermined significance (CCUS). Subsequent evaluations showed further deterioration in haematological status. Based on WHO revised 4$^{th}$ edition, AML with inv(3)(q21.3q26.2) requires the presence of ≥20% blasts. Cases with blast count less than 20% would otherwise be diagnosed as MDS with excess blasts (MDS-EB). The latest 5$^{th}$ WHO edition stated otherwise. In AML which involves the *MECOM* gene, a blast count <20% is acceptable as studies have demonstrated that these patients have clinical features resembling those with higher blast counts. Conclusion: This case highlights the significance of identifying chromosomal alterations in haematological assessments. Testing approaches should consider important rearrangements (e.g. *NUP98, KMT2A, MECOM*) which can be cryptic on conventional karyotyping.

**HM24: Implementation of Red Cell Depletion Using Optia Spectra in Paediatric Bone Marrow Transplant: Initial Experience and Refined Protocol in A Tertiary Centre**

Alia Suzana Asri[1], Nurliyana Jamaludin[1], Wafiq Azim Ismail[1], Nurassyikin Brahim[1], Koo Khai Nee[1], Yong Woon Lee[1], Doris Lau Sie Chong[2], Loh C-Khai[2], Farah Azima Abdul Muttlib[1], Shenaz Banu Said Khan[3]

*[1]Department of Diagnostic Laboratory, Hospital Tunku Ampuan Besar Tuanku Aishah Rohani, Wilayah Persekutuan Kuala Lumpur, Malaysia; [2]Department of Paediatrics, Hospital Tunku Ampuan Besar Tuanku Aishah Rohani, Wilayah Persekutuan Kuala Lumpur, Malaysia; [3]Department of Pathology, Hospital Tunku Azizah, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* Red cell depletion is critical in paediatric bone marrow transplantation (BMT), particularly in ABO-mismatched transplants to prevent haemolytic complications. However, the automated technique is not universally available. We report the first successful implementation of automated red cell depletion using the Optia Spectra system in our hospital, filling a critical gap in transplant support. *Materials & Methods:* The study evaluated the technical feasibility and early outcomes of Optia Spectra-based red cell depletion to establish a standardised protocol. The team underwent training and system testing using whole blood. Bone marrow harvests were processed using Optia Spectra, with pre-, during-, and post-processing measurements of total nucleated cells (TNC), haemoglobin and haematocrit levels. CD34+ and CD3+ enumeration was determined at pre- and post-processing. Operational challenges were documented, including the touchscreen calibration issue and adjusting parameters to achieve the best balance between effective red cell removal and preserving the viability and quantity of the desired cells. *Results:* Effective red cell depletion was successfully achieved in two patients; one with very severe aplastic anaemia (AB+ to B+), and one with transfusion-dependent beta thalassaemia (A+ to B+) yielding residual red blood cell volumes of 0.26 and 0.3 ml/kg, respectively. CD34 and TNC recoveries averaged 73% and 84% respectively. Blood cultures were negative. No technical failures or adverse events encountered, with SOPs finalised. *Discussion:* The implementation of red cell depletion via Optia Spectra demonstrates feasibility, safety and clinical effectiveness. This initiative facilitates advanced transplant support and multicentre Collaboration, improving outcomes for paediatric ABO-mismatched BMT patients.

**HM25: Mixed phenotype acute leukaemia: a case series of four patients with diverse genetic findings**

Dhamirah Nazihah bt Mohd Nasiruddin[1], Sarah Abdul Halim[1], Nurul Asyikin bt Nizam Akbar[23], Samilawati binti Mohd Arifin[4], Sumaiyah Adzahar[5]

*[1]Department of Pathology and Laboratory Medicine, Kulliyyah of Medicine, International Islamic University Malaysia (IIUM), Pahang, Malaysia; [2]Department of Haematology, School of Medical Sciences, Universiti Sains Malaysia, Kelantan, Malaysia; [3]Transfusion Medicine Unit, School of Medical Sciences, Universiti Sains Malaysia, Kelantan, Malaysia; [4]Pathology Department, Hospital Tengku Ampuan Afzan, Phang, Malaysia; Department of Pathology and Medical Laboratory, Faculty of Medicine, Universiti Sultan Zainal Abidin, Terengganu, Malaysia[5].*

*Introduction:* Mixed phenotype acute leukaemia (MPAL) is a rare, heterogeneous acute leukaemia characterised by blasts with both myeloid and lymphoid features. It poses diagnostic and therapeutic challenges due to overlapping features with acute lymphoblastic and myeloid leukaemias. We report a case series of four MPAL patients to highlight varied clinical presentations and genetic findings. *Case series:* Two cases were B/myeloid MPAL positive for the Philadelphia chromosome (BCR-ABL1) fusion: one arose from blast phase transformation of chronic myeloid leukaemia (CML), and the other was de novo. Another patient had de novo B/myeloid MPAL without BCR-ABL1 but with a *BCOR* gene mutation. The fourth case was a de novo T/myeloid MPAL with complex cytogenetic abnormalities. *Discussion:* These cases illustrate the heterogeneity of MPAL and the importance of comprehensive immunophenotypic and molecular evaluation. BCR-ABL1–positive MPAL may benefit from tyrosine kinase inhibitor therapy in addition to conventional chemotherapy. The presence of a *BCOR* mutation and complex karyotype in our patients underscores the value of genetic studies for classification and prognostication. Overall, MPAL remains an aggressive leukaemia with a need for tailored therapeutic approaches.

**HM26: Association of miR-92a expression and VCAM-1 in endothelial dysfunction and cardiovascular risk**

Nurul Izzati Abdullah[1], Fatin Syazwani Abd Malek[1], Fitri Kahar[1], Amrina Mohamad Amin[1], Md Parvez Eusof Izzudin[2], Sazlina Shariff Ghazali[3], Norshariza Nordin[4] and Sabariah Md Noor[1]

*[1]Department of Pathology, Faculty of Medicine and Health Sciences, Universiti Putra Malaysia, Selangor Darul Ehsan, Malaysia; [2]Hospital Sultan Abdul Aziz Shah, Family Medicine Clinic, Universiti Putra Malaysia, Selangor Darul Ehsan, Malaysia. [3]Department of Family Medicine, Faculty of Medicine and Health Sciences, Universiti Putra Malaysia, Selangor Darul Ehsan, Malaysia. [4]Department of Biomedical Sciences, Faculty of Medicine and Health Sciences, Universiti Putra Malaysia, Selangor, Malaysia.*

*Introduction:* Atherosclerosis is a chronic inflammatory disease characterised by endothelial dysfunction, lipid accumulation, and plaque formation, leading to thrombosis and vascular obstruction. MicroRNA (miRNA) plays a role in cell proliferation and vascular function. MiR-92a functions to promote atherosclerosis by upregulating the proinflammatory signalling in endothelial dysfunction. This study investigates the association between circulating miR-92a and VCAM-1 levels and their potential role in predicting cardiovascular disease (CVD). *Materials & Methods:* A cross-sectional analysis was conducted involving 46 participants with varying glycaemic profiles. Plasma levels of miR-92a were quantified using qRT-PCR, while VCAM-1 expression levels were measured using the Luminex assay. Spearman's correlation was used to assess the relationship between miR-92a and VCAM-1. *Results:* The study population had a median age of 58 years (IQR: 51-65), with 65% being male. Ethnic distribution was 87% Malay, 8.7% Chinese, and 4.3% Indian. A significant variation in fasting blood sugar (FBS) levels was observed ($H=20.15$, $p<0.001$). Correlation analysis revealed a positive but weak relationship between miR-92a and VCAM-1 ($\rho=0.198$, $p=0.294$). *Discussion:* These findings suggest that miR-92a expression is weakly associated with VCAM-1 levels, indicating a moderate role in endothelial activation. The significant FBS variation may reflect early metabolic stress, potentially influencing miR-92a and VCAM-1 expression through proinflammatory and prothrombotic mechanisms. This could contribute to endothelial dysfunction

and the progression of atherosclerosis. Future research with larger cohorts is needed to further explore the role of miR-92a in thrombosis and its potential as a biomarker for CVD risk.

**HM27: Association of miR-17 expression level in obesity and cardiovascular risk**

Nurul Izzati Abdullah[1], Fatin Syazwani Abd Malek[1], Fitri Kahar[1], Amrina Mohamad Amin[1], Md Parvez Eusof Izzudin[2], Sazlina Shariff Ghazali[3], Norshariza Nordin[4] and Sabariah Md Noor[1]*

*[1]Department of Pathology, Faculty of Medicine and Health Sciences, Universiti Putra Malaysia, Selangor Darul Ehsan, Malaysia; [2]Hospital Sultan Abdul Aziz Shah, Family Medicine Clinic, Universiti Putra Malaysia, Selangor Darul Ehsan, Malaysia; [3]Department of Family Medicine, Faculty of Medicine and Health Sciences, Universiti Putra Malaysia, Selangor Darul Ehsan, Malaysia; [4]Department of Biomedical Sciences, Faculty of Medicine and Health Sciences, Universiti Putra Malaysia, Selangor, Malaysia.*

*Introduction:* Obesity is a prothrombotic condition that increases cardiovascular disease (CVD) risk through endothelial dysfunction, platelet hyperactivation, and impaired fibrinolysis. MicroRNA-17 (miR-17), part of the miR-17-92 cluster, modulates haemostatic balance by targeting key vascular and thrombotic mediators including tissue factor, thrombomodulin, and PAI-1. It also regulates megakaryocyte differentiation and platelet reactivity—key processes in thrombosis and atherogenesis. This study aimed to assess plasma miR-17 expression in relation to body mass index (BMI) as a potential biomarker of obesity-related thrombotic and CVD risk. *Materials & Methods:* A cross-sectional study was conducted on 45 participants stratified by BMI. Plasma miR-17 levels were quantified using the qRT-PCR method, normalised with cel-miR-39 spike-in. Statistical analysis included Spearman's correlation and the Kruskal-Wallis test. *Results:* The study population had a median age of 58 years (IQR: 51–65), with 65% males and an ethnic distribution of 87% Malay, 8.7% Chinese, and 4.3% Indian. Participants were categorised by BMI into normal weight (n=12), overweight (n=16), and obese (n=17). Spearman's correlation showed a weak negative association between miR-17 and BMI ($r = –0.032$, $p = 0.853$). No significant differences were observed across BMI groups ($H = 1.597$, $df = 2$, $p = 0.450$). *Discussion:* Although miR-17 is known to influence endothelial and inflammatory pathways relevant to thrombosis and atherosclerosis, no significant correlation with BMI was found in this cohort. Future studies should assess miR-17 alongside platelet activation and coagulation markers to clarify its role in obesity-related CVD risk.

**HM28: Rare presentation of thrombotic thrombocytopenic purpura in a case of dengue fever: A case report**

Azizan Hanny Azahar[1], Zakiah Nurasyikin Mohamed Halim[1]

*Haematology Unit, Department of Pathology, Hospital Sultanah Nur Zahirah, Kuala Terengganu, Malaysia*

*Introduction:* Dengue virus infection is rarely associated with the occurrence of thrombotic thrombocytopenic purpura (TTP). Both conditions are fatal and can result in significant morbidity and mortality if left untreated. *Case Report:* We present a 16-year-old girl presented with fever for 4 days associated with rashes over the bilateral upper limb and lower limb, haematuria, dysuria and bruises over lip. On examination, liver palpable 1 finger breadth, dull traube space, multiple petechiae rashes over upper limb and bruises over lower limb. Dengue fever diagnosis was made from positive NS1 antigen. Full blood count showed bicytopenia of moderate anaemia and critically low platelets. Suspicion of haemolysis arises in view of high lactate dehydrogenase (LDH) (1016 U/l) with high indirect hyperbilirubinaemia (51umol/l), Direct coombs test positive and Reticulocyte count 2.1%. Peripheral blood smear suggestive of microangiopathic haemolytic anaemia (MAHA) with the presence of 2.6% schistocytes, keratocytes, spherocytes and microspherocytes. ADAMTS13 activity obtained was low. On day 1 of admission, the patient was transfused with 1 pint packed cell and 3 units of fresh frozen plasma. The patient then immediately started on plasma exchange on day 2 of admission and underwent a total of five sessions of plasma exchange and steroid therapy. The serial full blood picture noted improvement of schistocytes count with normal LDH and platelet count. *Discussion:* Prompt and accurate clinical recognition of TTP presentation in dengue fever as well early intervention with plasma exchange is warranted to improve clinical outcome and prevent further complications.

**HM29: Pre-analytical Dilemma: Interferences in FBC Analyser**

Agila Ganasagaran, Nur Dini Suliman, Aifa Osman, Chuah Khai Cyne, Jeevananthini Magsparam, M. Logashnee Manikam

*Department of Pathology, Hospital Tengku Permaisuri Norashikin, Kajang, Selangor Darul Ehsan, Malaysia*

*Introduction:* Full blood count (FBC) is a common laboratory test that enumerates blood cell counts. Thus, providing clues to certain illnesses in patients such as anaemia, infection, and malignancy when correlated with clinical history and physical examination. This case series highlights common interferences in the FBC analyser (Sysmex XN-1000) at our centre and measures taken to overcome these interferences. *Case Report:* This case series includes four cases. The first case involves a premature neonate sample with spurious leucocytosis caused by nucleated red blood cells interference, resolved by manual calculation of corrected WBC. The second case is a sample from a 63-year-old female presented with jaundice and tea-coloured urine. The red blood cells (RBC) parameters were abnormal caused by RBC agglutination, sorted by warming the sample at 37 degrees. The third case is a sample of a 1-year-old boy with spurious thrombocytopenia caused by platelet clumps. An accurate normal platelet count was obtained after reanalysing his new sample in a citrated tube instead. The last case involves a sample from a 37-year-old female with spurious thrombocytosis caused by fragmented cell interference, with correct platelet count obtained after repeating the sample with PLT-F (Platelet fluorescent). *Discussion:* Nucleated red blood cells, platelet clumps, RBC agglutination and fragmented red cells are pre-analytical errors contributed by patient conditions. These can be addressed by having excellent knowledge of the limitation and also advanced principle of detection of FBC analysers along with vigilant full blood picture reporting, correlated with the patient's clinical condition.

**HM30: When necrosis obscures the diagnosis: Uncovering a B-lymphoid neoplasm**

Geetha Nallappan, Kisa Khazanah Uthayarajah, Sukanya Banerjee Nair, Siti Zubaidah Mustapha
*Department of Pathology, Hospital Tengku Ampuan Rahimah, Klang, Selangor, Malaysia*

*Introduction:* Bone marrow necrosis (BMN) is rare and can obscure underlying malignancies. Here, we present a case of B lymphoid neoplasm diagnosed in the setting of marrow necrosis, highlighting the diagnostic challenges it poses. *Case report:* A 66-year-old male presented with a 2-day history of malaise, constipation, and decreased responsiveness. Laboratory investigations revealed hypercalcaemia, hyperferritinaemia, and isolated factor VII deficiency (5.2%). A full blood picture showed pancytopenia with a leukoerythroblastic picture and occasional blast-like cells. Initial bone marrow studies were suboptimal. Repeat marrow after one month showed a dry tap with blast cells on trephine imprint, indicating malignant infiltration. Immunophenotyping was inconclusive. Trephine biopsy was suboptimal and revealed necrotic tumour with crushed lesional cells. Immunohistochemistry showed CD20, CD79a, CD45, CD10, BCL6, and CD99 expression, with weak BCL2, suggesting B-lymphoid neoplasm. *Discussion:* BMN involves the destruction of haematopoietic or neoplastic cells, typically resulting from microvascular failure, and is frequently observed in hypercellular marrows. It is commonly linked to malignancy, infection, or sickle cell disease. Clinical manifestations include bone pain, fever, cytopenia, and elevated LDH and ferritin levels. Diagnosis depends on trephine biopsy findings of disrupted architecture, eosinophilic debris, and ghost cells. BMN should be distinguished from conditions such as aplastic anaemia, gelatinous transformation, and amyloidosis. Ancillary stains (e.g., CD3, CD20, CD34, GMS, AFB) assist in diagnosis, with nuclear markers avoided due to unreliable staining in necrotic tissue. TNF and CRP, as associated chemical mediators, may serve as useful biomarkers. This case emphasises that a comprehensive evaluation is essential for accurate diagnosis of BMN.

**HM31: A retrospective study on acute myeloid leukaemia (AML): Risk classification based on conventional cytogenetics and next-generation sequencing (NGS) in Subang Jaya Medical Centre (SJMC)**

Nurul Aida Ariffen[1], Yee Ling Sum[1], Ning Yi Yap[1], Nurul Shuhada Sukri[1], Noor Aziedayati Sairan[1], Bee Suan Tay[1], Che Zairieha Che Ainudin[1], Soo Chin Ng[1,2]
*[1]Laboratory, Subang Jaya Medical Centre, Subang Jaya, Selangor, Malaysia; [2]MK Faculty of Medicine & Health, Universiti Tunku Abdul Rahman, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* Genetic aberrations are significant in acute myeloid leukaemia (AML). The 2022 European LeukaemiaNet (ELN) Risk Classification for AML stratifies these into favourable, intermediate, and adverse risk groups. Thus, this study aims to analyse the prognosis of AML using this classification. *Materials & Methods:* Genetic aberrations were evaluated using karyotyping and Next-generation sequencing (NGS) in Subang Jaya Medical Centre (SJMC) (Approved by institutional ethics committee (Ref. no.: 202504.5)). Newly diagnosed AML cases (n=75) with concurrent karyotyping and NGS (year 2020 – 2024) were available for prognostication using the 2022 ELN guideline. *Results:* Karyotyping showed normal (42.7%), abnormal (56.0%), and culture failure (1.3%). Risk classification based solely on cytogenetics resulted in 13.3% favourable, 12.0% intermediate, and 30.7% adverse risk cases. NGS detected no genetic abnormalities (2.7%) and genetic aberrations (97.3%). Prognostication via NGS classified 26.7%, 26.7% and 33.0% of cases into favourable, intermediate, and adverse risk groups, respectively. Integrating both methods re-classified these groups into 26.7% favourable, 24.0% intermediate and 46.7% adverse risk. *Discussion:* The 2022 ELN Risk Classification involved both cytogenetics and NGS data. Using only one method showed that NGS detected higher prevalence of all risk groups. The incorporation of both methods appears to increase the detection of adverse risk aberrations in a range of 13.7~16.0%. In conclusion, both karyotyping and NGS are important complementary methods in classification of AML. This provides valuable insights and subsequently appropriate patient management since the adverse risk group will benefit more from bone marrow transplants.

**HM 32: Diagnostic and Minimal Residual Disease Monitoring in T-Cell Acute Lymphoblastic Leukaemia: A Two-Year Experience from Hospital Tunku Azizah**

Norazlina Azman, Siti Shahrum Muhamed Said, Suzana Zainol, Shenaz Banu Said Khan, Nurimatussolehah Sarijan, Koh Su Yee, Fatin Adlia Arifin, Siti Noraisyah Mahidin, Norhaslindawati Mohamad Ali, Nur Athirah Md Akhir, Tracyca Zuna Anak Nawang, Noor Syazwani Md Shakkeri, Salfeandy Salleh, Nurul Aida Abdul Rahman, Nurul Syahirah Syahril, Mimi Azura Aziz
*Department of Pathology, Hospital Tunku Azizah, Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* T-cell acute lymphoblastic leukaemia (T-ALL) is a high-risk ALL subtype that benefits from sensitive monitoring for risk stratification. Minimal residual disease (MRD) detection by flow cytometry (FCM) is a key prognostic tool. At Hospital Tunku Azizah (HTA), 8-colour FCM panels were developed for both diagnosis and MRD monitoring. This abstract presents HTA's two-year experience with T-ALL cases. *Materials & Methods:* We retrospectively analysed 58 diagnostic and 25 MRD-monitoring T-ALL cases (paediatric and adult) from June 2022 to June 2024. Immunophenotypic profiles were recorded at diagnosis. MRD was assessed at Day 15 (≥100,000 events, 0.1% sensitivity), Day 36, and Week 12 (≥1,000,000 events, 0.01% sensitivity). *Results:* At diagnosis, cyCD3 and CD7 were expressed in all cases. CD99, nTdT, and CD5 were also frequently expressed. CD34, CD1a, CD4, and CD8 showed variable expression. A significant proportion of T-ALL cases (50%) demonstrated a CD4-/CD8- immunophenotype. Six patients were identified as having early T-cell precursor ALL (ETP-ALL). MRD positivity was common at Day 15, often with large clone sizes. By Day 36, fewer patients remained positive, with some not achieving remission. MRD levels continued to decline by Week 12, and all tested cases were negative by Week 21. *Discussion:* Our experience demonstrates that MRD assessment using multiparameter flow cytometry is both feasible and reproducible in a resource-limited public healthcare setting. The establishment of panel design, acquisition targets, and coordinated clinician-laboratory workflows has ensured timely and clinically meaningful MRD reporting. Ongoing training and resource optimisation remain essential for sustaining and expanding this service.

**HM33: Immunophenotypic Characterisation and MRD Monitoring in Paediatric B-ALL: Flow Cytometry Insights from Hospital Tunku Azizah**

Norazlina Azman, Siti Shahrum Muhamed Said, Suzana Zainol, Shenaz Banu Said Khan, Nurimatussolehah Sarijan, Mohd Fikri Mustapha, Lai Ngan Shan, Norhaslindawati Mohamad Ali, Nur Athirah Md Akhir, Tracyca Zuna Anak Nawang, Noor Syazwani Md Shakkeri, Salfeandy Salleh, Nurul Aida Abdul Rahman, Nurul Syahirah Syahril ,Mimi Azura Aziz
*Department of Pathology, Hospital Tunku Azizah, Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* Acute Lymphoblastic Leukaemia (ALL) is the most common childhood cancer, with B-cell ALL (B-ALL) being the predominant subtype. Detecting minimal residual disease (MRD) using flow cytometry is essential for monitoring treatment response. This study aimed to characterise the immunophenotypic profiles of paediatric B-ALL patients at diagnosis and during MRD assessments, based on the BFM-ALL paediatric protocol. *Materials & Methods:* This retrospective study analysed 506 flow cytometry datasets of paediatric B-ALL patients tested at Hospital Tunku Azizah between June 2020 and December 2022. Bone marrow immunophenotyping data were collected at six time points: diagnosis, Day 15, Day 36, Week 12, Week 21, and end of treatment. Leukaemia-associated immunophenotypes (LAIPs) assessed included CD45 dim/negative, CD10 bright, CD38 downregulated, CD58 overexpressed, CD66c positive, CD81 negative, CD73 positive/dim, CD123 positive, and CD34/CD20 positive. *Results:* At diagnosis, most cases exhibited 2–4 leukaemia-associated immunophenotypes (LAIPs), with the most frequent being CD45 negativity (77%), CD58 overexpression (64%), and CD10 bright expression (49%). During measurable residual disease (MRD) assessment, MRD-positive samples typically showed 2–4 LAIPs, with some cases demonstrating up to 8. CD73 (positive/dim), CD123 (positive), and CD58 remained consistently detectable, indicating marker stability. Over time, MRD positivity decreased, with 224 out of 387 MRD samples showing no detectable LAIPs. *Discussion:* Hospital Tunku Azizah successfully integrates LAIP-based flow cytometry for MRD monitoring in paediatric B-ALL. Consistent LAIP expression and combined analytical strategies ensure accurate tracking, while close clinician-laboratory Collaboration enhances result interpretation and supports protocol-driven, high-quality patient care.

**HM34: Tosoh HLC-723G11 in Haemoglobinopathy Screening: A Tertiary Hospital Experience**

Siti Umairah Abd Rahman[1,2], Darnina Abdul Jalil[1], Munirah Abdul Razak[1], Thatcheiany Kumariah[1], Faridah Idris[2]
*[1]Haematology Unit, Department of Pathology, Hospital Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia; [2]Department of Pathology, Faculty of Medicine and Health Sciences, Universiti Putra Malaysia Serdang, Selangor, Malaysia*

*Introduction:* Accurate detection of thalassaemia and haemoglobinopathy is the key for its effective clinical management and national screening efforts. High-performance liquid chromatography (HPLC) analysers have been used as one of the methods for screening thalassaemia and haemoglobinopathies. This study evaluates the performance of the newly introduced Tosoh G11 HPLC analyser in comparison with two established platforms: Sebia Capillarys (capillary zone electrophoresis) and Bio-Rad Variant-II (HPLC). *Materials & Methods:* A prospective comparative study was conducted at the Haematology Unit, Pathology Department, Hospital Kuala Lumpur. 104 patient samples systematically selected were analysed using all three platforms. Chromatographic findings and presumptive diagnoses were compared. Agreement and bias of haemoglobin (Hb) fraction quantification (Hb $A_2$ and Hb F) were assessed using Intraclass Correlation Coefficient and Bland-Altman analyses. *Results:* The majority of screened patients were Malay (87.5%) and adolescents (51.9%) who underwent testing for the national Form 4 screening program. Tosoh G11 identified both common and rare Hb variants, including Hb H, Hb CS, Hb E, Hb S, Hb D, Hb J, Hb Lepore and Hb Q-Thailand. It demonstrated improved chromatographic distinction for Hb E and Hb H compared to Variant-II. Quantitative analysis showed good to excellent agreement in Hb $A_2$ and Hb F values across all platforms, with Tosoh G11 exhibiting significant positive bias against Sebia Capillarys and non-significant bias against Bio-Rad Variant-II for Hb $A_2$ quantification. *Discussion:* Tosoh G11 offers comparable Hb variants' detection and quantification to the existing instruments. Its incorporation into current laboratory workflows could strengthen national screening programmes.

**HM35: A Child With Myelodysplastic Syndrome – Cytomorphology and Cytogenetic Profile of Two Cases**

Farah Azima Abdul Muttlib[1], Julia Mohd Idris[2], Alia Suzana Asri[1], Yong Woon Lee[1]
*[1]Department of Laboratory Diagnostic Services, Hospital Tunku Ampuan Besar Tuanku Aishah Rohani, Hospital Pakar Kanak-Kanak UKM, Kuala Lumpur, Malaysia. [2]Department of Laboratory Diagnostic Services, Hospital Canselor Tuanku Muhriz UKM, Kuala Lumpur, Malaysia*

*Introduction:* Myelodysplastic syndrome (MDS) is a clonal haematopoietic stem cell disease characterised by cytopenias, ineffective haematopoiesis, morphological dysplasia and increase risk of leukaemia. Childhood MDS (cMDS) is rare. Here, we present 2-cases of cMDS, describing their clinical, morphological and genetic features. *Case report:* The first case is 12-years-old-girl presented with intermittent fever and weight loss for 5-months. No hepatosplenomegaly or lymphadenopathy present. Blood picture revealed pancytopenia, macrocytosis and the presence of abnormal mononuclear cells. BMAT revealed hypercellularity, erythroid hyperplasia and suppressed myelopoiesis. Megaloblastosis and dyserythropoiesis were prominent. Discrete dysplasia of myeloid and megakaryocytes was seen, with myeloblasts accounting for ~3.3%. Differential diagnosis of megaloblastic anaemia and MDS was suggested. Biochemical analysis showed low serum folate. Subsequent chromosomal analyses revealed monosomy 7, hence diagnosis of cMDS was made. The disease progressed to increase blasts with fibrosis 2-years later. Second case is 6-years-5-months-old-girl investigated for persistent pancytopenia. Neither lymphadenopathy nor hepatosplenomegaly was detected. Blood smear revealed leucoerythroblastic picture. BMAT revealed hypercellularity, erythroid hyperplasia, megaloblastic dyserythropoiesis, binuclearity, nuclear budding and karyorrhexis. Left shift maturation with dysgranulopoiesis and overt dysmegakaryopoiesis seen. Multilineage dysplasia was evident on immunophenotyping. Myeloblasts were increase(5.6%) with aberrant heterogenous CD13,nTdT,CD10 and CD7. Karyotyping revealed 46,XX,del(20)(q12)[5]/46,XX[27] and diagnosis of cMDS-IB was concluded. She remains in progression-free state, awaiting for HSCT. *Discussion:* MDS in children is extremely rare. Both cases show hypercellularity,

trilineage dysplasia, overt erythroid hyperplasia with megaloblastosis. Considering its rarity, folate deficiency seen in the first case compelled the diagnosis of megaloblastic anaemia. Morphological features are indistinguishable, thus differentiating both is challenging. The presence of clonality is crucial in helping the diagnosis.

**HM36: A Rare Case of Marrow Involvement by Lymphocyte-Depleted Classic Hodgkin Lymphoma**

Ngan Shan Lai, Kim Yan Poh
*Department of Pathology, Universiti Malaya, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* Lymphocyte-depleted classic Hodgkin lymphoma (LDCHL) is a very rare subtype of classic Hodgkin lymphoma (cHL), accounting for <2% of all HL cases. *Case report:* A 34-year-old Malay gentleman, presented with low back pain for 4 months, associated with bilateral lower limb weakness, urinary retention, and B-symptoms. Clinically there were bilateral palpable cervical lymph nodes and hepatosplenomegaly. Initial CT and MRI scans revealed extensive lymphadenopathy involving the cervical, thoracic, and abdominal nodal regions along with spinal cord compression at T4/T5 level. FBC showed severe anaemia and thrombocytopenia (Hb 22g/L, WBC $4\times10^9$/L, PLT $49\times10^9$/L). Infectious screening for HIV was negative. Bone marrow examination was performed and a dry tap on the aspirate. In the trephine biopsy, the marrow architecture was distorted by diffuse reticulin and collagen fibrosis. Occasional mononuclear Hodgkin cells, multinucleated Reed Sternberg cells (HRS cells) with prominent eosinophilic nucleoli and mummified cells could be observed. These cells are positive for IHC CD30 and CD15(weak), negative for CD20 and CD3. The background inflammatory cells are mainly fibroblasts with reactive T cells forming rosettes around the HRS cells. The histopathological features are therefore compatible with LDCHL. The patient had succumbed after one cycle of ABVD chemotherapy. *Discussion:* LDCHL is one of the 4 subtypes of cHL. There are two histologic patterns in LDCHL, one with diffuse fibrosis where fibroblasts are the main inflammatory cells while the other pattern is rich in anaplastic and pleomorphic HRS cells. LDCHL has the worst prognosis of all HL, usually presented at an advanced stage.

**HM37: Enhanced Identification of CNS Involvement in Childhood B-cell ALL: A Case Demonstrating the Utility of Immunophenotyping in CNS Relapse**

Nur Khairunnisa Aizan[1], Woon Lee Yong[2], Sie Chong Doris Lau[3], C-Khai Loh[3]
*[1]Department of Pathology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Wilayah Persekutuan Kuala Lumpur, Malaysia; [2]Department of Diagnostic Laboratory, Hospital Tuanku Ampuan Besar Tunku Aishah Rohani, Universiti Kebangsaan Malaysia, Wilayah Persekutuan Kuala Lumpur, Malaysia; Department of Pediatric, Universiti Kebangsaan Malaysia, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* Central nervous system (CNS) involvement in pediatric B-cell acute lymphoblastic leukaemia (B-ALL) may occur alongside with marrow disease or as an isolated relapse. Accurate detection of blasts in CNS is critical for timely management. Conventional CSF cytology lacks sensitivity, especially in low disease burden, while immunophenotyping offers a more sensitive detection tool. *Case Report:* A 5-year-old girl with relapsed B-ALL, achieved remission and on maintenance phase of UKALL R3 protocol, presented with bilateral eyelid swelling. MRI revealed leukaemic infiltration of both lacrimal glands and right optic nerve, raising concern for CNS involvement. Full blood picture showed mild anaemia (Hb 10.5 g/dL), normal WBC ($6.85\times10^9$/L), and normal platelets ($334\times10^9$/L) with no circulating blasts. Bone marrow aspiration showed no excess blasts. CSF cytology and cell count analysis was unremarkable, showing no blast detected. However, CSF immunophenotyping was performed within 60 minutes of collection, through acquiring 4,418 events and identified a distinct blast population (191 events; 9.1%), gated at CD45-negative and low side-scatter area, expressing CD19, CD10 (bright), under-expressed CD38 and CD81, CD66c+CD123 and CD73+CD304, matching her initial diagnostic immunophenotype, thus confirming an isolated CNS relapse. *Discussion:* This case highlights the superior sensitivity of CSF immunophenotyping over cytology in detecting CNS involvement in paediatric B-ALL. Flow cytometry enables earlier and more accurate diagnosis in cases with minimal disease, supporting its use in both diagnostic and relapse evaluations, which may improve outcomes through earlier intervention.

**HM38: A RARE HAEMOGLOBIN VARIANT: THE CLINICAL AND GENETIC UNRAVELING OF HAEMOGLOBIN LOUISVILLE**

Sharifah Sarah Syed Mohamad Alwi[1], Faidatul Syazlin Abdul Hamid[1], Syahzuwan Hassan[1], Ezzanie Suffya Zulkifle[1], Aisyah Aziz[1], Sharifah Suhana Syed Abd Rahman[1], Tze Shin Leong[2], Ermi Neiza Mohd Sahid[1], Azian Naila Md Nor[1], Suguna Somasundram[1], Ezalia Esa[1], Norafiza Mohd Yasin[1], Yuslina Mat Yusoff[1]
*[1]Haematology Unit, Cancer Research Centre (CaRC), Institute for Medical Research (IMR), National Institute for Health (NIH), Selangor, Malaysia; [2]Haematology Unit, Medical Department, Hospital Umum Sarawak.*

*Introduction:* Hb Louisville/Hb Bucuresti, a rare unstable haemoglobin variant characterised by a specific amino acid substitution which involves the replacement of phenylalanine with leucine at position 42 of the beta-globin chain, can lead to low oxygen affinity. *Case report*: An 8 months old girl was found to have low $SpO_2$ (80% on room air) during routine check-up. Clinically she was cyanosed but not in respiratory distress and investigations showed no cardiopulmonary abnormalities. Interestingly, arterial blood gas (ABG) analysis on room air revealed a PO2 of 113 mmHg. Her full blood count (FBC) showed RBC count of $2.51\times10^6$/uL, Hb of 6.9g/dL, MCV of 79.3fL, MCH of 24.7pg, RDW 22.3%. Full blood picture (FBP) showed normochromic normocytic anaemia with oxidative haemolysis features. Haemoglobin (Hb) analysis using High-performance liquid chromatography (HPLC) revealed borderline HbA2 (3.9%) with C window of 0.8%, while haemoglobin analysis capillary electrophoresis (CE) revealed borderline A2 (3.6%) and Z1 zone of 0.9%. Direct beta sequencing confirmed the presence of Hb Louisville/Hb Bucuresti. Her mother, aunt and grandfather's beta sequencing showed similar findings. *Discussion:* In carriers such as this case, features such as spuriously low SpO2 with lack evidence of respiratory distress or cardiorespiratory symptoms, with mild haemolytic anaemia observed, consistent with low oxygen affinity and unstable Hb. Hb analysis for this variant did not show a distinct abnormal peak

or may only present as minor, non-specific abnormalities. In view of the diagnostic limitation for unstable haemoglobin using Hb analysis hence the need for molecular testing for accurate diagnosis.

**HM39: Bone marrow morphology: a critical diagnostic tool in secondary hemophagocytic lymphohistiocytosis**

Sarah, Abdul Halim[1], Norlelawati A Talib[1], Ismail Ibrahim[2], Sumaiyah Adzahar[3]
*[1]Department of Pathology and Laboratory Medicine, Kulliyyah of Medicine, International Islamic University Malaysia, Pahang, Malaysia; [2]Department of Internal Medicine, Kulliyyah of Medicine, International Islamic University Malaysia, Pahang, Malaysia; [3]Department of Pathology and Medical Laboratory, Faculty of Medicine, Universiti Sultan Zainal Abidin (UniSZA), Terengganu, Malaysia*

*Introduction:* Hemophagocytic lymphohistiocytosis (HLH) is a life-threatening hyperinflammatory syndrome characterised by excessive immune activation and systemic inflammation. Timely diagnosis remains challenging due to nonspecific clinical presentations and overlapping laboratory abnormalities, particularly in secondary HLH where underlying triggers such as infections obscure the clinical picture. Bone marrow morphology can offer essential diagnostic evidence in such cases. *Case Report:* A 77-year-old man with squamous cell carcinoma of the lung and recent COVID-19 infection presented with pancytopenia and progressive clinical deterioration. Initial investigations were inconclusive and bone marrow examination was performed as part of pancytopenia workup. The bone marrow aspirate and trephine biopsy revealed prominent hemophagocytic activity. The calculated H-Score was 171, supporting a diagnosis of HLH. Immunohistochemistry showed strong CD68 and CD163 expression, with Glycophorin A confirming erythrophagocytosis. Despite initiation of corticosteroid therapy, the patient developed multiorgan failure and died. *Discussion:* This case highlights the diagnostic value of bone marrow morphology in identifying HLH, particularly when clinical features are ambiguous or overlapping with other conditions. The morphological evidence of haemophagocytosis, supported by immunohistochemical markers, was critical in establishing the diagnosis. In resource-limited settings or cases with diagnostic uncertainty, timely bone marrow assessment can expedite recognition and initiation of treatment. While haemophagocytosis alone is not pathognomonic, its presence within the appropriate clinical context strongly supports the diagnosis and may improve clinical decision-making. This approach is particularly valuable in secondary HLH cases where underlying conditions may complicate the clinical picture and delay recognition of this rapidly progressive, potentially fatal syndrome.

**HM40: When Gamma-Delta T-Cells Invade: A Sinusoidal Drama Unfolds**

Hari Priya Raghvan[1], Wee Shiang Yui[1], Caroline Ho Siew Ling[1], Ehram Jamian[1], Indhira Subbiah[1], Noraida Khalid[1]
*[1]Department of Pathology, Hospital Sultanah Aminah, Johor Bahru, Ministry of Health, Malaysia.*

*Introduction:* Hepatosplenic T-cell lymphoma (HSTL) is a rare and aggressive peripheral T-cell lymphoma that arises from cytotoxic T-cells, most commonly of the gamma-delta (γδ) T-cell receptor subtype. *Case report:* We present a case of a 32-year-old male with abdominal distension and constitutional symptoms. On examination, there is the presence of splenomegaly but no peripheral lymphadenopathies noted. A positron emission tomography (PET) scan depicted massive splenomegaly and enlarged liver. Full blood picture showed pancytopenia with no abnormal lymphoid cells/blasts noted. A bone marrow aspirate examination was undertaken and revealed the presence of abnormal lymphoid cells without lymphocytosis. Immunophenotyping confirmed the presence of abnormal T-cells with γδ restriction. Trephine biopsy displayed intrasinusoidal involvement of the abnormal lymphoid cells which were positive for CD3, CD56, TIA1 and negative CD8. He was then started on CHOP (cyclophosphamide, doxorubicin, vincristine and prednisolone) chemotherapy and subsequently planned for haematopoietic stem cell transplant. *Discussion:* HSTL primarily affects younger adults and can be difficult to diagnose because its symptoms may resemble other myeloid or lymphoid neoplasms and morphology may be subtle. Unlike most other lymphomas, HSTL typically does not present with lymphocytosis or a leukaemic appearance, making it harder to be identified. Key indicators, such as massive splenomegaly and abnormal lymphoid cells in the sinusoids with γδ restriction in flow cytometry, can help pinpoint HSTL. Early detection requires high suspicion and additional studies, as the prognosis is poor. Allogeneic stem cell transplantation is currently the only potential curative treatment.

**HM41: Evaluation And Improvement Strategy of Laboratory Turnaround Time for Group, Screen and Hold**

Ameera Ashyila Kamaruzaman[1], Zalizah Khalid[1,2], Wan Asmuni Wan Mohd Saman[1,2], Nurhazrina Hashim[2], Muhammad Fakhri Sallehussin[2]
*[1]Department of Pathology, Faculty of Medicine, Universiti Teknologi MARA, Sg. Buloh Campus, Selangor, Malaysia; [2]Haematology and Transfusion Medicine Unit, Department of Clinical Diagnostic Laboratories, Hospital Al-Sultan Abdullah, Universiti Teknologi MARA, Selangor, Malaysia*

*Introduction:* Laboratory turnaround time (LTAT) is an important quality indicator in clinical laboratories. Group, Screen and Hold (GSH) is a pre-transfusion procedure that consists of ABO and RhD grouping test and antibody screening test. This study aims to evaluate the overall LTAT for GSH requests and identify factors contributing to the delays. *Materials & Methods:* This retrospective study was conducted over a 6-month period at the Haematology and Transfusion Medicine Unit (HTMU) of a tertiary care teaching hospital in Malaysia. We analysed the LTAT of all GSH requests received which comprised received-to-preparation time and validation time. Cases with prolonged LTAT were further evaluated for causes of delay. *Results:* A total of 2687 GSH requests were analysed. Of these, 1658 (61.70%) requests exceeded the internally mandated LTAT threshold (more than 4-hour). Blood bank validation time comprised 96.14% (1594 requests) of this delay, and most (70.7%) requests involved sample arrival after office hour. Sample arrival after office hour contributed 70.44% (1168 request) of the delays in GSH LTAT, with (1128 request) occurring during validation time. *Discussion:* Most of GSH LTAT requests were delayed, and occurred in the validating process. Most of the delay in validation of results occurred on samples arriving after office hours, especially during weekends and public holidays. We identified validation of GSH results by Scientific Officer (SO) and SOs' office hours work schedule contributes to delay in LTAT of GSH. This result will be used to change our current workflow practices to improve LTAT and customer satisfaction.

**HM42: A Diagnostic Dilemma in An Adolescent Male**

Ameera Ashyila Kamaruzaman[1], Azzatul Husna Ahmad[1,2], Nor Hafiza Saad[2], Sharifah Mai Sarah Syed Azmi[2], Salmi Abdullah[2], Asmawiza Awang[3], Zalizah Khalid[1]

*[1]Department of Pathology, Faculty of Medicine, Universiti Teknologi MARA, Sg. Buloh Campus, Selangor, Malaysia; [2]Department of Pathology, Hospital Selayang, Selangor Malaysia; [3]Department of Pathology, Hospital Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* Incidence of Non-Hodgkin lymphoma (NHL) increases with age; however, diffuse large B-cell lymphoma (DLBCL) is one of the commonest subtypes in adolescent and young adulthood (AYA). We present the difficult diagnostic procedure and the complicated course in an adolescent patient with DLBCL. *Case Report:* The 16-year-old male presented with a history of prolonged fever for the past 7 months, B symptoms and hepatosplenomegaly. There was no palpable lymphadenopathy. Extensive investigations including infectious workups were negative. CT scan showed multiple paraaortic, portal and subhepatic lymph nodes, but the biopsy only showed reactive histiocytes. There was no malignancy detected. Later, patient deteriorated, developed pancytopenia (Hb 2.5 g/dL, WBC $3.65 \times 10^3$/uL, Plt $92 \times 10^3$/uL), and bone marrow biopsy was further performed which reported marrow infiltration by High Grade Large B Cell Lymphoma, non GCB-type. The course of disease was complicated by worsening anaemia (Hb dropped from 8 g/dL to 4.7 g/dL), anuric Acute Kidney Injury requiring dialysis, liver failure and coagulopathy which was not corrected even after administration of blood products, PCC and Fibrinogen Concentrate. The patient was subsequently critically ill, needing double inotropes support and finally succumbed to death due to multiorgan failure. *Discussion:* This case of DLBCL in an adolescent male is extraordinary in many ways. DLBCL, especially the non-GCB type, is a relatively rare disorder in AYA patients. Predominant bone-marrow involvement has been described in only a few older patients with non-GCB-type DLBCL and mostly aggressive clinical courses.

**HM43: A Case of HbA1c Interference Revealing a Rare Beta-Globin Variant in a Malaysian Patient**

Mohd. Fauzi Mohd. Yusoff

*Department of Pathology, Hospital Sultan Abdul Halim, Kedah, Malaysia*

*Introduction:* Haemoglobin A1c (HbA1c) is widely used to assess glycaemic control in diabetic patients. Inheritance of haemoglobin variants can interfere with HbA1c tests and cause glycaemic status to be misinterpreted. This example highlights the diagnostic challenge posed by an unreported beta-globin variant found in an asymptomatic person. *Case report:* A 64-year-old Indian man with diabetes mellitus presented to the primary care clinic for a routine follow-up. However, the result suggested possible assay interference due to a haemoglobinopathy. A complete blood count done revealed normochromic normocytic anaemia, with a haemoglobin level of 9.9 g/dL. Haemoglobin capillary electrophoresis revealed a normal HbA2 level and presence of an abnormal peak at Zone 8, which appeared fused with HbA. High-Performance Liquid Chromatography revealed normal HbA2 and HbF, and the presence of unknown peak of 39.5% at a retention time of 2.78 minutes, shouldering with HbA. DNA analysis revealed the heterozygous condition of the Codon 25 [GGT>GCT] variant. The findings indicated heterozygosity for a beta variant. *Discussion:* The medical literature and global haemoglobin variant databases have not yet documented this variant. The clinical importance is hence undetermined. This example illustrates the diagnostic complications associated with unexplained HbA1c interference and underscores the necessity of evaluating haemoglobin variants, particularly in the ethnically diverse population of Malaysia. Hence, it is worth noting that screening for haemoglobinopathy is important when HbA1c interference is present, regardless of Mean Corpuscular Volume and Mean Corpuscular Haemoglobin values. Further research is required to ascertain the clinical significance of this distinct beta-globin mutation.

**HM44: Comparative genomic profiling of circulating tumour DNA and FFPE tissue using targeted next-generation sequencing in Diffuse Large B-Cell Lymphoma**

Yuslina Mat Yusoff[1], Zahidah Abu Seman[1], Fatin Sofia Mohamad[1], Sharifah Suryani Syed Rahim[2], Ermi Neiza Mohd Sahid[1], Ezalia Esa[1], Mohd Fadzly Shaharuddin[3], Asmawiza Awang[3] and Norhayati Omar[3]

*[1]Haematology Unit, Cancer Research Centre, Institute for Medical Research, National Institutes of Health, Ministry of Health Malaysia, Selangor, Malaysia; [2]Department of General Medicine, Hospital Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia; [3]Department of Pathology, Hospital Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* Diffuse large B-cell lymphoma (DLBCL) is a genetically heterogeneous malignancy, in which precise molecular profiling is essential for classification, risk stratification and therapeutic targeting. While formalin-fixed paraffin-embedded (FFPE) tissue biopsy remains the diagnostic gold standard, it is invasive and may not adequately capture tumour heterogeneity. This study aimed to evaluate the performance of circulating tumour DNA (ctDNA) obtained through liquid biopsy, as a minimally invasive alternative for mutation profiling in DLBCL. *Materials & Methods:* Fifteen (15) ctDNA and 11 tissue samples (≥20 ng/μL, high purity) underwent library preparation using a custom 305 kb SureSelect XT HS2 DNA panel targeting 70 DLBCL-related genes. Mutational profiles were analysed and compared across both sample types. *Results:* ctDNA revealed a broader mutation spectrum than tissue samples. High mutation frequencies in ctDNA were observed for ID3, MGA, KMT2D, TNFRSF14, CD22, CREBBP, ANKRD17, EP300, FOXO1 and NOTCH2, many of which were absent or minimally detected in tissue samples. In paired samples (n = 11), overlapping mutations were identified in 33 out of 70 genes. The most frequently mutated genes across both sample types included ID3, MGA, TNFRSF14, TGFBR2, PIM1, FOXO1, GNA12, CD22, PRDM1 and KTM2D. *Discussion:* This study represents one of the first efforts in Malaysia to explore ctDNA-based profiling in DLBCL. The broader mutation detection in ctDNA suggests its higher sensitivity and ability to capture aspects of tumour heterogeneity. These findings demonstrate the feasibility and potential of ctDNA as a complementary or alternative tool for molecular profiling, particularly when tissue access is limited.

**HM45: Delta Beta Thalassaemia in Pregnancy: Molecular Subtypes and Haematological Profiles from a Malaysian Cohort**

Ermi Neiza Mohd Sahid[1], Samsol Kamal Mohd Bahari[2], Ezalia Esa[1], Faidatul Syazlin A Hamid[1], Syahzuwan Hassan[1], Yuslina Mat Yusoff[1], Azian Naila Md Nor[1], Norafiza Mohd Yasin[1], Sabariah Md Noor[2]

*[1]Institute for Medical Research, National Institute of Health, Shah Alam, Selangor, Malaysia; [2]Department of Pathology, Faculty of Medicine and Health Sciences, Selangor, Malaysia*

*Introduction:* Delta beta (δβ) thalassaemia is a rare haemoglobinopathy characterised by elevated foetal haemoglobin (HbF). Pregnancy may influence its clinical presentation. This study evaluated the molecular subtypes and haematological profiles of δβ-thalassaemia in pregnant Malaysian women compared to non-pregnant females. *Methods:* A retrospective cross-sectional study was conducted on 224 confirmed heterozygous δβ-thalassaemia cases. Molecular subtyping, haemoglobin fraction analysis, and full blood count (FBC) assessments were performed. Comparisons were made between pregnant women (n=24) and non-pregnant females from a school-based screening cohort (n=95). Iron studies were unavailable. *Results:* Seven δβ-thalassaemia subtypes were identified, with Gγ(Aγδβ)$^0$ Siriraj (32.6%) and (δβ)$^0$ Thai (29.9%) being the most common. Pregnant women exhibited significantly lower haemoglobin (10.8 ± 1.4 g/dL) and RBC counts (4.7 ± 0.9 × $10^6$/$mm^3$) than non-pregnant females (13.6 ± 1.2 g/dL; 5.8 ± 0.5 × $10^6$/$mm^3$). Mean corpuscular haemoglobin (MCH) and mean corpuscular volume (MCV) were slightly reduced during pregnancy. RDW was significantly higher in pregnant women (18.4 ± 2.8% vs. 17.1 ± 2.9%, p=0.017). HbF levels remained elevated (mean 18–20%) with no significant difference between groups. *Discussion:* Pregnancy may exacerbate anaemia in δβ-thalassaemia by further lowering Hb and RBC indices. Co-inheritance with alpha thalassaemia might also be a contributing factor. Elevated RDW suggests anisopoikilocytosis, aiding differential diagnosis. Despite the absence of iron studies, consistently elevated HbF supports the diagnosis. These findings emphasise the importance of antenatal screening and haematological monitoring during pregnancy.

**HM46: Novel missense mutation in F8 gene causing severe Haemophilia A**

Gowrisankari Navaretnam[1], Ermi Neiza Mohd Sahid[1], Norafiza Mohd Yasin[1], Azian Naila Md Nor[1], Suguna Somasundram[1], Nursaedah Abdullah Aziz[1], Lam Kah Yuen[1], Siti Nor Assyuhada Mat Ghani[1], Zulaiha Muda[2], Yuslina Mat Yusoff[1]

*[1]Haematology Unit, Cancer Research Centre, Institute for Medical Research, National Institutes of Health, Wilayah Persekutuan Kuala Lumpur, Malaysia; [2]Department of Paediatrics, Hospital Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* Haemophilia A is a congenital X-linked recessive bleeding disorder caused by mutations in F8 gene, which encodes coagulation factor VIII. Severe Haemophilia A is defined by factor VIII levels below 1%, often results from large gene inversions, though missense mutations can also be causative. We report a novel missense mutation in the F8 gene in a severe Haemophilia A patient. *Case report:* A 4-year-old male presented with easy bruising and joint bleeds onset at day 12 of life. Factor VIII activity <1%, consistent with severe Haemophilia A. There was no family history of bleeding disorders. Further testing revealed that the patient did not develop inhibitors. Molecular testing began with inverse-shifting PCR and multiplex PCR to screen for intron 22 and intron 1 inversions, which were negative. PCR and bidirectional Sanger sequencing of the promoter and all coding exons (1–26) of F8 revealed a novel hemizygous missense mutation, c.1236G>C (p.Trp412Cys), in exon 8. The variant substitutes tryptophan with cysteine at a conserved site within the A2 domain of factor VIII, and is predicted to be deleterious by in-silico tools. The variant was not previously described in disease variant databases, confirming its novelty. Maternal testing confirmed carrier status. *Discussion:* The c.1236G>C (p.Trp412Cys) mutation represents a novel cause of severe Haemophilia A. Although large structural rearrangements are frequent in severe cases, full sequencing is essential for patients without common inversions. This case expands the spectrum of pathogenic mutations in F8 and emphasises the diagnostic value of genetic testing.

**HM47: Silent Genes, Loud Symptoms: Early-Onset Haemoglobin H Disease in an Infant with Compound Heterozygosity for $-\alpha^{3.7}$ Deletion and Hb Adana Mutation**

Nor Ainiza Mansor[1], Siti Fatihah Zulaikha Shamsul Kamal[1], Azly Sumanty Ab Ghani[1], Wan Amal Hayati Wan Hassan[1], Wan Zuhairah W. Embong[1], Zakiah Nurasyikin Mohamed Halim[1]

*[1]Department of Pathology, Hospital Sultanah Nur Zahirah, Terengganu, Malaysia*

*Introduction:* Haemoglobin H (Hb H) disease is a form of α-thalassemia caused by the dysfunction of three α-globin genes. Non-deletional variants, particularly those involving unstable haemoglobins such as Hb Adana, are associated with more severe phenotypes and earlier clinical manifestations. *Case report:* We report a term Malay-Indonesian newborn boy with an uneventful antenatal period, born to a mother with deletional Hb H disease (--SEA/$-\alpha^{3.7}$). At 10 hours old, his haemoglobin dropped from 14.2 to 11.1 g/dL, requiring packed-cell transfusion. The mother was O+ and the baby A+, raising concerns for ABO incompatibility, supported by blood film and haemolytic markers. He was discharged with Hb 8.7 g/dL. At follow-up, worsening anaemia was noted (Hb 7.2 g/dL at 6 weeks and 6.8 g/dL at 2 months), prompting a second transfusion. Hb analysis at 3-month-old was suggestive of Hb H disease. DNA analysis confirmed compound heterozygosity for the $-\alpha^{3.7}$ deletion and a codon 59 mutation (Hb Adana). The father was identified as a Hb Adana carrier. The child remains clinically well and non–transfusion-dependent under haematology follow-up. *Discussion:* Non-deletional Hb H disease, especially with unstable Hb Adana, can present in neonatal period due to haemolysis and ineffective erythropoiesis. While ABO incompatibility may have contributed to early anaemia, the persistent haemoglobin decline suggests an underlying intrinsic haemoglobinopathy. Diagnosis is challenging due to nonspecific early findings and limitations of routine newborn Hb analysis. Early molecular testing is essential for accurate diagnosis, family counselling, and ongoing management.

**HM48: Verifying EE score for differentiation of homozygous haemoglobin E and haemoglobin E $\beta^0$-thalassaemia in Malaysian population : A Study in Hospital Kuala Lumpur**

Faridah Ahmad Maulana[1], Munirah Abdul Razak[1], Norafiza Mohd Yasin[2], Ezalia Esa[2], Noraesah Mahmud[1]
[1]Department of Pathology, Hospital Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia; [2]Haematology Unit, Cancer *Research Centre (CaRC), Institute for Medical Research (IMR), National Institute for Health (NIH), Selangor, Malaysia*

*Introduction:* Differentiating between homozygous HbE and HbE-$\beta^0$ thalassaemia can be a problem during haemoglobin (Hb) analysis. The objective of this study was to verify the EE score formula in differentiating between these two HbE-related disorders which is helpful to reduce the number of referral cases for molecular testing. *Materials & Methods:* Laboratory results from thalassaemia DNA analysis database at Hospital Kuala Lumpur (HKL) in 2023 and 2024 were analysed in which molecular analysis for the diagnosis of β mutation and HbE were performed on these cases. EE scores were calculated using the HbA2 and HbF levels measured by capillary electrophoresis using the published formula of 7.3HbA2 + HbF. Verification of this formula was subsequently performed. *Results:* 66 cases of homozygous HbE and 185 cases of HbE-$\beta^0$ thalassaemia were included. The EE score of >60 indicated HbE-$\beta^0$ thalassaemia, which was found in all HbE-$\beta^0$ thalassaemia cases and only 3 of homozygous HbE cases. Application of this score showed accurate prediction of HbE-$\beta^0$ thalassaemia with 100% sensitivity, 95.5% specificity, 98.4% positive predictive value and 100% negative predictive value. *Discussion:* EE score formula with cut-off point of above 60 could identify potential HbE-$\beta^0$ thalassaemia cases and be helpful in differentiation between these two HbE-related disorders. Although the EE score has been established based on the Thai population, this formula could also be applied in our population, provided the Hb analysis is done by a method capable of reporting HbA2 in the presence of HbE with clinical correlation.

**HM49: Utilising whole genome sequencing for breakpoint characterisation of the multi-species conserved sequence (MCS) in the Human α-Globin Locus**

Norafiza Mohd Yasin[1,2], Anaelle Vigne[1], Veronique Baudin[1], Tamara Koopman[1], Sandra J.G. Arkesteijn[1], Maaike Verschuren[1], Linda Vijfhuizen[1], Jeanet ter Huurne[1], Rianne Schaap[1], Jelmer Legebeke[1] Joroen Knijnenburg[1], Femke de Vries[1], Cornelis L. Harteveld[1]
*[1]Department of Clinical Genetics/LDGA, Leiden University Medical Centre, Leiden, The Netherland; [2]Haematology Unit, Cancer Research Centre (CaRC), Institute for Medical Research (IMR), National Institute for Health (NIH), Selangor, Malaysia*

*Introduction:* Alpha-thalassaemia is an inherited haemoglobin disorder characterised by microcytic anaemia due to reduced expression of α-globin genes. While most cases are caused by deletions within the α-globin gene cluster on chromosome 16, some result from deletions in upstream regulatory regions. These deletions, often arising through homologous or non-homologous recombination between repetitive elements, can disrupt critical enhancers such as the multi-species conserved sequence (MCS-R) cluster, essential for erythroid-specific α-globin gene expression. *Materials and Methods:* We investigated three patients with microcytic anaemia and intact α-globin genes, who were identified by multiplex ligation-dependent probe amplification (MLPA) as having deletions affecting the MCS-R cluster. Breakpoint analysis was performed using whole genome sequencing (WGS), and the deletions were characterised via read-depth and split-read analysis in Integrative Genomics Viewer (IGV), with breakpoint sequences reconstructed. *Results:* The identified deletions among Dutch patients ranged from 3.3 kb to 61 kb and included two novel deletions not previously reported. Of particular note, we describe for the first time an $\alpha\alpha^{ALT}$ deletion in a Dutch individual, involving a complex rearrangement between chromosome 16 and chromosome 3. This finding expands the known ethnic and geographic spectrum of such rearrangements. *Discussion:* These results underscore the critical role of the MCS-R region, especially MCS-R2, in the long-range regulation of α-globin expression. Comprehensive characterisation of regulatory deletions enhances our understanding of erythroid gene regulation and highlights the utility of WGS in diagnosing complex structural variants causing α-thalassaemia.

**HM 50: Pitfalls in Diagnosing Haemoglobin E Beta Thalassaemia from Haemoglobin Analysis: Possible Genotypes and Diagnostic Clues for an Accurate Diagnosis**

Munirah Abdul Razak[1], Darnina Abdul Jalil[1], Faridah Ahmad Maulana[1], Ezalia Esa[2], Ahmad Faizal Sabri[1], Noraesah Mahmud[1]
*[1]Department of Pathology, Hospital Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia, [2]Haematology Unit, Cancer Research Centre (CaRC), Institute for Medical Research (IMR), National Institute for Health (NIH) Setia Alam, Selangor, Malaysia*

*Introduction:* A presumptive diagnosis of haemoglobin E-beta zero (HbE-$\beta^0$) thalassaemia is commonly established based on haemoglobin (Hb) analysis, typically showing predominant HbE and HbF with the absence of HbA. Although the diagnosis may appear straightforward, the underlying genotype could instead be different. *Case Report:* We report five cases, aged 16–67 years, suspected HbE-$\beta^0$ thalassaemia based on Hb analysis, each later molecular study revealed the following genotypes: Homozygous HbE, compound heterozygous HbE-$\beta^0$, HbE-Lepore, HbE-δβ and HbE-HPFH. Hb levels ranged from 6.1 to 12.5 g/dL. Clinically, severity varied based on genotype: HbE-$\beta^0$ in the patient with severe anaemia, HbE-Lepore and HbE-HPFH in those with moderate anaemia, HbE-δβ with mild anaemia, and homozygous HbE in the patient with normal Hb. In all cases, Hb analysis showed the absence of HbA with predominance of HbE and HbF. One case demonstrated a peak at Zone 6 (10.7%), initially misinterpreted as degraded HbE, later identified as Hb Lepore. $HbA_2$ levels were elevated in HbE-$\beta^0$ and homozygous HbE (4.1% and 4.0%) and within the normal range in HbE-HPFH and HbE-δβ (2.9% and 2.8%). EE scores were 77 for HbE-$\beta^0$ and 50 for homozygous HbE. *Discussion:* This poster highlights the diagnostic pitfalls in interpreting similar haemoglobin patterns that mask distinct genotypes in HbE-related disorders. Although HbE and HbF are predominant on Hb analysis, differences in phenotype, $HbA_2$ percentage, chromatogram pattern, and EE score can help distinguish the underlying genotype. A comprehensive approach involving phenotype correlation, Hb analysis, EE score, and molecular testing are essential for accurate diagnosis.

**HM51: Haemoglobin Phnom Penh (HBA1:c.354_355insATC): a rare alpha globin variant in Malaysia**

Nur Azura Suliman[1], Darnina Abdul Jalil[1], Ermi Neiza Mohd. Sahid[2], Norafiza Mohd Yasin[2], Munirah Abdul Razak[1]
*[1]Department of Pathology, Hospital Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia; [2]Haematology Unit, Cancer Research Centre, Institute for Medical Reseacrh (IMR), Shah Alam, Malaysia*

*Introduction:* Haemoglobin (Hb) Phnom Penh is a rare alpha (α) globin variant due to mutation at codons 117/118 (+ATC) in exon 3 of α-1 globin gene. This report presents the first documented case of Hb Phnom Penh in Malaysia. *Case report:* We describe a family with Hb Phnom Penh and $\alpha^0$-thalassaemia Southeast Asian (SEA) deletion. The index case, a healthy 16-year-old girl, presented with hypochromic microcytic RBC indices during thalassaemia school screening programme. Capillary electrophoresis (CE) showed low HbA2 level with normal shape of HbA and HbA2 peaks. There was no peak observed in other zones. High-performance liquid chromatography (HPLC) revealed mildly low HbA2 level with widening and shouldering patterns of both HbA and HbA2 peaks. No pre-run peaks were observed. Molecular tests of the alpha gene confirmed compound heterozygous Hb Phnom Penh and $\alpha^0$-thalassaemia SEA deletion. Parental testing identified heterozygous Hb Phnom Penh in the father and heterozygous $\alpha^0$-thalassaemia SEA deletion in the mother. *Discussion:* This case was highlighted due to its rarity. Although Hb Phnom Penh has distinct features on HPLC, it may be missed on CE due to co-elution with HbA and its HbA2 variant is present at a low level, often undetectable, resulting in only low HbA2. Importantly, despite the interaction between Hb Phnom Penh and $\alpha^0$-thalassaemia appears silent, the clinical consequences of this variant when co-inherited with non-deletional α-thalassaemia mutations or unstable α-globin variants remain unknown. Such combinations may potentially result in more severe phenotypes and warrant careful genetic counselling and further investigation.

**HM52: Early Detection of Haematological Malignancies through Slide Review Practice: A Six-Year Retrospective Study**

Nor Ayuni Khuzaimah[1], Nabeelah Abdul Khalid[1]
*[1]Department of Pathology, Hospital Pulau Pinang, Pulau Pinang, Malaysia.*

*Introduction:* Slide review is a key part of the Full Blood Count validation, performed for samples with cytopenia or analyser-generated flags. In our lab, Medical Laboratory Technologists (MLT) conduct initial screening. Cases exhibiting significant morphological abnormalities will be escalated to a Medical Officer and Pathologist for confirmation. Cases suggestive of haematological malignancies or haemolysis will be reported as urgent, and the turnaround time for slide review is 24 hours. *Materials and Methods:* A retrospective analysis was conducted from the data in the Lab Information System at Haematology Unit, Pathology Department, Hospital Pulau Pinang, between 2019 and 2024, encompassing 25,994 slide review reports. *Results:* Among the reviewed reports, 130 cases were reported as suggestive of haematological malignancies (0.5% positive detection rate). The malignancies included: Acute Leukaemia (52%, n=68), Myeloproliferative Neoplasm (21%, n=27), Lymphoproliferative Disease (15%, n=20), Myelodysplastic/Myeloproliferative Neoplasm (6%, n=8), Myelodysplastic Neoplasm (3%, n=4), and Multiple Myeloma (2%, n=3). On average, our lab detected around 20 to 30 cases of haematological malignancies per year, with nearly 50% of these slide reviews originating from FBC samples collected in the Emergency Department. *Discussion:* Slide review remains a critical tool in the early detection of haematological malignancies, enabling prompt diagnosis and intervention. Our findings underscore the importance of integrating slide review into routine FBC validation protocols. Furthermore, this study highlights the essential role of MLTs as first-line screeners, emphasising that their morphological competency is crucial for the accurate and timely identification of abnormal cases.

**HM53: Myelodysplastic/Myeloproliferative Neoplasm, Not Otherwise Specified with Isolated Isochromosome 17q: A Case Report**

Seunghwan Kim, Seo Wan Kim, Minkyung So, Jungwon Huh
*Ewha Womans University College of Medicine, Seoul, South Korea*

*Introduction:* Myelodysplastic/Myeloproliferative Neoplasms, Not Otherwise Specified (MDS/MPN, NOS) are heterogeneous clonal haematopoietic disorders. The 2022 ICC and WHO 5th edition provisionally recognise MDS/MPN with isolated isochromosome 17q (i(17q)) as a distinct sub-entity under MDS/MPN, NOS. This entity is associated with aggressive clinical courses and rapid AML progression. This report details a rare case, highlighting its unique morphological, molecular, and cytogenetic features. *Case report:* A 76-year-old female presented with chronic kidney disease and anaemia. Initial CBC showed mild thrombocytosis (603 x $10^9$ /L), normalizing after 6 months, with persistent anaemia (Hb 5.8-8.2 g/dL). Bone marrow (BM) was hypercellular with prominent multilineage dysplasia. Distinct morphological findings included markedly increased and dysplastic megakaryocytes (micromegakaryocytes, hypolobation). Dysgranulopoiesis (hypolobation) and dyserythropoiesis (nuclear budding, megaloblastic change) were also evident. BM biopsy showed no fibrosis. Cytogenetic analysis revealed isolated i(17q). FISH showed TP53 deletion (77%) and monosomy 17 (3%). NGS identified pathogenic variants in SRSF2 (VAF 60.5%), SETBP1 (VAF 41.1%), and ASXL1 (VAF 29.8%). Diagnosis: MDS/MPN, NOS with isolated isochromosome 17q. *Discussion:* This case exemplifies diagnostic complexities in MDS/MPN, NOS, particularly with fluctuating peripheral blood counts, underscoring the need for detailed morphological evaluation. The combination of hypercellular BM with marked dysmegakaryopoiesis and i(17q) is highly characteristic of this recently recognised entity. Co-occurrence of SRSF2 and SETBP1 mutations is frequent in this subtype, with TP53 mutations being rare despite 17p loss. This case emphasises integrating unique morphological patterns with cytogenetic and molecular findings for precise classification and understanding of these aggressive myeloid neoplasms.

**HM54: Comprehensive molecular characterisation of three new α-thalassemia deletions (--$^{SA}$), (--$^{CR}$) and (-α$^{16.6}$) in the Malaysian population**

Faidatul Syazlin Abdul Hamid[1], Syahzuwan Hassan[1], Ezalia Esa[2], Ermi Neiza Mohd Sahid[1], Azian Naila Md Nor[1], Norafiza Mohd Yasin[1], Yuslina Mat Yusoff[1]

*[1]Haematology Unit, Cancer Research Centre, Institute for Medical Research, National Institutes of Health, Selangor, Malaysia; [2]Virology Unit, Infection Disease Research Centre, Institute for Medical Research, National Institutes of Health, Selangor, Malaysia Institutes of Health, Selangor, Malaysia*

*Introduction:* α-thalassemia is a genetic disorder caused by reduced production of the α-globin chain, often due to large gene deletions. This study investigates rare α-thalassemia deletions in the Malaysian population. *Materials & Methods:* Whole blood samples of 23 cases were referred to the Institute for Medical Research (IMR) for further molecular analysis of α-thalassemia between 2016 and February 2025. Multiplex ligation-dependent probe amplification (MLPA) was used to detect large deletions, and deletion breakpoints were further characterised using published primers and confirmed by Sanger sequencing. *Results:* Three rare α-thalassemia deletions were identified among the 23 cases: the (--$^{SA}$) deletion (n = 15), the (--$^{CR}$) deletion (n = 7), and the (-α$^{16.6}$) deletion (n = 1). Among the 15 (--$^{SA}$) deletion cases, the majority were Malay (n = 6), followed by Indian (n = 4), Chinese (n = 2), Dusun (n = 1), Iban (n = 1), and others (n = 1). For the (--$^{CR}$) deletion, most cases were Malay (n = 5), with the remainder being Chinese (n = 2). The single case of the (-α$^{16.6}$) deletion was identified in a Malay individual. *Discussion:* The (--$^{SA}$) deletion was first reported in South Africa, then in Indian and North American populations. (--$^{CR}$) was initially found in Chiang Rai and Southern China, while (-α$^{16.6}$) was previously identified in Thailand. The presence of these deletions in Malaysians suggests possible intermarriage with other ethnic groups, contributing to the discovery of new α-thalassemia genotypes in Malaysia.

**HM55: Performance Evaluation of the AI-100 Digital Morphology Analyser for White Blood Cell Differential Counts: A Comparative Study with Automated Haematology Analyser and Manual Microscopy**

Fatin Adlia Arifin, Suzana Zainol, Nurimatussolehah Sarijan, Siti Maryam Abdul Mujib, Norhaslindawati Mohamad and Mimi Azura Aziz

*Department of Pathology, Hospital Tunku Azizah, Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia.*

*Introduction:* This study evaluated the performance of the AI-100 digital morphology analyser (Sigtuple) compared to automated haematology analysers and manual microscopy for white blood cell (WBC) differential assessment. *Materials & Methods:* Forty-three stained blood smears, encompassing a range of normal and pathological WBC morphologies, were analysed using the AI-100 and compared to automated haematology analyser (Sysmex XN-3000) results and manual microscopy (gold standard) by 3 experienced pathologists. Statistical analyses included Pearson correlation coefficients, coefficient of determination ($r^2$), and Passing-Bablok regression to assess agreement and systematic biases. *Results:* For neutrophils, the AI-100 demonstrated excellent agreement with both automated (r=0.971, $r^2$=0.94, slope=0.973) and manual assessments (r=0.976, $r^2$=0.953, slope=0.951). Lymphocyte counts showed moderate to strong correlations; the AI-100 underestimated counts compared to automated analysers (r=0.918, $r^2$=0.843, slope=0.908) but overestimating them relative to manual counts (r=0.681, $r^2$=0.464, slope=0.998). Monocyte classification by the AI-100 showed poor correlation with automated analysers (r=0.119, $r^2$=0.014) but moderate correlation with manual microscopy (r=0.676, $r^2$=0.457). Eosinophil counts demonstrated strong agreement (r=0.893–0.862, $r^2$=0.797–0.743). Basophil counts showed very poor correlation (r=0.195, $r^2$=0.038). *Discussion:* Our findings align with previous studies evaluating digital morphology analysers, highlighting strong performance for neutrophil and eosinophil identification but challenges with monocytes and basophils. While the AI-100 can enhance laboratory efficiency through rapid, consistent classification of common WBCs, manual verification remains essential, particularly for rare or morphologically variable cells. Manual microscopy remains the cornerstone for confirming critical morphological assessments and ensuring safe, accurate clinical decision-making.

**HM56: Insights From a Homozygous β$^+$-Thalassemia Case: Haemoglobin Analysis Similarities with Classical Heterozygous β-Thalassemia**

Nor Syazana Jamali[1], Kisa Khazanah Uthayarajah[2], Wan Hayati Mohd Yaakob[2], Azian Naila Md Nor[3]

[1]Department of Pathology, Hospital Banting, Selangor, Malaysia; [2]Department of Pathology, Hospital Tengku Ampuan Rahimah, *Klang, Malaysia; [3]Molecular Genetic Laboratory, Haematology Unit, Cancer Research Centre, Institute Medical Research, National Institute of Health, Selangor, Malaysia*

*Introduction:* Homozygous β$^+$-thalassemia often presents with variable clinical severity, typically as thalassemia intermedia. We report the haematological characteristics of a case involving a homozygous β$^+$-thalassemia mutation. *Case report:* This patient is a 31-years-old, Malay lady noted to have thalassaemic indices from peripheral blood film. Her red cell indices were; haemoglobin 8.9g/dL, red cell count 5.15 x10$^{12}$/L, mean cell volume 56.5fL, mean cell haemoglobin 17.3pg. Normal serum ferritin (120ug/L). Peripheral blood film shows anisopoikilocytosis, hypochromic microcytic red cells, target, cigar, irregular contracted, and tear drop cells with no nucleated red cells. Haemoglobin analysis by capillary electrophoresis (CE) shows raised $HbA_2$ (6.2%) and HbF (2.2%) with $HbA_0$ 91.6%. High Performance Liquid chromatography (HPLC) shows raised $HbA_2$ (6.2%) and HbF (2.4%) $HbA_0$ 82.5%. DNA analysis on beta-globin gene by Sanger sequencing identified homozygous Poly A [AATAAA>AATAGA] (β$^+$) mutation. DNA analysis on alpha-globin gene/cluster did not detect any abnormality. *Discussion:* The Poly A mutation affects the polyadenylation signal of the β-globin gene, disrupting mRNA processing and leading to β$^+$-thalassemia. The patient's haematological parameters and borderline upper limit level of $HbA_2$ raise suspicion of a more severe phenotype than a classical β-thalassemia trait. Without further DNA analysis, the homozygous status for this patient could be missed. This case demonstrates a mild thalassemia intermedia phenotype that currently does not require transfusion. A similar previously reported case presented later in life and eventually required regular transfusions, underscoring the importance of genetic confirmation and clinical monitoring.

**HM57: The Interaction of Mesenchymal Stem Cell Secretions on the Growth, Invasion and Gene Expressions of Double-Hit Diffuse Large B-Cell Lymphoma**

Xi Zeng Low[1], Soon Keng Cheong[2], Alan Han Kiat Ong[1], Bee Sun Lee[2]
*[1]Department of Pre-clinical Sciences, MK Faculty of Medicine and Health Sciences, Universiti Tunku Abdul Rahman, Malaysia; [2]Department of Medicine, MK Faculty of Medicine and Health Sciences, Universiti Tunku Abdul Rahman, Malaysia*

*Introduction:* The interaction between MSCs and cancer cells is complicated, exhibiting both pro-tumourigenic and anti-tumourigenic effects. In this study, we aim to investigate the effect of human umbilical cord-derived MSCs (hUC-MSCs) on a double-hit diffuse large B cell lymphoma (DH-DLBCL) cell line. *Materials & Methods:* The hUC-MSCs were seeded in 100mm petri dishes and cultured in 37 °C, 5% $CO_2$ incubator for 3 days. Once confluence, batches of medium were supplied to the cells and further cultured 1 day. The hUC-MSCs medium was collected, filtered, and stored as conditioned medium (CM). A DH-DLBCL cell line with c-MYC and BCL-2 gene expression was used in the study. The CM was co-cultured with the cell line in 0%, 25% and 100% concentration for 3 days. The treated cell line was subjected to cell count assay (CCK8), cell cycle assay, invasion assay and qPCR. *Results:* After co-culturing with hUC-MSCs CM, CCK8 study demonstrated that the cell count of DH-DLBCL decreased in trend when the concentration of CM was increased, cell cycle of the treated DH-DLBCL was arrested at S-phase, invasiveness of the cells was suppressed, and qPCR analysis showed down-regulation of *c-MYC* and *BCL6* genes expression. *Discussion:* Our study demonstrated co-culturing of DH-DLBCL cells and hUC-MSC CM resulted in an inhibitory effect to the growth and invasive potential of the cancer cells. Further studies are needed to confirm these findings, which could be a potential therapeutic approach in the DLBCL treatment paradigm.

**HM:58 Warm AIHA in a newly diagnosed Lymphoma: A Case Report**

Azzatul Husna Ahmad[1,2], Ameera Ashyila Kamaruzaman[2], Nor Hafiza Saad[1], Sharifah Mai Sarah Syed Azmi[1], Salmi Abdullah[1], Asmawiza Awang[3], Ummi Mohlisi Mohd Asmawi[2], Zalizah Khalid[2]
*[1]Department of Pathology, Hospital Selayang, Selangor, Malaysia; [2]Department of Pathology, Faculty of Medicine, Universiti Teknologi MARA, Sg. Buloh Campus, Selangor, Malaysia; [3]Department of Pathology, Hospital Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* Warm Autoimmune Hemolytic Anaemia (wAIHA) can be primary or secondary. In this case, we found NHL as the underlying disease of wAIHA. Non-Hodgkin Lymphoma can coexist with AIHA, known as AIHA-associated Non-Hodgkin Lymphoma. Approximately 1 from 5 AIHA patients develop lymphoma, while 7% to 10% of lymphoma patients have co-existing AIHA. *Case report:* We report a 54-year-old lady presented with fever and anaemic symptoms for a week. Clinically, she had mild hepatosplenomegaly with no lymphadenopathy. Full blood count showed severe anaemia (Hb 3.9g/dL), mild leucocytosis (WCC 12.33 × $10^3$/uL) with lymphocytosis (Absolute Lymphocyte Count 8.11 × $10^3$/uL) and normal platelet (Plt 179 × $10^3$/uL). Full blood picture showed 91% abnormal lymphoid cells, polychromasia and spherocytes. Direct Coombs Test was positive (IgG 4+, C3d 3+) and elution showed nonspecific Auto IgG, thus suggestive of wAIHA. Bone marrow aspirate, flow cytometry and trephine immunohistochemistry stains are suggestive of marrow infiltration by B-cell lymphoma (60% infiltration), low-grade, with weak heterogeneous CD5 positivity. Differential diagnosis includes marginal zone lymphoma and lymphoplasmacytic lymphoma. For the management of AIHA, this patient received packed cell transfusion and was given IV Hydrocortisone, IV MTP, IVIG and subsequently oral prednisolone. Her Hb increased to 9.3g/dl and was then transferred to Hospital Ampang for further management. *Discussion:* The differential diagnosis of lymphoma should be considered in patients presented with AIHA.

**HM59: The Eye That Opened a Myeloma Mystery: A Case Report of Ptosis Preceding Plasma Cell Myeloma Diagnosis**

Siti Nurrazan Zulkifli[1], Elina Subramaniam[1], Sukanya Banerjee Nair[1], Zainura Anita Zainal Abidin[1], Siti Zubaidah Mustapha[1], Wan Hayati Mohd Yaakob[1], Wan Muhammad Jalaluddin Wan Mohamed[2], Ahmad Zakiyy Mohamed[2]
*[1]Department of Pathology, Hospital Tengku Ampuan Rahimah, Selangor, Malaysia; [2]Department of Medicine, Hospital Tengku Ampuan Rahimah, Selangor, Malaysia*

*Introduction:* Plasma cell myeloma, a malignant proliferation of clonal plasma cells, is a systemic haematological malignancy typically characterised by bone lesions, renal dysfunction, hypercalcemia, and anaemia. While its diverse clinical presentations are well-documented, initial manifestations are rarely confined to isolated ocular symptoms such as proptosis, diplopia, or visual impairment, which usually occur in later stages often due to orbital plasmacytomas or direct infiltration. This case report highlights an unusual instance where isolated ptosis served as the sentinel symptom, ultimately leading to the diagnosis of plasma cell myeloma. *Case report:* This is a case of a 69-year-old lady with underlying diabetes mellitus and hypertension presented with right eye ptosis for 1 week. Clinical examination discovered right 3rd cranial nerve palsy. No signs of increased intracranial pressure or organomegaly. Full blood picture showed leucoerythroblastic anaemia with occasional abnormal mononuclear cells. Bone marrow examination with immunohistochemistry staining revealed infiltration by the clonal plasma cells. Other myeloma workups also fulfilled the diagnosis of plasma cell myeloma. *Discussion:* This case highlights that patient's presentation which is a seemingly benign ophthalmic complaint, can be the sole initial indicator of a systemic malignancy, underscores the critical need for clinicians, to maintain a high index of suspicion for underlying systemic diseases, even in the presence of isolated and non-specific symptoms. Early recognition of such atypical presentations is paramount, as prompt diagnosis of plasma cell myeloma allows for timely initiation of appropriate systemic therapy, potentially improving patient outcomes and preventing further disease progression.

**HM60: Therapy-Related B-Acute Lymphoblastic Leukaemia Transformation Following Refractory Classical Hodgkin Lymphoma: A Case Report**

Alina Md Fauzi[1,2], Wong Chee Yong, Liew Pek Kuan[1], Veena Sevaratnam[1], Tan Sen Mui[1]
*[1]Department of Haematology, Hospital Ampang, Selangor, Malaysia; [2]Department of Medical Sciences II, Faculty of Medicine and Health Sciences, Universiti Sains Islam Malaysia, Negeri Sembilan, Malaysia*

*Introduction:* We present a rare case of therapy-related B-acute lymphoblastic leukaemia (B-ALL) in a 33-year-old woman with a history of refractory classical Hodgkin lymphoma (cHL). Initially diagnosed in 2017 with stage IVB cHL, she was given six cycles of ABVD. Due to persistent disease, she received prolonged oral methotrexate and 6-mercaptopurine, followed by second-line bendamustine and brentuximab in 2019–2020, however defaulted treatment between 2022-2023. The disease progressed and the patient underwent stem cell transplant in late 2024, achieving temporary remission. In April 2025, patient presented with new-onset leukocytosis (WCC 100 ×10⁹/L), anaemia (Hb 7 g/dL), and thrombocytopenia (platelet 16 ×10⁹/L). Peripheral blood morphology and flow analysis revealed 65% blasts of B-cell lineage with aberrant expression of CD304+CD73, absent CD45, CD34, TdT, and light chains—consistent with therapy-related B-lymphoblastic leukaemia. Although refusing bone marrow examination, this diagnosis was sufficiently made in the context of extensive prior chemotherapy and immunotherapy exposure. *Discussion:* Therapy-related ALL is a rare but recognised complication of cytotoxic treatment, diverging from the typical progression to acute myeloid leukaemia. In addition, therapy related ALL, often associated with more adverse molecular and cytogenetic aberrations, have poorer outcomes than de novo ALL.The pathogenesis likely involves genotoxic insults to haematopoietic progenitors, with emerging evidence suggests overlapping mutational profiles with myeloid malignancies (e.g., DNMT3A, ASXL1, RUNX1), as well as classical ALL-associated genes (e.g., CDKN2A, IKZF1).This case underscores the need for long-term monitoring in patients undergoing intensive, multimodal therapies for Hodgkin lymphoma, and highlights the diagnostic and therapeutic challenges associated with therapy-related lymphoid neoplasms.

**HM61: Mimicry Unmasked: A Case of Haemoglobin G-Makassar Misidentified as Sickle Cell Trait**

Mohd Fauzi[1], Nurul Asyikin Nizam Akbar[2,3]
*[1]Haematology Unit, Department of Pathology, Hospital Sultan Abdul Halim, Kedah, Malaysia; [2]Department of Haematology & Transfusion Medicine Unit, Kelantan, Malaysia, [3]Hospital Pakar Universiti Sains Malaysia (HPUSM), Kelantan, Malaysia.*

*Introduction:* Haemoglobin G-Makassar is a rare β-globin variant that is clinically benign but presents a diagnostic challenge because its electrophoretic similarity to haemoglobin S (Hb S). This case report describes a 30-year-old pregnant woman in Malaysia initially suspected to have sickle cell trait underscores the importance of molecular testing for accurate identification of haemoglobin variants. *Case report:* A 30-year-old pregnant woman presenting with persistent mild hypochromic microcytic anaemia underwent further evaluation during a routine prenatal visit. Capillary electrophoresis showed Hb A at 60.3%, Hb A2 at 3.0%, and Hb S at 36.7%, while HPLC revealed Hb A at 51.5%, Hb A2/E at 5.6%, Hb F at 0.6%, and an abnormal peak in the S window. Initially suspected to be heterozygous for Hb S, molecular testing confirmed a heterozygous mutation at codon 6 of the β-globin gene (GAG→GCG), consistent with haemoglobin G-Makassar. *Discussion:* Haemoglobin G-Makassar is a rare variant in Malaysia with a low prevalence, though reports of its presence are increasing. It often causes diagnostic confusion because its haemoglobin analysis pattern closely resembles that of Hb S. Regional studies from Thailand and Malaysia have shown that Hb G-Makassar is clinically benign and does not cause sickling, unlike Hb S. This case highlights the necessity of molecular testing for the accurate identification of haemoglobin abnormalities, crucial for preventing incorrect treatment, alleviating patient anxiety, and avoiding misdiagnosis. The clinically benign attributes of Hb G-Makassar highlight its potential as a subject for further exploration in gene therapy.

**HM62: Unravelling the Cost of Thalassaemia Genotyping in Malaysia's Multi-Ethnic Government Sector**

Ezalia Esa[1], Ezzanie Suffya Zulkifle[2], Faidatul Syazlin Abdul Hamid[2], Syahzuwan Hassan[2], Nur Aisyah Aziz[2], Ermi Neiza Mohd Sahid[2], Azian Naila Md Nor[2], Norafiza Mohd Yasin[2], Yuslina Mat Yusoff[2]
*[1]Virology Unit, Infectious Disease Research Centre (IDRC), Institute for Medical Research (IMR), National Institute for Health (NIH) Setia Alam, Selangor, Malaysia; [2]Haematology Unit, Cancer Research Centre (CaRC), Institute for Medical Research (IMR), National Institute for Health (NIH) Setia Alam, Selangor, Malaysia*

*Introduction:* Thalassaemia in Malaysia shows high genetic diversity due to its multi-ethnic population, requiring multiple molecular methods for accurate genotyping. To optimise resources, a stepwise diagnostic approach screens samples first for common variants based on demographic and phenotypic data, followed by testing for rarer mutations if needed. *Materials & Methods:* A retrospective cost analysis was performed on samples received in 2023. Genotyping of the alpha and beta globin gene clusters employed multiplex ARMS-PCR, multiplex Gap-PCR, MLPA, and direct sequencing. Test costs included reagents, consumables, external quality assurance, and equipment usage. *Results:* Of 2,947 samples received nationwide, 107 (3.6%) were rejected. The majority of samples (n=703; 23.9%) originated from Wilayah Persekutuan Kuala Lumpur. Among 2,840 analysed samples, 1,990 (70.1%) had positive genotypes, 849 (29.9%) were negative, and one (<1%) was inconclusive. A total of 274 test combinations were used, with 85% (n=2,425) requiring more than one method. The total testing cost was RM923,190.00, with per-sample costs ranging from RM110.00 to RM1,050.00. Most samples (n=1,137; 40%) were tested with three methods, averaging RM319.15 per sample. The most frequently used combination was multiplex alpha ARMS-PCR, multiplex alpha Gap-PCR, and beta-globin gene sequencing, costing RM340.00 per sample. A subset of 122 samples (4.3%) exceeded RM600.00, accounting for RM89,480.00 (9.7%) of total costs. *Discussion:* The complexity of thalassaemia genotyping in Malaysia contributes to high costs, as most samples require multiple tests. Enhancing diagnostic algorithms and genotype-phenotype correlations may reduce this burden. Although currently expensive, targeted next-generation sequencing holds promise for future cost-effective diagnosis of complex cases.

**HM63: Rare Fusion, Rare Phenotype: SET::NUP214 Links ETP-ALL and Aberrant B-Cell Antigen Expression?**

Alia Suzana Asri[1], Siti Nurrazan Zulkifli[2], Izyan Khalidah Mohd Arif[1], Malisa Mohd Yusoff[1], Yong Woon Lee[1], Farah Azima Abdul Muttlib[1], Yong Woon Lee[1], Loh C-CKhai[3], Doris Lau Sie Chong[3], Hafiza Alauddin[2]

*[1]Department of Diagnostic Laboratory, Hospital Tunku Ampuan Besar Tuanku Aishah Rohani, Cheras, Wilayah Persekutuan Kuala Lumpur, Malaysia; [2]Department of Pathology, Hospital Canselor Tunku Muhriz, Cheras, Wilayah Persekutuan Kuala Lumpur, Malaysia, [3]Department of Paediatrics, Hospital Tunku Ampuan Besar Tuanku Aishah Rohani, Cheras, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* Early T-cell precursor acute lymphoblastic leukaemia (ETP-ALL) is a high-risk neoplasm with a distinct immunophenotype and molecular profile. While typically expressing stem cell and myeloid antigens, aberrant B-cell expression poses a diagnostic challenge. The *SET::NUP214* fusion gene, typically associated with T-ALL, activates ABL1 kinase. This report details a unique case of ETP-ALL expressing aberrant B-cell markers with *SET::NUP214* fusion. *Case report:* An eight-year-old boy, presented with fever, hepatosplenomegaly, lymphadenopathy and mild cytopaenias (Hb 10.0 g/dL, WBC 7.58x$10^9$/L, Platelet 114 × $10^9$/L, ANC 2.15x$10^9$/L) with 36% bone marrow blasts compatible with ETP-ALL immunophenotype (CD45dim, CD7bright, cyCD3+, CD5dim, CD34partial, HLA-DR+, CD38+, CD33dim). A subclone (13%) expressed dim CD19/cyCD79a, prompting MPAL consideration but disfavoured due to weak intensity and lack of other B-cell markers (CD10, cyCD22). Genetic analysis confirmed *SET::NUP214* fusion and ABL1 deletion. He was treated per UK ALL 2011, escalating to regimen C (addition of cytarabine and asparaginase) due to persistent disease. He achieved MRD negativity during consolidation and is currently in chemotherapy maintenance. *Discussion:* Integrated diagnostics are key for distinguishing ETP-ALL with aberrant B-cell markers from MPAL. This case highlights a potential association of specific molecular finding with aberrant B-cell expression. The *SET::NUP214* fusion, primarily found in T-ALL, occasionally in AML, disrupts nucleocytoplasmic transport and alters gene regulation, promoting proliferation and apoptosis resistance. With only two published worldwide ETP-ALL cases with aberrant B-markers and *SET::NUP214,* investigation into prognostic significance and targeted therapies is warranted.

**HM64: Blood Group Dynamics: Investigating the Link Between ABO/Rh Blood Groups and Metabolic Health Among the University Students**

Madzlifah Ahadon[1], Victoria Chu[2], Kamaleswaran Rajan[2], Kamalia Aqilah Khairul Anwar[2], Petricia Charle[2], Arlizan Bazura Ariffin[1], Norashikin Samsudin[1]

*[1]Department of Pathology, Faculty of Medicine and Health Sciences, Universiti Malaysia Sarawak; [2]Faculty of Medicine and Health Sciences, Universiti Malaysia Sarawak, Malaysia*

*Introduction:* The ABO system is present on the surface of red blood cells as well as in various human tissues, including platelets, epithelium, sensory neurons, and vascular endothelium. Increasing evidence suggests a link between the ABO blood group and the emergence of several disorders, particularly cardiovascular diseases. *Materials & Methods:* A total of 104 medical undergraduates participated in this cross-sectional study from January to June 2024. Sociodemographic data and relevant family history were obtained from each student. Clinical parameters such as the ABO blood group, body mass index (BMI), fasting blood glucose (FBG), fasting total cholesterol, and triglyceride of each student were measured and recorded. These data were then analysed using the IBM SPSS (version 27.0). *Results:* Blood group B was observed to be the most prevalent (n=36), followed by O (n=34), A (n=24), and AB (n=10), with a significant majority (n=102) being Rhesus positive. A statistically significant association between the specific ABO blood group and the different BMI classes was observed (p=0.02). However, no statistically significant associations were observed between O and non-O blood groups with the fasting blood glucose, fasting lipid and the different BMI classes (p>0.05). *Discussion:* The findings of this study indicate a possible connection between a person's blood type and their BMI. Additional studies involving a larger sample size are required to explore this further and validate any potential genetic influences on health.

**HM65: Anaemia Assessment Using the Mindray's BC-6200: Prevalence, Severity and Types in a Newly Established Hospital Setting**

Daniel Shukri[1] , Adibah Daud[1,2], Syamihah Razak[1,2], Kamariah Jalil[1,2], Azzahra Azhar[1,2], Aqil Nazahah[1], Hidayah Wahab[1], Sumaiyah Adzahar[1,2]

*[1]Department of Pathology and Medical Laboratory, Hospital Sultan Zainal Abidin, Kuala Terengganu, Terengganu, Malaysia; [2]Department of Pathology and Medical Laboratory, Faculty of Medicine, Universiti Sultan Zainal Abidin (UniSZA), Kuala Terengganu, Terengganu, Malaysia.*

*Introduction:* Anaemia remains a major global health concern, particularly in developing regions. Early detection and classification are essential for effective management. This study aimed to assess the prevalence, severity, and morphological types of anaemia among patients attending Hospital Sultan Zainal Abidin, a newly established healthcare facility in Terengganu, Malaysia. *Materials & Methods:* A cross-sectional study was conducted over 12 months using complete blood count (CBC) results from patients undergoing routine haematological testing. Anaemia was defined and classified according to World Health Organization (WHO) criteria. Red cell indices obtained from the BC-6200 haematology analyser were used to determine anaemia types (microcytic, normocytic, or macrocytic) and severity (mild, moderate, or severe). *Results:* Among the 387 cases reviewed, 252 (65.1%) patients were found to be anaemic. Of these, 45.3% had mild, 31.1% moderate, and 23.6% severe anaemia. Microcytic anaemia was the most common morphological type (53.7%), followed by normocytic and macrocytic types. Anaemia was more prevalent among females and elderly patients, with statistically significant associations ($p < 0.05$). *Discussion:* This study highlights the substantial burden of anaemia in the population served by a new hospital and supports the utility of automated haematology analysers like the BC-6200 for routine anaemia screening and classification. These findings emphasise the need for early detection and targeted intervention in primary care settings.

**HM66: Factor VII Deficiency in a Pregnant Lady with Hepatitis C Infection: Acquired or Inherited?**

Azly Sumanty AG[1], Nor Ainiza M[1], KH Yip[2], K Ganesh[3], Suzana Z[4]

*[1]Department of Pathology, Hospital Sultanah Nur Zahirah Kuala Terengganu, Terengganu; [2]Department of Medicine, Hospital Sultanah Nur Zahirah Kuala Terengganu, Terengganu; [3]Department of Haematology, Hospital Ampang, Selangor; [4]Department of Pathology, Hospital Tunku Azizah, Kuala Lumpur*

*Introduction:* Factor VII deficiency is a rare bleeding disorder which can be acquired or inherited. Acquired factor VII deficiency may occur in conditions such as severe liver impairment, sepsis or vitamin K deficiency. *Case report:* We report a 21 year old pregnant lady who presented with acute epigastric pain and found to have Hepatitis C with liver transaminitis and isolated prolonged Prothrombin Time (PT) which was corrected on mixing study. Coagulation factor assay showed Factor VII (FVII) activity level of < 1.0%. Prophylactic recombinant activated FVII (rFVIIa) was administered prior to delivery and 4 hours post-delivery. She successfully delivered a live infant vaginally without any complication. Combination antiviral therapy for Hepatitis C commenced 1 week after delivery. She remains well after completion of treatment. However, her PT result remains prolonged despite normalization of liver function. *Discussion:* Regardless whether acquired or inherited, clinical manifestation of FVII deficiency can range from asymptomatic to severe life-threatening bleeding. For this patient, prophylactic rFVIIa was given during delivery at appropriate dosing and interval to reduce incidence of postpartum haemorrhage. Prophylactic rFVIIA before delivery is very important in a pregnant lady with severe disease in the prevention of bleeding complications. A repeat FVII activity assay after improvement of liver function will assist clinician to differentiate between acquired and inherited deficiency.

## MEDICAL MICROBIOLOGY (MM)

**MM01: Clinical and microbiological characteristics of culture-confirmed tuberculous lymphadenitis in adult patients at Universiti Malaya Medical Centre, Kuala Lumpur, Malaysia: a 7-year retrospective cohort study**

Nadia Atiya[1,2 *], Choy Yoong Miin[3], Tai Hui Tian[3], Chandramathi Samudi Raju[2], Azwani Abdullah[1,2]

*[1]Department of Medical Microbiology, Universiti Malaya Medical Centre, Kuala Lumpur, Malaysia; [2]Department of Medical Microbiology, Faculty of Medicine, Universiti Malaya, Kuala Lumpur, Malaysia; [3]Faculty of Medicine, Universiti Malaya, Kuala Lumpur, Malaysia*

*Introduction:* Tuberculosis (TB) is an endemic disease of public health importance in Malaysia. Tuberculous lymphadenitis is a common form of extrapulmonary TB. However, there is a lack of local data on TB lymphadenitis. Hence, our study aimed to determine the clinical and microbiological characteristics of TB lymphadenitis among adult Malaysian patients. *Materials & Methods:* All adult patients aged ≥18 years diagnosed with culture- confirmed TB lymphadenitis at Universiti Malaya Medical Centre from 1 January 2016 to 31 December 2022 were retrospectively analysed. Clinical and microbiological data were collected from patient electronic medical records and the laboratory information system, respectively. Statistical analyses were performed using SPSS version 28.0. *Results:* Thirty- eight adult patients with culture-confirmed TB lymphadenitis were identified, comprising 9.5% of the 399 adult patients diagnosed with extrapulmonary TB during the study period. The cervical lymph node was the most commonly affected (n = 30, 78.9%). The majority of the 38 patients were female (n = 27, 71.1%), aged 18–40 years (n = 26, 68.4%), were smear-negative (n = 29, 76.3%), and HIV-negative (n = 35, 92.1%). Only 7 patients (18.4%) had concomitant pulmonary TB and 4 patients (10.5%) had drug-resistant TB. Xpert MTB/RIF Ultra was performed in 6 patients (15.8%), all of whom tested positive. *Discussion:* Our study provides valuable insights into the clinical and microbiological characteristics of TB lymphadenitis in Malaysian adults. However, our study was limited by its relatively small sample size. Bigger studies are needed to better characterise the epidemiology of TB lymphadenitis in Malaysia.

**MM02: Clinical and microbiological characteristics of extrapulmonary non-tuberculous mycobacterial disease in adult patients at Universiti Malaya Medical Centre, Kuala Lumpur, Malaysia: an 8-year retrospective cohort study**

Nadia Atiya[1,2 *], Si Wei David Fan[3], Minyie Lim[3], Chandramathi Samudi Raju[2], Azwani Abdullah[1,2]

*[1]Department of Medical Microbiology, Universiti Malaya Medical Centre, Kuala Lumpur, Malaysia; [2]Department of Medical Microbiology, Faculty of Medicine, Universiti Malaya, Kuala Lumpur, Malaysia; [3]Faculty of Medicine, Universiti Malaya, Kuala Lumpur, Malaysia*

*Introduction:* The isolation of non-tuberculous mycobacteria (NTM) from clinical samples may indicate transient colonisation or true infection/disease. Local data on extrapulmonary NTM disease (EP-NTMD) is limited. Hence, our study aimed to determine the clinical and microbiological characteristics of EP-NTMD among adult Malaysian patients. *Materials & Methods:* All adult patients aged ≥18 years with NTM isolated from at least one extrapulmonary sample and identified by real-time polymerase chain reaction and speciated using hsp65 gene sequencing at the Diagnostic Mycobacteriology Unit, Department of Medical Microbiology, Universiti Malaya Medical Centre from 1 January 2015 to 31 December 2022 were retrospectively analysed. The following data were retrieved from the patient's electronic medical records: age, gender, auramine O smear microscopy result, NTM species isolated, and whether the patient was diagnosed with EP-NTMD. Statistical analyses were performed using SPSS version 28.0. *Results:* Seventy-nine adult patients had NTM isolated from at least one extrapulmonary sample, of whom 38 (48.1%) were deemed to have NTM colonisation, while 41 (51.9%) were diagnosed with EP-NTMD. The majority of the EP-NTMD patients were males (n=27; 65.9%), aged 18-40 years (n=17; 41.5%), were smear-positive (n = 23; 56.1%) and had disseminated infection (n = 14; 34.1%). Mycobacterium avium complex was the most common causative NTM species causing EP-NTMD (n = 14; 34.1%). *Discussion:* To our knowledge, this is the first study to describe the characteristics of adult EP-NTMD in Malaysia. Further studies among the Malaysian population are required to elucidate the local risk factors for and clinical outcomes of this disease to guide clinical management.

**MM03: Accidental Case of Ancylostoma ceylanicum in the descending colon**

Karshini Jeya Pirathaba[1,2 *], Meng Yee Lai [1], Yee Ling Lau [1]

*[1]Department of Parasitology, Faculty of Medicine, Universiti Malaya, Kuala Lumpur, Malaysia; [2]Department of Medical Microbiology, Universiti Malaya Medical Centre, Kuala Lumpur, Malaysia*

*Introduction: Ancylostoma ceylanicum* is a zoonotic hookworm species primarily infecting dogs and cats but has increasingly been recognised as a cause of human enteric infections, especially in Southeast Asia. Human infections are often associated with environmental exposure or close contact with animals. *Case report:* We report an incidental finding of *A. ceylanicum* in a 68-year-old man with no known medical illness who underwent routine colonoscopy for colorectal cancer screening. The patient was asymptomatic, with no gastrointestinal complaints. Physical and biochemical assessments were unremarkable. He had no identifiable risk factors such as pet ownership, walking barefoot, or gardening. During colonoscopy, a live nematode was observed in the descending colon and retrieved using forceps. The worm measured approximately 11 mm in length with characteristic teeth in the buccal capsule and a pointed tail, morphologically resembling a female *Ancylostoma* spp. Partial sequencing of the internal transcribed spacer (ITS) region showed 100% identity with *A. ceylanicum*. The patient was treated with oral albendazole for three days and remained well. *Discussion:* Although *Ancylostoma duodenale* and *Necator americanus* are well-established as the primary hookworms infecting humans, zoonotic species like *A. ceylanicum* are increasingly recognised yet often remain underdiagnosed. This incidental finding draws attention to the often-silent burden of zoonotic hookworm infections and emphasises the growing need for vigilance, even within urban and suburban settings. Incorporating molecular diagnostics into routine parasitological investigations is essential to improve detection accuracy, strengthen surveillance, and deepen our understanding of zoonotic transmission dynamics.

**MM04: Ultra-Sensitive MTB/RIF: Is 'Trace Detected' Diagnostically Helpful, or a Mere False Positive? A 3-year Clinical Audit**

Nurnabilah Zainuddin[1 *], Nur Zulieffa Zakaria[1], Nor Hafizah Jentera@Yahya[1], Abigail Terah Iben[1], Alisa Hanum Arba'eni @ Arbaen[1], Norashikin Samsudin[2]

*[1]Department of Pathology, Sarawak General Hospital, Sarawak, Malaysia; [2]Department of Pathology, Faculty of Medicine & Health Sciences, Universiti Malaysia Sarawak, Sarawak, Malaysia*

*Introduction:* As a molecular WHO-recommended rapid diagnostic test (mWRD) for tuberculosis, GeneXpert MTB/RIF has been a significant game-changer in the fight against the global pandemic. However, with improved sensitivity in the revised assay, GeneXpert MTB/RIF Ultra also has an increased risk of false positives due to its lower specificity, particularly in reporting trace detected samples. This clinical audit aims to determine the reliability of MTB/RIF GeneXpert trace detected results in diagnosing Mycobacterium tuberculosis (MTB) compared to MTB culture. *Materials & Methods:* This retrospective clinical audit was conducted in the Microbiology Laboratory, Sarawak General Hospital (SGH). Data on all samples tested for GeneXpert MTB/RIF Ultra yielding MTB trace detected from 1st January 2022 until 31st December 2024 were collected and compared with their corresponding specimens sent for MTB culture using solid Ogawa media. *Results:* From 6630 samples tested in SGH, 161 yielded trace MTB detected. Most trace detected samples were from male aged older than 25 years, outside SGH, and sputum samples. With 117 culture-negative samples, the TB GeneXpert false positivity rate is 73%. There was a significant association between patient age and culture positivity ($\chi^2$ (3) = 8.905, $p < .05$). *Discussion:* High false positivity rate among trace detected GeneXpert samples compared to MTB culture remains a management dilemma to clinicians. Although MTB culture serves as a gold standard method for TB diagnosis, it is still imperfect, with many variables influencing growth yield. Further research with the integration of a composite reference standard is needed.

**MM05: Phocaiecola vulgatus bacteraemia: The Chicken-and-egg in Colorectal Carcinoma**

Nurnabilah Zainuddin[1], Nur Zulieffa Zakaria[1], Alisa Hanum Arba'eni @ Arbaen[1], Habib Abdul Hakim Esa[2], Norashikin Samsudin[3]

*[1]Department of Pathology, Sarawak General Hospital, Kuching, Sarawak, Malaysia; [2]Bacteriology Unit, Infectious Diseases Research Centre, Institute for Medical Research, National Institutes of Health, Ministry of Health Malaysia, Setia Alam, Selangor, Malaysia; [3]Department of Pathology, Faculty of Medicine & Health Sciences, Universiti Malaysia Sarawak, Sarawak, Malaysia*

*Introduction: Phocaeicola vulgatus*, formerly known as *Bacteroides vulgatus*, is a Gram-negative anaerobic bacterium, exclusively inhabiting the human colon. While mankind benefited from its role in digestion and maintaining a healthy microbiome, more research links this opportunistic bacterium to inflammatory diseases. Recent study has also demonstrated a link between anaerobic bacteraemia and colorectal carcinoma. We describe a *P. vulgatus* bacteraemia in a patient with colorectal carcinoma. *Case report:* A 32-year-old Malay gentleman presented to the emergency department with a sudden onset of delirium, two weeks of weakness and poor oral intake. He was diagnosed with KRAS-positive rectal adenocarcinoma two years ago, underwent abdominoperineal resection, and remains on adjuvant chemoradiation. On arrival, he was lethargic, disorientated to time, albeit alert and afebrile. Abdominal and neurological examinations were unremarkable. While treating for symptomatic hyponatraemia, his percutaneous blood culture taken on admission grew *P. vulgatus*, identified by MALDI-TOF MS and confirmed with 16S rRNA sequencing. The isolate was tested susceptible for amoxicillin/clavulanate, metronidazole and imipenem. After completing eight days of amoxicillin/clavulanate, the patient recovered and discharged well. *Discussion:* Colorectal cancer can cause bacterial translocation, enabling intestinal bacteria to enter the bloodstream. A Danish cohort study identified *P. vulgatus* as the second most common anaerobic bacterium associated with the highest rates of colorectal cancer following bacteraemia. The relationship between colorectal cancer and anaerobic bacteraemia, whether it contributes to the development of colorectal cancer, or if it is a consequence of the disease remains unclear. More research is needed to determine its causative linkage.

**MM06: Stop the Waste, Trust the Fluid: Using CSF Clues to Justify Qiagen ME Panel Requests**
Norafandi Mohd Noor, Rayuwani Mohamad Kamal, Janice Tham Jia Mei, Wong Shou Chen
*Department of Pathology, Hospital Sibu, Sarawak, Malaysia*

*Introduction:* The QIAstat Meningitis/Encephalitis (ME) panel allows for rapid and accurate identification of pathogens, allowing for timely treatment. However, due to its high cost, selective and evidence-based criteria is necessary. This study aims to identify cerebrospinal fluid parameters that may support appropriate utilisation of QIAstat ME testing, improving diagnostic value and reducing unnecessary costs. *Materials and Methods:* A retrospective study was conducted at the Microbiology Unit of Hospital Sibu from January 2022 to December 2024. The study examined CSF samples submitted for QIAstat ME testing. Samples that exhibited significant blood contamination or were referred without CSF biochemistry and cell count results were excluded. Chi-square tests were used to evaluate relationships and associations between CSF biochemistry and cell count findings and QIAstat positivity. Binary logistic regression was used to identify independent predictors. A p-value of less than 0.05 was considered statistically significant. *Results:* A total of 130 CSF samples were evaluated. The overall QIAstat positive rate was 15.4% (20/130). Chi-square analysis showed associations with both abnormal CSF cell counts ($p = 0.016$) and combined abnormal biochemistry (high protein and low CSF: blood glucose ratio) ($p = 0.004$). Logistic analysis confirmed them as independent predictors ($p=0.013$ and $p=0.029$ respectively). The model had an overall 85.6% accuracy rate, with a high specificity of 98.7%. *Discussion:* The positivity rate of 15.4% indicated that numerous QIAstat requests produced no actionable results; nevertheless, true positives case correlated significantly with abnormal CSF profiles, illustrating that established CSF criteria could be used to guide the approval of test requests, thereby exemplifying diagnostic stewardship and rationalizing the application of molecular diagnostics to avert resource wastage.

**MM07: One Host, Two Invaders: Molecular Detection Triumphs at Borneo's First Parasitology Centre**
Norafandi Mohd Noor, Rayuwani Mohamad Kamal, Gokullshautri Sinalthan, Lo Feng Feng
*Department of Pathology, Hospital Sibu, Sarawak, Malaysia*

*Introduction: Strongyloides stercoralis* and *Ancylostoma duodenale* are helminthic-associated illnesses linked to soil in tropical and subtropical areas. Co-infections are infrequent, especially in immunocompetent individuals. We present a rare case of a co-infection involving two parasites in a previously healthy adult and examine the significance of molecular diagnostics in identifying such co-infections. *Case report:* A 45-year-old male from a rural region in Sarawak arrived at the hospital with chronic abdominal discomfort, intermittent diarrhoea, and eosinophilia of indeterminate origin. A preliminary stool analysis indicated the presence of rhabditiform larvae indicative of potential *Strongyloides stercoralis* however, confirmation was obtained using helminth multiplex PCR at our first regional parasitology reference facility revealing dual infection of *Strongyloides stercoralis* and *Ancylostoma duodenale*. The patient received treatment with ivermectin and albendazole, resulting in a normalised eosinophil count at the follow-up appointment. *Discussion:* While co-infection with *Strongyloides stercoralis* and *Ancylostoma duodenale* is uncommon, it may create challenges in diagnosis, especially by standard microscopy. Confirmation of diagnosis with molecular diagnostics such as PCR increases the likelihood of finding rarer mixed infections and enables previously undetected cases. Sarawak is endemic for parasitic diseases; however, it is just starting to provide molecular diagnostics with our first regional parasitology centre in Borneo. When there is accurate and timely diagnosis, it will greatly tailor patient treatments. In the case of a mixed infection, this will ensure they are sufficiently diagnosed; therefore, the proper medication will be prescribed for each parasite, and if necessary, complications attributed to undiagnosed strongyloidiasis, such as hyperinfection syndrome, will be avoided. This case has demonstrated how PCR can improve patient outcomes with the identification of parasites and develop capacity in a region that is of high endemicity for parasitic diseases.

**MM08: Unmasking the Hidden: Cerebral Toxoplasmosis in a Newly Diagnosed Retroviral Patient**
Nor Liyana Fitriah MK, Kamariah AJ, Nur Farhanim CAH, Salwani Ismail, Nor Iza A. Rahman, Nor Rasidah Rasid, Aimi Khairuddin
*Department of Pathology and Medical Laboratory, Hospital Sultan Zainal Abidin, Terengganu, Malaysia*

*Introduction:* Cerebral toxoplasmosis is one of the most common opportunistic central nervous system (CNS) infections seen in patients with acquired immunodeficiency syndrome (AIDS). *Toxoplasma gondii*, a neurotropic parasite, can cause a wide spectrum of neurological and neuropsychiatric manifestations, particularly in immunocompromised individuals. In typical scenarios, cerebral toxoplasmosis is encountered in patients with known HIV/AIDS; however, we report a reverse diagnostic case in which an opportunistic infection unveiled an underlying retroviral disease in a previously well man. This case underscores the importance of considering HIV-related opportunistic infections even in patients without apparent risk factors. *Case report:* A 35-year-old male, with a background of well-controlled bronchial asthma and no prior history of immunodeficiency, presented with a one-month history of intermittent dizziness, progressive nausea, vomiting, and photophobia. Collateral history revealed subtle neurological deficits, including slurred speech and left-sided weakness. Despite multiple evaluations for nonspecific symptoms, neuroimaging ultimately demonstrated bilateral parietal cerebral abscesses with eccentric target signs, raising suspicion for cerebral toxoplasmosis. Subsequent investigations confirmed advanced HIV infection with severe immunosuppression. *Discussion:* This case highlights the critical need for clinicians to maintain a high index of suspicion for retroviral disease in patients presenting with atypical CNS infections—even in those who appear previously healthy and deny high-risk behaviour. A broader awareness of atypical presentations among healthcare providers is crucial to improving early detection, optimising treatment outcomes, and reducing the burden of undiagnosed HIV-related complications. Early recognition and prompt treatment are essential to prevent irreversible neurological damage and improve patient outcomes.

**MM09: Aztreonam Plus Ceftazidime-Avibactam Broth Disc Elution (BDE): In vitro study on carbapenemase-producing Enterobacterales (CPE)**

Amira Amir[1], Mafuzah Mohd Said[1], Farrah Hanum Abdul Kadir[1], Subashini A/P Sathasivan[1], Rinusha A/P Manogaran[1,2], Sahlawati Mustakim[1], Rohaidah Hashim[3]

*[1]Department of Pathology, Hospital Sungai Buloh, Selangor, Malaysia; [2]Universiti Putra Malaysia, Selangor, Malaysia; [3]Bacteriology Unit, Institute for Medical Research, National Institute of Health*

*Introduction:* The management of carbapenemase-producing Enterobacterales (CPE) remains highly challenging, particularly in South-East Asia, where most isolates harbour Metallo-β-lactamases (MBL), notably NDM-1. Clinical outcomes have favoured ceftazidime-avibactam over colistin-based regimens, and for specific MBL-producing isolates, the combination of aztreonam plus ceftazidime-avibactam has been associated with lower 30-day mortality compared to polymyxins[1]. However, these novel therapies come at significantly higher costs, and there have been reports of emergent resistance[2]. *Materials & Method:* A total of 76 CPE isolates confirmed by modified carbapenem-inactivation method (mCIM) and/or CPE genotyping done at Bacteriology Unit, Institute for Medical Research, National Institute of Health Reference Laboratory were subjected to 2024 CLSI recommendations for aztreonam plus ceftazidime-avibactam synergy test using the broth disk elution (BDE) method. *Results:*Among the organisms identified included *Klebsiella pneumoniae* (51%, 39/76), *Enterobacter hormaechei* (21%, 16/76), *Enterobacter cloacae* (9%, 7/76) and *Escherichia coli* (7%, 5/76). The majority of isolates were NDM-1 producers (72%, 55/76), followed by OXA-48 producers (8%, 6/76). However, a few isolates (6%, 5/76) could not be characterised by multiplex PCR, as the assay targets only the five common CPE genes (*NDM, OXA-48, IMP, VIM, KPC*). Genotypic data were unavailable for the remaining 10 isolates. Synergy testing demonstrated excellent susceptibility to aztreonam plus ceftazidime-avibactam across all isolates, except for one OXA-48-producing *E. coli*, which was verified as non-susceptible by the reference laboratory. *Discussion:* This in vitro study aligns with existing evidence supporting the use of combination antimicrobial therapy with aztreonam plus ceftazidime-avibactam for treating CPE in regions where Metallo-β-lactamase (MBL) producers are the predominant genotypes. Although the only non-susceptible isolate was identified as an OXA-48 producer, further characterisation through sequencing is necessary to detect co-producing rare carbapenemase genes. Therefore, this synergy test should be integrated into clinical microbiology laboratories to guide treatment decisions for highly challenging CPE infections.

**MM10: Serological and molecular detection of seropositive occult hepatitis B virus infection at Hospital Pakar USM (HPUSM)**

Athirah Mohammad[1], Sharmilah Nehru[1], Muhammad Imran Kamarudin[2], Mohd Nazri Hassan[3], Nik Haszroel Hysham Nik Hashim[1]

*[1]Department of Medical Microbiology & Parasitology, School of Medical Sciences, Universiti Sains Malaysia, Health Campus, Kelantan; [2]Department of Haematology, School of Medical Sciences, Universiti Sains Malaysia, Health Campus, Kelantan; [3]Chronic kidney disease unit, Hospital Pakar Universiti Sains Malaysia, Universiti Sains Malaysia Kampus Kesihatan, Kelantan*

*Introduction:* Occult hepatitis B virus infection (OBI) is defined as the presence of replication-competent HBV DNA in the liver and/or HBV DNA in the blood of people who test negative for hepatitis B surface antigen (HBsAg) by currently available assays (European Association for the Study of the Liver, 2018). This condition poses a diagnostic challenge, as standard serological screening methods may fail to detect the infection. Although the ideal sample for diagnosis is the detection of HBV DNA in the liver, the detection of anti-HBc in the blood may be used as a surrogate marker. We aim to determine the prevalence of seropositive OBI in Hospital Pakar USM (HPUSM) by using hepatitis B core antibody (anti-HBc) as a surrogate marker and nested polymerase chain reaction (PCR) for detection of HBV DNA. *Materials & Methods:* Between August 2021 until August 2022, sera from blood donors at the Blood Donation Unit HPUSM and residual samples at the Medical Microbiology & Parasitology Laboratory HPUSM that were Hepatitis B surface antigen (HBsAg)-negative were tested using anti-HBc antibody. Samples that were reactive to anti-HBc were further tested using hepatitis B surface antibody (anti-HBs) and nested PCR of the S gene. *Results:* 56 of the 955 (5.9%) HBsAg negative sera from blood donors and lab samples were found to be reactive to anti-HBc. Out of the 56, anti-HBs was reactive in 53. Nested PCR detected HBV DNA in eight out of the fifty-five cases (14.5%). Five out of the eight were blood donors. This study has found seropositive OBI in 0.83% of HBsAg-negative sera from blood donors and lab samples. *Discussion:* Seropositive OBI rate of 0.83% is much lower to a previous Malaysian study but comparable to several other studies. In conclusion, this study shows the usefulness of anti-HBc test as a surrogate marker for screening of OBI prior to confirmation.

**MM11: Utility of M2-3E/BPO autoantibodies in primary biliary cholangitis with seronegative AMA-M2: A retrospective study of a Malaysian cohort using EUROLINE.**

Ainur Yusniza Yusof *, Nur Liyana Roslan, Siti Asma Bakar, Siti Fatimah Abdullah

*Autoimmune Unit, Allergy and Immunology Research Centre, Institute for Medical Research, National Institute of Health, Setia Alam, Shah Alam, Selangor, Ministry of Health Malaysia, Malaysia*

*Introduction:* Primary Biliary Cholangitis (PBC) is an autoimmune liver disease strongly associated with anti-mitochondrial antibodies (AMA), particularly AMA-M2. The M2-3E/BPO epitope, derived from the E2 subunit of the pyruvate dehydrogenase complex (PDC-E2), may increase diagnostic sensitivity, especially in AMA-M2–negative and early-stage cases. This study aimed to evaluate diagnostic utility and seropositivity of anti-AMA-M2 and anti-M2-3E/BPO antibodies in PBC patients in a Malaysian cohort. *Materials & Methods:* A retrospective cohort of 1221 sera with autoimmune liver disease were conducted from 2021-2022. Samples were tested for anti-AMA-M2 antibodies and anti-M2-3E/BPO antibodies determined by EUROLINE- Autoimmune Liver Disease (IgG) immunoblot strips – (EUROIMUN). The test kit contains a test strip coated with lines of purified antigens. *Results:* Hundred and thirteen (9.25%) sera were seropositive to at least one of the PBC autoantibodies. Out of 113 sera, 50 (44.25%) were positive to both AMA-M2 and M2-3E/BPO, 41 (36.28%) were AMA-M2 positive but M23E /BPO negative and 22 (19.47%) were M2-3E/BPO positive with AMA-M2 negative, respectively. *Discussion:* This study showed that anti-M2-3E/BPO antibody improved PBC detection which may be missed in AMA-M2 seronegative patients, supporting its use in routine diagnostics.

**MM12: Concordance between VITEK-2 N374 sensitivity card and Liofilchem MIC strips in measuring antibiotic susceptibility towards Burkholderia pseudomallei**

Noor Hamidah Che Ali[1], Anita Sulong[1], Zalina Ismail[1], Roesnita Baharudin[2]
*[1]Department of Medical Microbiology & Immunology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Wilayah Persekutuan Kuala Lumpur, Malaysia; [2]Department of Pathology, Hospital Tengku Ampuan Afzan, Pahang, Malaysia*

*Introduction:* Melioidosis is an infection caused by Burkholderia pseudomallei, a Gram-negative bacillus commonly found in soil and contaminated water. It predominantly occurs in tropical and subtropical regions and is endemic in Pahang. Due to its intrinsic resistance to numerous antibiotics, antimicrobial susceptibility testing (AST) is essential for optimising melioidosis treatment. *Materials & Methods:* This prospective cross-sectional study evaluated the concordance between the VITEK-2 N374 card and Liofilchem MIC strips of ceftazidime, trimethoprim-sulfamethoxazole, and meropenem. *Results:* Concordance between methods was assessed using essential agreement, categorical agreement, and Cohen's kappa. Meropenem exhibited excellent concordance with essential and categorical agreements exceeding 90% and a Cohen's kappa of 0.758 ($p < 0.001$). Ceftazidime demonstrated high categorical agreement (95.6%) but moderate essential agreement (73.8%) and a Cohen's kappa of 0.550 ($p < 0.001$), indicating variability in clinical breakpoints. Trimethoprim-sulfamethoxazole showed significant variability, with lower essential and categorical agreements (<82%) and negligible Cohen's kappa (0.01, $p = 0.845$). *Discussion:* The comparison between VITEK-2 and Liofilchem MIC strips showed strong agreement for meropenem but variable results for ceftazidime and trimethoprim-sulfamethoxazole, highlighting the need for careful result interpretation.

**MM13: Inflammatory biomarkers for prediction of sepsis in febrile patients**

Siow-Phing Tay[1], Jin-Shyan Wong[2], Chuan-Joon Lau[1], Alice Joe[1], Vanessa Claudia Musa[1], Arni Nazera Azahar[1], Henry Rantai Gudum[1]
*[1]Faculty of Medicine and Health Sciences, Universiti Malaysia Sarawak, Sarawak, Malaysia; [2]Borneo Medical Centre, Kuching, Sarawak, Malaysia*

*Introduction:* Sepsis, an infection-induced systemic inflammatory response syndrome, has high morbidity and mortality rates. Rapid recognition of sepsis with appropriate management saves lives. Blood cultures remain the gold standard diagnostic tool, results that are only available after 24-48 hours have hampered the effort of minimising mortality in sepsis care. Several inflammatory biomarkers have emerged as new rapid tools, but large discrepancy exists in their reported diagnostic values. *Materials & Methods:* This retrospective study investigated the clinical significance of white blood cells (WBC), absolute neutrophil count (ANC), platelet count (PLT), procalcitonin (PCT), C-reactive protein (CRP) and erythrocyte sedimentation rate (ESR) in prognosticating sepsis. *Results & Discussion:* From 814 febrile cases with blood cultures done, prevalence of sepsis was 9.8% with 12.5% mortality. Majority (57.5%) grew Gram negative cultures with *Escherichia coli* being the most common isolates. Occurrence of sepsis was significantly associated with older age. Significantly higher ANC, PCT, CRP and lower PLT were observed in septic patients. PCT was superior to the others in terms of diagnostic accuracy (85% sensitivity, 55% specificity). Multivariate analysis by combining all six biomarkers with age revealed that PCT (OR: 1.032; 95%CI: 1.013-1.051; p=0.001) and CRP (OR: 1.005; 95%CI: 1.001-1.008; p=0.006) were the only two significant biomarkers for prediction of sepsis (86.5% accuracy). *Conclusion:* This study demonstrated the significant role of PCT in diagnosing and predicting sepsis. In cases where sepsis is suspected, PCT should be included in the test panel to allow rapid detection of sepsis that requires prompt clinical intervention to ensure better outcome.

**MM14: Prevalence of Respiratory Pathogens Detectable via Automated Multiplex Polymerase Chain Reaction (PCR): Findings from 18-Month Utilisation in Malaysian Public Hospitals**

Mahirah Kamil Puat[1], Siti Hawa Hamzah[2], Sahlawati Mustakim[3]
*[1]Department of Pathology, Hospital Tengku Ampuan Rahimah, Klang, Selangor, Kementerian Kesihatan; Malaysia; [2]Department of Pathology, Hospital Seberang Jaya, Pulau Pinang, Kementerian Kesihatan Malaysia; [3]Department of Pathology, Hospital Sungai Buloh, Selangor, Kementerian Kesihatan Malaysia*

*Introduction:* Infectious diseases affecting the upper respiratory tract present diagnostic challenges due to diverse aetiologies and overlapping clinical presentations. The objective of this study is to identify the prevalence of respiratory pathogens detectable via the automated multiplex PCR analyser QIAstat-Dx Respiratory SARS-CoV-2 panel. *Materials & Methods:* Data from 1st January 2023 to 30th June 2024 were obtained from 29 public hospitals in Malaysia using QIAstat-Dx integrated with QIAsphere. *Results:* From 1st January 2023 to 30th June 2024, a total of 7145 valid tests were performed using the QIAstat-Dx Respiratory SARS-CoV-2 panel. Monthly, the positive detection rate ranged from 55.04% to 72.27%, with the highest detection rate in November 2023. The three most common pathogens detectable were Rhinovirus/Enterovirus (1728; 24.18%), Respiratory syncytial virus A+B (RSV A+B) (935; 13.09%) and Influenza A (618; 8.65%). The most common bacterial pathogen detected was *Mycoplasma pneumoniae* (270; 3.77%). Other detectable pathogens accounted for a third of the total valid tests (2429; 34%). *Chlamydophila pneumoniae* was the only pathogen in the panel that was not detected during this study period. The co-detection rate, in which more than one pathogen is detected in the same sample, ranges from 9.09% to 24.82%. The most common co-detected pathogens were *Mycoplasma pneumoniae* with Rhinovirus/Enterovirus. *Discussion:* The prevalence of detectable respiratory pathogens in this study is similar to the prevalence prior to the COVID-19 pandemic. In view of low detection of SARS-CoV-2 in the post-pandemic period, attention should be shifted to other respiratory pathogens through utilisation of automated multiplex PCR technology that enable simultaneous detection of multiple respiratory pathogens including SARS-CoV-2.

**MM15: Rhizobium radiobacter bacteraemia in a neonate: A case report**

Siti Hafsyah Mohd Hariri[1,2], Muhammad Haris Fadillah Muhamad[1], Zeehaida Mohamed[1,2 *]
[1]Department of Medical Microbiology and Parasitology, School of Medical Sciences, Universiti Sains Malaysia, 16150, Kubang Kerian, Kelantan; [2]Hospital Pakar Universiti Sains Malaysia, Universiti Sains Malaysia Health Campus, Jalan Raja Perempuan Zainab II, 16150 Kubang Kerian, Kelantan.

*Introduction: Rhizobium radiobacter*, formerly known as *Agrobacterium radiobacter*, is a tumourigenic plant pathogen that is infrequently associated with human disease. Typically, it acts as an opportunistic pathogen in immunocompromised individuals and is often linked to indwelling medical devices. Reports of neonatal infections are rare, especially in the absence of risk factors. *Case report:* A full-term male neonate, born via spontaneous vaginal delivery, presented with leukocytosis ($29 \times 10^9$/L) during routine screening for presumed sepsis in the postnatal ward. He was otherwise clinically well with no obvious signs of sepsis or underlying conditions, apart from maternal gestational diabetes mellitus. The C-reactive protein was less than 10 mg/L. Despite clinical stability, blood culture later grew Gram-negative bacilli identified as *Rhizobium radiobacter* via VITEK2 GN card (97% confidence); therefore, he was treated with IV piperacillin-tazobactam and gentamicin. Subsequent blood cultures showed no growth, and his white blood count normalized. He was discharged home in good condition on the seventh day of life. *Discussion: R. radiobacter* is a rare cause of bacteraemia in neonates, particularly in the absence of common risk factors such as prematurity, indwelling catheters, or immunosuppression. Its identification often raises concern about contamination; however, clinically relevant infections have been reported. In this case, the absence of clinical symptoms, negative inflammatory markers, and resolution without complications suggest possible pseudobacteremia. Nonetheless, given its potential pathogenicity in vulnerable patients, *R. radiobacter* should be considered significant when risk factors and clinical features support the presence of infection. Prompt identification and targeted antibiotic therapy contribute to favourable outcomes.

**MM16: A case of Streptococcus gordonii infective endocarditis complicated by intracranial mycotic aneurysm and cerebral abscess**

Siti Hafsyah Mohd Hariri[1,2], Muhammad Haris Fadillah Muhamad[1], Zeehaida Mohamed[1,2 *]
[1]Department of Medical Microbiology and Parasitology, School of Medical Sciences, Universiti Sains Malaysia, Kelantan, Malaysia; [2]Hospital Pakar Universiti Sains Malaysia, Universiti Sains Malaysia Health Campus, Kelantan, Malaysia.

*Introduction: Streptococcus gordonii*, a member of the viridans group streptococci, is an uncommon cause of infective endocarditis (IE). Though typically low in virulence, it can lead to severe complications, particularly in patients with predisposing cardiac conditions. We present a rare case of *S. gordonii* IE complicated by intracranial mycotic aneurysm and cerebral abscess. *Case report:* A 31-year-old woman with known mitral valve regurgitation presented with syncope, fatigue, and constitutional symptoms. Blood investigations showed anaemia and raised inflammatory markers. Echocardiogram revealed severe mitral regurgitation and vegetations measuring 0.13 $cm^2$. She was started on IV penicillin and gentamicin. Four separate blood cultures were sent, and all grew *S. gordonii.* On day five of admission, she developed left-sided weakness and facial palsy. Neuroimaging revealed multifocal infarctions with haemorrhagic transformation, cerebral abscesses, and a mycotic aneurysm. Dental evaluation indicated poor oral hygiene. Ophthalmologic examination showed bilateral Roth spots. Serial imaging showed a reduction in vegetation size and resolution of abscesses, with residual aneurysms. She completed an 8-week antibiotic course and was discharged with no neurological deficits. *Discussion: S. gordonii* IE is rare but may cause severe neurological complications, especially in patients with valvular heart disease and poor dental hygiene. Mycotic aneurysms and cerebral abscesses are life-threatening conditions and require prompt diagnosis through imaging. Conservative management with prolonged IV antibiotics may suffice in unruptured aneurysms, though careful monitoring is essential. This case underscores the importance of early detection and multidisciplinary care in managing complex IE cases with neurological involvement.

**MM17: False-Positive (1-3)-β-D-Glucan Results Associated with Specific Serum Separation Tube**

Soo-Kyung Kim
*Department of Laboratory Medicine, Ewha Womans University College of Medicine, Seoul, Korea*

*Introduction:* (1-3)-β-D-glucan (BDG) is a key biomarker for diagnosing invasive fungal infections. However, false-positive results may occur due to various preanalytical factors, including the use of cellulose membrane dialyzers, administration of intravenous immunoglobulin, transfusion of blood products, certain antibiotics (such as amoxicillin-clavulanate and piperacillin-tazobactam), bacterial endotoxins, use of gauze, and contamination from central venous catheters. At our institution, the BDG positivity rate increased significantly from a historical average of 16% to 79.6% after March 28, 2025. We aimed to identify the cause of this sudden rise. *Materials & Methods:* We reviewed ward-specific positivity rates, medication changes, transfusion history, phlebotomist staffing, and blood collection procedures but found no contributing factors. Suspecting preanalytical contamination, we collected six lots of serum separation tubes (SSTs). Under sterile conditions, 2 mL of sterile distilled water was added to each tube, vortexed for 5 seconds, and centrifuged at 3500 rpm for 10 minutes. Three tubes per lot were tested using a BDG assay (Beijing Gold Mountainriver Tech Development, China). Control testing was performed with plain tubes. *Results:* Of the six SST lots evaluated, four tested negative while two consistently yielded positive BDG results. The mean BDG values were 127.1 pg/mL (standard deviation [SD] 0.6) and 811.4 pg/mL (SD 85.7), both significantly exceeding the 10 pg/mL cutoff. *Discussion:* Contamination associated with specific SST lots can cause false-positive BDG results. Preanalytical factors involving blood collection tubes must be considered. Continuous monitoring of BDG positivity rates is essential to identify underlying preanalytical issues.

**MM18: Genotypic detection of plasmid-mediated AmpC beta-lactamases in Escherichia coli and Klebsiella pneumoniae in Hospital Canselor Tuanku Muhriz**

Mohd Syazwan Mohd Saaid[1], Zalina Ismail[1], Wong Kon Ken[1], Ramliza Ramli [1]
[1]*Department of Medical Microbiology & Immunology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia*

*Introduction:* Plasmid-mediated AmpC (pAmpC) beta-lactamases in Enterobacterales are challenging to identify due to lack of standardised laboratory detection test. This study aimed to identify the presence of pampC genes in *E. coli* and *Klebsiella pneumoniae* isolated from clinical samples at Hospital Canselor Tuanku Muhriz with molecular methods. *Materials & Methods:* 39 archived non-repetitive strains of *E. coli* (n = 20) and *Klebsiella pneumoniae* (n = 19) were included in this study. These organisms were isolated from various clinical specimens from 31 January 2020 until 30 January 2021 and were positive for extended spectrum beta-lactamase (ESBL) screening test (zone of inhibition of ≤ 22mm for ceftazidime or ≤ 27mm for cefotaxime) as well as positive for AmpC disc test. Conventional polymerase chain reaction (PCR) was used to detect the presence of pampC genes, which were subsequently confirmed with sequencing. *Results:* Thirty six of 39 (92.3%) isolates were positive for pampC genes (20 *E. coli* and 16 *Klebsiella pneumoniae*). Nineteen isolates harboured DHA group genes (15 *Klebsiella pneumoniae*, four *E. coli*), 17 isolates harboured CIT group genes (17 *E. coli*), and one harboured EBC group gene (one *Klebsiella pneumoniae*). One particular *E. coli* isolate was found to harbour dual ampC genes (DHA and CIT gene groups). *Discussion:* The presence of pampC genes in *E. coli* and *Klebsiella pneumoniae* from clinical samples highlights the need for standardised phenotypic methods in clinical microbiology laboratories for AmpC detection. Inaccurate reporting of AmpC beta-lactamase producers could result in suboptimal antimicrobial treatment potentially leading to treatment failure.

**M19: Challenges in Borderline Oxacillin-Resistant Staphylococcus aureus (BORSA): A Case Report and Discussion**

Mohd Syazwan Mohd Saaid , Zalina Ismail*
*Department of Medical Microbiology & Immunology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia*

*Introduction:* Borderline oxacillin-resistant *Staphylococcus aureus* (BORSA) is *Staphylococcus aureus* strains with reduced oxacillin susceptibility. In contrast, methicillin-resistant *Staphylococcus aureus* (MRSA) has high-level oxacillin resistance mediated by the mecA gene via altered penicillin-binding protein (PBP2a). BORSA strains typically lack this gene. Thus, laboratory tests using cefoxitin to identify MRSA often precludes the detection of BORSA *Case report:* We present two cases of BORSA-related bacteraemia in Hospital Canselor Tuanku Muhriz. Both patients had end stage renal failure, on haemodialysis via central venous catheter following failures of arteriovenous fistulas. Both peripheral and central blood cultures of both patients grew *Staphylococcus aureus*. Automated antimicrobial susceptibility testing showed discrepancy between cefoxitin screening and oxacillin MIC for *Staphylococcus aureus* isolates of both patients, with negative cefoxitin screening but MIC oxacillin of ≥ 4 µg/mL. Additionally, these isolates were positive for nitrocefin test, and viable on mannitol salt agar supplemented with 4.5 µg/mL oxacillin. Both patients were initially treated empirically with intravenous (IV) vancomycin and ceftazidime for suspected catheter-related bloodstream infection. The antibiotics were switched to IV cefazolin upon identification of BORSA. Both patients' central venous lines were also changed. The second patient was changed back to IV vancomycin due to delayed culture clearance. *Discussion:* BORSA poses diagnostic complexities due to distinct resistance mechanisms from MRSA. The clinical management of BORSA infections can be variable due to lack of universal clinical guidance. Infection prevention and control measures are also a concern in preventing BORSA spread within healthcare settings. Further research into BORSA epidemiology and impact is required to inform evidence-based management strategies and optimise patient care.

**MM20: Capnocytophaga canimorsus bacteraemia following cat bite**

Fairuz Abdul Rashid[1,2], Normi Ngah Mohamed[1,2], Nurul Azira Mohd Shah[1,2], Siti Norbahiyah Awad[1,2].
[1]*Microbiology & Parasitology Unit, Clinical Diagnostic Laboratories, Hospital Al-Sultan Abdullah, Universiti Teknologi MARA, Selangor;* [2]*Department of Microbiology & Parasitology, Faculty of Medicine, Universiti Teknologi MARA, Sungai Buloh Campus, Selangor*

*Introduction: Capnocytophaga canimorsus* is a fastidious, gram-negative rod found in the oral flora of dogs and cats. Although it is part of the normal microbiota in animals, it can cause serious and potentially fatal infections in humans, especially following bites or scratches. Risk factors include asplenia, alcohol abuse, and immunosuppression. Early recognition and treatment are crucial, given the organism's slow growth and potential for sepsis. Here, we report a case of *C. canimorsus* bacteremia in an elderly woman following contact with a cat bite. *Case report:* An 84-year-old woman with a background history of hypertension presented with a one-week history of fever, chills, rigors, myalgia, and nausea. Two weeks prior to admission, she sustained bite injuries to the right middle finger and the right lateral shin from her pet cat and a stray cat. On examination, she was febrile and appeared systemically unwell. A petechial rash was observed over both shins, along with a blanchable erythaematous rash over the bilateral calves. Laboratory investigations revealed elevated white blood cell count and C-reactive protein (CRP), indicating an inflammatory response. Empirical antibiotic therapy with intravenous ceftriaxone was initiated. Blood cultures taken on admission grew a gram-negative, fastidious, and slow-growing organism after several days of incubation. Identification using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) confirmed *Capnocytophaga canimorsus*. The patient showed clinical improvement with resolution of symptoms and a decreasing trend in inflammatory markers. After completing two weeks of intravenous ceftriaxone, she was transitioned to oral amoxicillin-clavulanate for an additional seven days. She continued to recover well on follow-up. *Discussion: Capnocytophaga* infections are not nationally notifiable, therefore there is no national estimate of incidence, furthermore the case reports are rarely reported. This case highlights the importanreported. Thisring *Capnocytophaga canimorsus* as a potential pathogen in elderly or immunocompromised patients presenting with systemic symptoms following

animal bites. Despite its fastidious nature and slow growth, timely identification using advanced techniques such as MALDI-TOF MS and prompt initiation of appropriate antibiotic therapy can lead to favorable outcomes. Early recognition and treatment are crucial to prevent severe complications associated with this potentially life-threatening zoonotic infection.

**MM21: Beyond the Toxin: A Case Series on Diverse Presentations of Corynebacterium diphtheriae Infection in Adults and Adolescents**

Puvanesvari Purusothma Naido[1], Nik Noramalina Binti Rozik[1], Muhamad Izrin Syukri Bin Mohd Nasri[2],
*[1]Department of Pathology, Hospital Duchess of Kent, Sabah, Malaysia, [2]Department of Pathology, Hospital Kinabatangan, Sabah, Malaysia*

*Introduction: Corynebacterium diphtheriae (C.diphtheriae)* infections, historically associated with respiratory diphtheria, is now re-emerging with diverse clinical manifestations. Recent evidence shows increasing isolation of both toxigenic and non-toxigenic strains from cutaneous and systemic sites, including among vaccinated individuals. We report three cases illustrating diverse clinical manifestations. *Case report:* Case 1: A 45-year-old male with unknown immunization history presented with facial myiasis involving left cheek swelling, purulent discharge, and maggot infestation. Blood cultures grew toxigenic *C. diphtheriae* (Elek test and PCR positive); pus swab showed mixed growth. He remained stable and recovered with antibiotics and wound debridement. Case 2: A 36-year-old female admitted for hypertensive emergency developed acute respiratory failure requiring mechanical ventilation. Tracheal aspirate grew non-toxigenic *C.diphtheriae* with negative blood cultures. She was treated with azithromycin and discharged uneventfully. Case 3: A 14-year-old vaccinated adolescent presented with fever and lethargy, rapidly progressing to septic shock. Despite intensive care, he succumbed to multiorgan failure. Blood cultures revealed non-toxigenic *C.diphtheriae.* The role of *C.diphtheriae* as a primary pathogen versus an incidental finding remains uncertain. *Discussion:* This case series highlights the evolving clinical spectrum of *C.diphtheriae* infections, from cutaneous to fatal systemic disease irrespective of toxin production. Although traditionally associated with toxigenic respiratory illness, non-toxigenic strains have caused severe infections, particularly in the setting of critical illness. Molecular characterisation, including toxin gene testing, remains crucial for clinical decision-making and public health management. Further research is needed to clarify pathogenicity and significance of non-toxigenic *C.diphtheriae* strains.

**MM22: Automated PCR Syndromic Panel Accelerates Early Diagnosis of Listeria Rhombencephalitis Compared to Culture**

Umi Ali[1], Ummu Afeera Zainulabidin[2], Petrick Periyasamy[3], Najma Kori[3], Xiong Khee Cheong[3], Kon Ken Wong[1]
*[1]Department of Medical Microbiology & Immunology, Faculty of Medicine, UKM, Wilayah Persekutuan Kuala Lumpur, Malaysia; [2]Department of Internal Medicine, Kulliyah of Medicine, International Islamic University Malaysia, Pahang, [3]Department of Medicine, Faculty of Medicine, UKM, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* Listeria rhombencephalitis, a rare but serious form of brainstem encephalitis caused by *Listeria monocytogenes*, typically manifests as a biphasic illness beginning with flu-like prodromal symptoms followed by neurological signs, such as cranial nerve palsies and cerebellar dysfunction. Conventional culture methods for identifying *Listeria monocytogenes* are reliable but often slow, delaying the initiation of targeted antibiotic therapy. The use of automated multiplex PCR meningitis/encephalitis panel (QIAstat-Dx Meningitis/Encephalitis Panel (QIAGEN, Hilden, Germany) offers rapid pathogen identification, enabling earlier diagnosis and treatment initiation. *Case report:* A 58-year-old patient with underlying hypertension presented with complex ophthalmoplegia, neck stiffness, gait instability, and progressive neurological deterioration. Clinical findings were consistent with rhombencephalitis. Cerebrospinal fluid (CSF) analysis showed markedly elevated protein (1758 mg/dL) and low glucose (1.01 mmol/L), initially raising suspicion for tuberculous meningitis. However, an automated multiplex PCR-based meningitis syndromic panel rapidly detected *Listeria monocytogenes* within 24 hours. Prompt initiation of targeted therapy with high-dose intravenous ampicillin significantly improved the patient's neurological condition. Conventional CSF cultures subsequently confirmed *Listeria monocytogenes*, but results were only available several days later, highlighting the diagnostic advantage of automated PCR in accelerating pathogen identification. *Discussion:* Early pathogen identification enabled timely targeted antibiotic therapy, reducing the risk of severe complications. The utilisation of an automated PCR panel significantly outperforms conventional culture in rapidly diagnosing *Listeria monocytogenes* rhombencephalitis, facilitating early treatment and improved patient outcomes.

**MM24: Unmasking Resistance: A Fatal Case of Refractory Melioidosis Revealed by Whole-Genome Sequencing**

Jayamalar Pitchaimuthu[1], Mohammad Ridhuan Mohd Ali[2], Hana Farizah Zamri[2], Rayuwani Mohamad Kamal[3]
*[1]Department of Pathology, Hospital Serdang, Selangor, Malaysia; [2]Bacteriology Unit, Infectious Disease Research Centre (IDRC), Institute for Medical Research (IMR), National Institutes of Health, Shah Alam, Malaysia; [3]Department of Pathology, Hospital Sibu, Sarawak, Malaysia*

*Introduction:* Melioidosis, caused by *Burkholderia pseudomallei*, is a potentially fatal infection with high relapse rates due to intrinsic antimicrobial resistance. Conventional methods such as culture and susceptibility testing remain the gold standard. However, in complex cases with treatment failure, molecular sequencing provides crucial insights into resistance mechanisms and guides targeted therapy. *Case report:* A 55-year-old male with diabetes, hypertension, dyslipidaemia, and chronic kidney disease presented with fever, cough, weight loss, and respiratory distress. Initial blood cultures confirmed *B. pseudomallei*, and susceptibility testing indicated resistance to trimethoprim/sulfamethoxazole but susceptibility to β-lactams. He was started on ceftazidime, but his condition worsened, requiring multiple admissions. He developed recurrent bacteraemia, severe pneumonia, septic shock, and pulmonary embolism. Despite escalation to meropenem, amoxicillin/clavulanate, and doxycycline, the infection persisted, leading to multi-organ failure. Whole-genome sequencing later identified the isolate as sequence type ST881 and revealed numerous $bla_{\text{OXA-42}}$ and $bla_{\text{PEN}}$ genes, explaining resistance to β-lactams. No plasmid was detected, confirming intrinsic resistance mechanisms. *Discussion:* This case highlights limitations of conventional diagnostics in drug-resistant melioidosis. WGS uncovered

resistance mechanisms undetectable by routine testing. Early genomic analysis could have enabled more effective, tailored therapy. Integrating molecular diagnostics such as WGS into clinical workflows is vital to optimise antimicrobial stewardship and improve outcomes in complex infections.

**M25: More Than Just a Cough: A Dual Diagnosis of Lung Carcinoma and Hidden Hookworm Infection**

Alisa Hanum Arba'eni[1], Nurdiyana Zakaria[1], Norashikin Samsudin[2], Nurnabilah Zainuddin[1], Romano Ngui[3]
*[1]Department of Pathology, Sarawak General Hospital, Kuching, Sarawak, Malaysia; [2]Department of Pathology, Faculty of Medicine & Health Sciences, Universiti Malaysia Sarawak, Sarawak, Malaysia; [3]Department of Paraclinical Sciences, Faculty of Medicine & Health Sciences, Universiti Malaysia Sarawak, Sarawak, Malaysia*

*Introduction:* Chronic respiratory symptoms often raise suspicion for pulmonary tuberculosis (PTB), especially in high-prevalence regions. However, a broad differential diagnosis is essential, particularly when initial investigations return negative. This case illustrates the value of comprehensive assessment in uncovering multiple underlying pathologies in an apparently straightforward presentation. *Case report:* A 60-year-old man, a chronic smoker with no known medical history, presented with progressive breathlessness and a 3-month history of chronic cough, weight loss, and anorexia. He also reported right-sided pleuritic chest pain for two days, increasing fatigue and dizziness, suggestive of long-standing anaemia. Physical examination was unremarkable, but chest X-ray showed right middle zone opacity with pleural effusion. Initial microbiological investigations for *Mycobacterium tuberculosis* (MTB) were negative on auramine staining and culture. A thoracocentesis was performed and pleural fluid was sent for histopathology, which revealed metastatic small cell squamous carcinoma. Blood tests showed microcytic hypochromic anaemia, prompting stool microscopy, which showed hookworm ova. The stool specimen was then referred to Faculty of Medicine and Health Sciences, Universiti Malaysia Sarawak for further species identification via molecular analysis, which subsequently confirmed the presence of *Necator americanus*. Despite chronic parasitic infection, his eosinophil count was low, suggesting long-standing parasitaemia. He was treated with albendazole and supportive therapy for respiratory symptoms. Despite appropriate interventions, the patient's condition deteriorated and unfortunately, he succumbed to death. *Discussion:* This case underscores the importance of considering alternative diagnosis in chronic respiratory presentations, especially when MTB tests were negative. A multidisciplinary approach revealed not only advanced lung malignancy but also an overlooked parasitic infection contributing to chronic anaemia. Thus, highlighting the challenges in managing late-stage presentations with multiple coexisting conditions.

**MM26: Mimicking Mycobacterium Tuberculosis: A Diagnostic Pitfall of Mycobacterium abscessus**

Alisa Hanum Arba'eni[1], Nor Hafizah Jentera@Yahya[1], Nurnabilah Zainuddin[1], Norashikin Samsudin[2]
*[1]Department of Pathology, Sarawak General Hospital, Kuching, Sarawak, Malaysia; [2]Department of Pathology, Faculty of Medicine & Health Sciences, Universiti Malaysia Sarawak, Sarawak, Malaysia.*

*Introduction:* This is a case of a patient with multiple comorbidities presented with symptoms suggestive of *Mycobacterium tuberculosis* (MTB) and was treated accordingly. However, culture later identified as *Mycobacterium abscessus* complex, highlighting the diagnostic challenges in differentiating non-tuberculous mycobacteria (NTM) from MTB cases. *Case report:* A 28-year-old Pakistani man with underlying myasthenia gravis (post-thymomectomy and radiotherapy in 2021, complicated by oesophageal stricture and pulmonary fibrosis), presented with chronic constitutional symptoms, productive cough, and intermittent fever. He was hypoxic and hypotensive on arrival, requiring oxygen therapy. Microbiological investigation began with auramine staining of sputum, which showed scanty acid-fast bacilli (AFB), leading to a presumptive diagnosis of MTB and was incubated for growth. Anti-tuberculosis therapy was initiated per standard protocol. However, his clinical course was complicated by intolerance to oral MTB medications necessitating adjustments from oral to intravenous and finally syrup-based regimens. After two weeks of MTB cultures incubation, colonies morphologically resembling MTB were observed and referred to a national reference laboratory for species identification. He was discharged with medications for MTB, but his conditions did not improve, leading to repeated hospital admissions. Molecular testing later confirmed the isolate was *Mycobacterium abscessus* complex, a rapidly growing non-tuberculous mycobacterium. This case report emphasised the importance of confirmatory culture and species-level identification in AFB-positive cases, especially in patients with underlying comorbidities. Accurate microbiological diagnosis is key in guiding appropriate therapy and avoiding prolonged empirical treatment for tuberculosis. *Discussion:* This case highlights the importance of considering non-tuberculous mycobacteria in patients with atypical presentations and complex comorbidities. Early species identification is crucial to guide appropriate treatment and improve patient outcomes.

**MM27: Exploring HLA-A & -B Loci: Uncovering the Genetic Links in Generalized Pustular Psoriasis from Sarawak**

Norhazlin Mustafa[1], Ingrid Pao Lin Ting[2], Asmadamia Abdul Aziz[1], Bee Tee Koay[1], Hock Gin Teo[3], Norfarhana Khairul Fahmy[1], Min Moon Tang[2], Masita Arip[1]
*[1]Transplantation Immunology Unit, Allergy and Immunology Research Centre (AIRC), Institute for Medical Research, National Institutes of Health, Malaysia; [2]Department of Dermatology Sarawak General Hospital, Sarawak, Ministry of Health Malaysia; [3]Dermatology Unit, Sibu Hospital, Sarawak, Ministry of Health Malaysia*

*Introduction:* Generalized pustular psoriasis (GPP) is a rare but severe chronic skin disorder characterised by the sudden appearance of sterile pustules. Association between human leukocyte antigen (HLA) and GPP, particularly HLA-C*06:02 has been identified as a significant risk factor for early-onset psoriasis. A previous study on the Sarawakian population showed no association between HLA-C and GPP. This study aims to investigate further the HLA-A and HLA-B loci in the Sarawakian population. *Materials & Methods:* Whole blood samples were collected from 40 GPP patients across three major hospitals in Sarawak, representing four ethnic groups: Malay, Chinese, Iban and Bidayuh. The patients ranged in age from 12 to 92 years. Extracted DNAs were subsequently genotyped for HLA-A and -B alleles, using the sequence-specific oligonucleotide (SSO) method. The odds ratios (OR) and p-values for each allele were calculated using 2 × 2 contingency tables. *Results:* For HLA-A, the Malay group exhibited the highest allele

diversity with 9 alleles, followed by the Chinese with 8 alleles, the Iban with 6 alleles, and the Bidayuh with 5 alleles. Similarly, for HLA-B, the Malay group showed the greatest variation with 18 alleles, followed by the Iban with 14 alleles, the Chinese with 11 alleles, and the Bidayuh with 8 alleles. No statistically significant associations were found for HLA-A or HLA-B alleles in our cohort. *Discussion:* A larger sample size is likely needed to clarify the HLA and GPP relationship in the Sarawakian population. Exploring HLA associations in GPP remains promising, with potential for novel therapies and the development of targeted treatments.

**MM28: Unmasking Bullous Pemphigoid in Malaysia: A 3-year Retrospective Analysis of Incidence and Demographic Disparities**

Siti Fatimah Abdullah[1], Ainur Yusniza Yusof[1], Siti Asma Bakar[1], Shuwahida Shuib, Nurhanani Mohamed Nor[1], Syuriatika binti Dionysius[1], Bavithra A/P Venu[1], Masita Arip[1].
*[1]Autoimmune Unit, Allergy and Immunology Research Centre, Institute for Medical Research, National Institutes of Health, Ministry of Health Malaysia*.

*Introduction:* Bullous pemphigoid (BP) is a chronic autoimmune blistering disorder primarily affecting the elderly. It is characterised by the immune system's attack on the skin layer beneath the outer surface, resulting in blisters. This study investigates BP's incidence and demographic characteristics in Malaysia's multiethnic population. *Materials & Methods:* The research retrospectively analysed the demographic data of 601 patients from 57 hospitals between January 2022 and December 2024, using mosaic BIOCHIPS with anti-BP180 and anti-BP230 antibodies for diagnosis. *Results:* The study found that 39.4% (237) of patients tested positive for at least one anti-BP antibody, with 20.0% for anti-BP180, 1.5% for anti-BP230, and 18.0% for both. The annual incidence of BP was 0.23 per 100,000 people, while the prevalence was 0.69 per 100,000. Among the positive patients, 55.7% were female, 44.3% were male (1.3:1 ratio), and the ages ranged from 1.83 to 98 years, with a median age of 75.5. Notably, 78.9% of positive patients were over 60 years ($p<0.0001$). Variances in BP cases across ethnicities were statistically significant ($p<0.0001$) with 39.7% Chinese, 36.7% Malay, 15.6% Indian, and 8.0% from other backgrounds. Regional differences in BP cases also showed varying rates across Malaysia: 26.6% in Wilayah Persekutuan, 15.6% in Selangor, 13.9% in Penang, and 11.0% in Perak. *Discussion:* This study highlights a non-uniform distribution of bullous pemphigoid across ethnic groups in Malaysia, with a notable predominance in older adults and Chinese ethnicity. These findings underscore the need for improved awareness and targeted dermatological care in high-risk populations.

**MM29: Antimicrobial Susceptibility Patterns and Vancomycin-Ceftaroline Relationship in MRSA Bloodstream Isolates: A Retrospective Analysis**

Jayamalar Pitchaimuthu[1], Mariani Maasaoom[1], Nurathirah Mat Nasir[1], Munirah Abdul Aziz[1]
*[1]Department of Pathology, Hospital Sultan Idris Shah, Selangor, Malaysia*

*Introduction:* Methicillin-resistant *Staphylococcus aureus* (MRSA) is a major cause of bloodstream infections (BSI) in healthcare settings. While vancomycin remains the mainstay of treatment, concerns about increasing antimicrobial resistance have prompted interest in alternative therapies such as ceftaroline. This study evaluates the antimicrobial susceptibility patterns of MRSA bloodstream isolates at Hospital Sultan Idris Shah, Serdang, focusing on vancomycin and ceftaroline susceptibility. *Materials & Methods:* A retrospective analysis was performed on MRSA-positive blood cultures from January to December 2024, including only the first isolate per patient. Data on demographics and antimicrobial susceptibility were extracted from the laboratory information system. Susceptibility was interpreted according to CLSI guidelines. Vancomycin minimum inhibitory concentrations (MIC) and ceftaroline disc susceptibilities were analysed using Spearman's rank correlation. Empirical utility was Categorised as: >80% (suitable), 60–80% (use with caution), and <60% (not suitable). *Results:* Among 69 MRSA isolates, 68.1% were from male patients (mean age: 52 years). All were resistant to cloxacillin. Susceptibility was low for penicillin (1.5%, n=69) and erythromycin (26.1%, n=69) moderate for clindamycin (42.7%, n=68) and fusidic acid (51.5%, n=68) and high for gentamicin (88.4%, n=69), rifampicin (98.6%, n=69), linezolid (100%, n=69), vancomycin (100%, n=69), and trimethoprim-sulfamethoxazole (97.1%, n=69), Ceftaroline showed 78.2% (n=55) susceptibility. Vancomycin MIC ranged from 0.38–1.5 μg/mL and were not significantly correlated with ceftaroline susceptibility ($\rho = 0.224$, $p = 0.101$). *Discussion:* Despite universal vancomycin susceptibility, treatment failure in some patients necessitates combination therapy. The absence of correlation with ceftaroline susceptibility suggests independent activity, supporting its alternative use. High susceptibility to trimethoprim-sulfamethoxazole, rifampicin, and linezolid reinforces their value in empirical and step-down regimens. Ongoing surveillance remains essential.

**MM30: Sequence analysis of MPB64 Gene in Mycobacterium tuberculosis complex (MTBC) from clinical samples**

Mohammad Ismim Putera bin Nawawi[1], Zetti Zainol Rashid[1,2], Asiyah Nordin[1,2]
*[1]Department of Medical Microbiology and Immunology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia; [2]Department of Laboratory Diagnostic Services, Hospital Canselor Tuanku Muhriz (HCTM), Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia*

*Introduction:* Accurate detection of *Mycobacterium tuberculosis* complex (MTBC) in clinical samples is crucial for appropriate and timely management. Molecular methods for MTBC enable rapid detection with high sensitivity and specificity. We aim to confirm the presence of MTBC DNA in PCR-positive but culture-negative specimens by sequence analysis of the *MPB64* gene. *Materials and Methods:* We tested 1695 clinical specimens from HCTM using the Lytestar™ 3.0 TB/NTM real-time PCR assay, acid-fast bacilli (AFB) smear, and mycobacterial culture. A total of 138 specimens (8.1%) were MTBC positive by PCR, of which 91 were negative by culture and AFB smear. Only 18/91 fulfilled the cycle threshold (Ct) value of <30 for sequence analysis of *MPB64* gene (178 base pairs), which were performed for these specimens. The curated sequences were analysed with Molecular Evolutionary Genetics Analysis version 12 (MEGA12) software to evaluate chromatogram quality and execute multiple sequence alignment (MSA) using the MUSCLE algorithm. The sequences were then matched to the National Centre for Biotechnology

Information (NCBI) GenBank database using Basic Local Alignment Search Tool (BLAST). *Results:* 17 samples showed 100% match to *Mycobacterium tuberculosis*, while 1 sample was inconclusive. The phylogenetic tree generated by MEGA12 showed that the sequences from these 17 samples belonged to a group of closely related strains. *Conclusion:* Sequence analysis confirmed that 17 out of 18 MTBC PCR positive samples were true positives, while 1 sample remained inconclusive. These findings reaffirm the specificity of real-time PCR method for MTBC detection in culture-negative specimens.

**MM31: Clostridium perfringens bacteraemia: A Tale from Two Cases**

Mohammad Ismim Putera Nawawi[1], Anita Sulong[1]
*[1]Department of Medical Microbiology & Immunology, Faculty of Medicine, Universiti Kebangsaan Malaysia*

*Introduction: Clostridium perfringens* bacteraemia is extremely rare but clinically lethal if treatment is delayed or misdiagnosed. Most clinical conditions are usually associated with the pathology of the gastrointestinal tract. Nevertheless, non-gastrointestinal origins can be the foci of infection. This case report describes and compares clinicopathological features of two occurrences of *C. perfringens* bacteraemia of gastrointestinal and urinary origin, respectively. *Materials & Methods:* The first case describes an 89-year-old lady who arrived with symptoms suggestive of acute gastroenteritis while the second case describes a 72-year-old gentleman who presented symptoms of septic shock secondary to urinary tract infection. For both cases, *C. perfringens* was isolated in their peripheral blood cultures. *Results:* A Gram stain showed Gram-positive rods with anaerobic agar displaying grey, β-haemolytic colonies susceptible to metronidazole. The identification is aided by a reversed CAMP test and confirmed using Matrix-assisted laser-desorption/ionisation time-of-flight mass spectrometry (MALDI-TOF MS). The antibiotic sensitivity test was done using an Epsilometer test (E-test), which showed sensitivity towards metronidazole, amoxicillin/clavulanic acid and ampicillin/sulbactam. *Discussion: Clostridium perfringens* bacteraemia is an exceptionally uncommon condition that presents challenges in diagnosis and exhibits fast progression, leading to a significant risk of fatality. The diagnosis requires a strong level of suspicion, which is based on the patient's medical history, physical examination, microbiological data, biomarkers for sepsis, and other laboratory findings. Swift and accurate diagnosis, surgical intervention, effective management of the source of infection, and appropriate administration of antibiotics that target anaerobic bacteria are vital for successful therapy.

**MM33: Unexpected Pneumococcal Infection: A Rare Case of Pneumococcal Chorioamnionitis**

Praveena A/P Samy[1], Habib Abdul Hakim Bin Esa[1], Revathy A/P Arushothy[1], Nur Humairah Binti Thangarajah[2], Nalini A/P Ragandaran[1], Rohaidah Binti Hashim[1].
*[1]Bacteriology Unit, Infectious Disease Research Centre, Institute for Medical Research, National Institute of Health, Ministry of Health Malaysia.; [2]Bacteriology unit, Hospital Sultan Haji Ahmad Shah Temerloh, Pahang, Malaysia.*

*Introduction:* Maternal genital tract colonisation by *Streptococcus pneumoniae* is extremely rare but can lead to severe obstetric and neonatal complications. Here, we report a case that highlights the importance of a prenatal high vaginal swab (HVS), which uncovered the pathogenic potential of *S. pneumoniae*, serotype 3. *Case report:* A 24-year-old gravida 2, para 1, at 31 weeks and 2 days of gestation, presented with preterm premature rupture of membranes and active labour. Her antenatal history was complicated by persistent tachycardia and anaemia. A prenatal HVS was performed at 28 weeks due to symptomatic presentation, which detected *S. pneumoniae*, later identified as serotype 3. She subsequently delivered a live female infant prematurely via vaginal birth after caesarean. Clinical signs of chorioamnionitis were evident intrapartum and later confirmed by placental histopathology. Post-delivery, the infant developed respiratory distress, requiring intubation, surfactant therapy, and high-frequency oscillatory ventilation. She was diagnosed with moderate-to-severe respiratory distress syndrome, congenital pneumonia, and bilateral intraventricular haemorrhage. Although blood cultures were negative, the clinical presentation suggested congenital infection secondary to maternal chorioamnionitis. The infant required prolonged NICU care with oxygen support and antimicrobial therapy, gradually improved, and was discharged on room air at 36 weeks corrected gestation. *Discussion:* This case underscores the rare but serious risk of neonatal morbidity associated with maternal *Streptococcus pneumoniae* colonisation. It also highlights the importance of vigilant prenatal monitoring in primary healthcare and emphasises appropriate clinical measures when unexpected organisms are detected.

**MM34: Recurrent Abscesses in a Healthy Adolescent with Complex Paediatric Melioidosis: A Case Report**

Nurdiyana Mohamed[1], Muhammad Zakwan Yahya[2], Norhidayah Kamarudin[1], Wan Husna Barakah Meor Jamaludin[2], Asiyah Nordin[3]
*[1]Department of Pathology and Laboratory Medicine, Kulliyyah of Medicine, International Islamic University Malaysia, Pahang, Malaysia, [2]Department of Radiology, Kulliyyah of Medicine, International Islamic University Malaysia, Pahang, Malaysia, [3]Department of Medical Microbiology and Immunology, Universiti Kebangsaan Malaysia, Cheras, Kuala Lumpur, Malaysia*

*Introduction:* Melioidosis, caused by the environmental Gram-negative bacillus *Burkholderia pseudomallei*, exhibits diverse clinical syndromes from localised infection to fatal sepsis. Paediatric cases represent 5–15% of all melioidosis, with mortality ranging from 7–59%. *Case report:* A 13-year-old Malay boy presented with recurrent right inguinal abscesses extending into the iliopsoas muscle and anterior abdominal wall; initially misdiagnosed as a simple skin infection, definitive therapy was consequently delayed. Due to his unresolved pain and swelling progression despite antibiotics, he was admitted, and the contrast-enhanced CT confirmed abscess extension, necessitating tissue debridement. The tissue cultures isolated *B. pseudomallei*, susceptible to ceftazidime but resistant to trimethoprim–sulfamethoxazole (SXT). He received four weeks of intravenous ceftazidime followed by twelve weeks of oral amoxicillin–clavulanate. Investigations revealed impaired glucose tolerance, folate deficiency, and hypochromic microcytic anaemia. The patient attained full clinical and biochemical recovery at the completion of the maintenance phase. *Discussion:* This case highlights an unusual paediatric presentation with minimal environmental exposure and identifies host vulnerability mild hyperglycaemia, folate deficiency, and anaemia—that may impair innate and adaptive immunity, facilitating intracellular proliferation. The SXT resistance disrupts standard oral eradication, increasing relapse risk and necessitating alternative regimens. Emergent SXT resistance underscores the urgent need for surveillance of resistance genotypes and development of novel oral

eradication strategies. Complex paediatric melioidosis demands multidisciplinary management, vigilant clinical and laboratory monitoring, and adherence to prolonged antimicrobial therapy. Prospective studies on subclinical host variables in paediatric melioidosis are critically needed to enhance and refine risk stratification and therapy methods.

**MM35: Double trouble: Mixed Plasmodium falciparum and Plasmodium vivax infection with hepatic involvement and thrombocytopaenia**

Norafandi Mohd Noor, Sia Chew Guan, Rayuwani Mohamad Kamal, Gokullshautri Sinalthan, Roshatika Azhar
*Department of Pathology, Hospital Sibu, Sarawak, Malaysia*

*Introduction:* While mixed-species malaria infections are uncommon, they pose a substantial challenge in both diagnosis and treatment. *Plasmodium falciparum* is highly virulent, while Plasmodium vivax has the potential for relapse due to hypnozoites in the liver that are dormant and usually exhibit lower-level activity. Dual infection cases are difficult to diagnose, and microscopic examination can positively identify mixed-species infection in only 16.6% of the patients seen. The recognition of mixed-species disease necessitates the development of improved clinical recognition and better sensitivity in diagnosis in the future. *Case Report:* A 49-year-old male patient presented with high-grade fever, vomiting, and gastrointestinal symptoms two months after returning from Papua New Guinea and two months after being diagnosed with Plasmodium vivax which the patient claimed to be treated completely. A laboratory examination demonstrated a mixed infection of *P. falciparum* (55,680 T/µL) and *P. vivax* (1,600 T/µL). Laboratory assessment also noted thrombocytopenia, anaemia, and increased liver transaminases (AST 243 U/L, ALT 220 U/L). After initiation of treatment with artemether-lumefantrine, the patient began to improve rapidly and there was complete clearance of parasites by Day 5. Due to the possibility of P. vivax relapse, the patient was planned for follow-up treatment with primaquine to eliminate hepatic hypnozoites. *Discussion:* This case serves as an illustration of the importance of considering mixed-species malaria infections when returning from co-endemic areas. Patients with concurrent *P. vivax* infections may be masked by predominance of *P. falciparum* infection, making diagnosis and treatment challenging. *P. vivax* can notoriously relapse after *P. falciparum* infection and there is evidence from studies that approximately 21.5% of individuals treated for *P. falciparum* will develop recurrent *P.vivax* parasitaemia by Day 63. This presents a need for follow-up treatment rationales and monitoring strategies that acknowledge species specificity. The complexity of the clinical picture is further heightened by both malaria-induced hepatic dysfunction and haematological factors, reinforcing the need for ongoing monitoring. For favourable outcomes to occur in such complex diseases, a prompt, sequential assessment of parasitemia and appropriate treatment approaches is essential.

**MM36: Antimicrobial resistance of methicillin-sensitive versus methicillin-resistant Staphylococcus aureus**

Syahrul Azlin Shaari[1,2 *], Noor Aini Abu Bakar[2], Fairuz Abdul Rashid[1]
*[1]Medical Microbiology & Parasitology Department, Faculty of Medicine, University Teknologi MARA, Malaysia; [2]Medical Microbiology Unit, Hospital Al-Sultan Abdullah, University Teknologi MARA, Malaysia*

*Introduction:* Phenotypically, methicillin-sensitive *Staphylococcus aureus* (MSSA) and methicillin-resistant *Staphylococcus aureus* (MRSA) are identified by being cefoxitin sensitive and cefoxitin resistant, respectively. This study is intended to establish the differences in antimicrobial resistance between them, with regards to other routinely tested antibiotics. *Materials & Methods:* Antibiotic susceptibility results for *Staphylococcus aureus* isolated from clinical specimens processed by Medical Microbiology unit of Hospital Al-Sultan Abdullah UiTM, from January 2023 to December 2024, were retrieved and retrospectively analysed. Other than cefoxitin susceptibility was used to differentiate MSSA from MRSA, susceptibility profiles for erythromycin, clindamycin, gentamicin, rifampicin and fusidic acid were also evaluated. *Results:* There were a total of 365 MSSA and 93 MRSA isolated for the two years' duration. Antimicrobial resistance rates calculated for MSSA in comparison to MRSA were as follows. For erythromycin it was 4.5% vs 64%, for clindamycin 1.5% vs 22%, gentamicin 2.5% vs 18%, rifampicin was 1% vs 4% and finally resistance rates for fusidic acid was 9% vs 64%. *Discussion:* Almost two-thirds of MRSA isolates were resistant to either erythromycin or fusidic acid. About one-fifths of MRSA isolates were resistant to either clindamycin or gentamicin. In contrast, less than one-tenths of MSSA were resistant to either erythromycin, clindamycin, gentamicin or fusidic acid. However, resistance rates of MSSA and MRSA isolates against rifampicin were rather similar, both at less than 5%. This study suggests that antibiotics such as clindamycin remain a feasible alternative treatment, potentially in cases of skin and soft tissue infections due to community-acquired MRSA.

**MM37: Training Deficits and Quality Control Gaps in Parasitology Diagnostics: Findings from a Malaysian Pilot Survey**

Karshini Jeya Pirathaba
*Department of Parasitology, Faculty of Medicine, Universiti Malaya, Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* Intestinal parasitic infections (IPIs) remain a significant diagnostic and public health challenge in Malaysia. Accurate detection depends on trained laboratory personnel, appropriate techniques, and the implementation of internal quality control (IQC) systems. This pilot study aimed to assess baseline knowledge, diagnostic practices, and challenges faced by laboratory personnel prior to a parasitology hands-on workshop. *Materials & Methods:* A structured questionnaire was distributed via Google Form to 31 registered participants, with 29 valid responses collected. The survey assessed demographics, years of service, previous parasitology training, diagnostic techniques used, self-assessed proficiency, and laboratory quality practices. *Results:* Respondents included medical laboratory technologists (n=11), scientific officers (n=8), microbiology doctors (n=9), and one clinical doctor. Most participants were from government hospitals (n=14), followed by private laboratories (n=9) and university hospitals (n=6). Eleven had more than 10 years of experience, and 72% had not received formal parasitology training in the past five years. In terms of proficiency, 24 participants reported needing more practice in direct wet mount, 18 lacked confidences in concentration techniques, and 17 were not confident in permanent staining methods (e.g., trichrome, MZN). Key challenges included limited training opportunities (93.1%), limited sample access for quality control (58.6%), and lack of reference materials (58.6%). Alarmingly, 100% of participants reported performing stool examinations without positive or negative controls, citing both difficulty

in obtaining control materials and a perceived lack of necessity. *Discussion:* The findings underscore urgent gaps in parasitology diagnostic training and quality assurance. Structured education, standardised protocols, and implementation of IQC systems are essential to improve diagnostic reliability and patient outcomes.

**MM38: ANA positivity in post-COVID-19 era within Major Specialist Hospital. Is it Significance?**

Siti Fazilah Situ[1], Maznah Mohammad[1], Suhaiza Mohamad[1], Nur Zulaikhar Zakaria[1], Nur Fatini Shahime[1], Nurzahratul Hikma Binti Mohamad Zakaria[2]

*[1]Microbiology Unit, Pathology Department Hospital Tengku Permaisuri Norashikin, Selangor, Malaysia; [2]Clinical Research Unit (CRU), Hospital Tengku Permaisuri Norashikin, Selangor, Malaysia*

*Introduction:* ANA, an antibody targeting cell nuclei, is linked to Systemic Autoimmune Rheumatic Disease (SARD). Immunology laboratories have noted increased antinuclear antibody (ANA) test requisitions following COVID-19 for the past few years. This trend could substantially increase our annual reagent costs. Therefore, we studied the positivity rate among patients at a major specialist hospital and the significance of positive ANA results among post-COVID-19 cases. *Methodology:* This is a retrospective cross-sectional study analysing all ANA test results from January 2019 to December 2023 at HTPN, Kajang. Patient demographic data (age, gender, ethnicity) and COVID-19 status (confirmed via RTK or PCR) were extracted from the hospital laboratory information system. *Results:* Since 2019, testing requests have increased by over 15-21% in 2022 and 2023. Our data shows an average ANA positivity rate of 30-40% annually. Most requests were from female and Malay patients. In post-COVID years (2021, 2022 & 2023), the mean age groups are 36.3 to 39.1(SD16.3-18.1). From 870 ANA-positive cases, only 33 patients had confirmed COVID-19 infection before ANA testing. Chi-square analysis revealed a statistically significant association between gender and ANA results ($\chi^2 = 5.1$, $p = 0.024$), with females more likely to test positive for ANA. There was no statistically significant association between ANA results and ethnicity ($\chi^2 = 7.6$, $p = 0.058$) or age group ($p = 0.6$). *Discussion:* Other studies have explored the relationship between the presence of Antinuclear Antibodies (ANA) and post-COVID-19 infection. This study's findings are consistent with previous research from the pre-COVID year, which indicated that approximately 13-20% of healthy individuals exhibit ANA positivity, with higher rates observed in females compared to males.

**MM39: A Fatal Invasive Meningococcal Disease caused by Non-Typeable Neisseria meningitidis in Infant with G6PD Deficiency: A Rare but Lethal Combination**

Muhammad Zaki Amali Basiron[1,2], Amizah Othman[1], Siti Asma' Hassan, Syazwani Mohd Tajuddin[2]

*[1]Microbiology Unit, Department of Pathology, Hospital Sultanah Bahiyah, Kedah, Malaysia; [2]Department of Medical Microbiology & Parasitology, School of Medicine, Universiti Sains Malaysia, Kelantan, Malaysia*

*Introduction:* Non-typeable *Neisseria meningitidis* strains are generally less virulent but can cause severe infections in immunocompromised individuals, including infants. *Case report:* A 5-month-old, full-term girl with G6PD deficiency presented with a 2-day history of fever, diarrhea, and a generalized purpuric rash. Initially, her condition was stable, but she rapidly deteriorated the following day. The purpuric rash spread cephalocaudally across her body, and she progressed into respiratory distress, requiring intubation with a working diagnosis of meningoencephalitis. Later, the patient experienced a seizure, and her condition worsened, leading to purpura fulminans, disseminated intravascular coagulation, and multiorgan failure. The diagnosis shifted to meningococcal septicemia after blood culture and serotyping revealed a non-typeable *Neisseria meningitidis* strain. She required triple inotropic support, FFP transfusion, and was given intravenous ceftriaxone 250 mg q12h for 13 days. However, she succumbed to death after 13 days of admission. Discussion: While there is limited direct evidence linking G6PD deficiency specifically to *Neisseria meningitidis* infections, studies have shown that G6PD deficiency predisposes individuals to more severe infections in general, particularly when oxidative stress and immune function are compromised. G6PD deficiency impairs immune function, allowing *Neisseria meningitidis*' immune evasion mechanisms, such as factor H binding and sialylation of lipooligosaccharides, to be more effective. *Conclusion:* This case underscores that even non-typeable strains can lead to fatal outcomes in vulnerable populations, and the correct antibiotic treatment is crucial for patient outcomes.

**MM40: Invasive fungal diseases in patients with COVID-19: demographics, risk factors and outcomes**

Mohd Nizam Tzar[1,2], Chuan Hun Ding[1,2], Ahmad Firdaus Salleh[2], Asiyah Nordin[1,2], Asrul Abdul Wahab[1,2]

*[1]Department of Medical Microbiology and Immunology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia; [2]Department of Diagnostic Laboratory Services, Hospital Canselor Tuanku Muhriz, Kuala Lumpur, Malaysia*

*Introduction:* The COVID-19 pandemic has caused a rise in secondary infections, including invasive fungal diseases (IFDs), which have greatly increased morbidity and mortality. This study aimed to explore the demographics, risk factors and outcomes of IFDs in COVID-19 patients admitted to our centre. *Materials & Methods:* We retrospectively reviewed data from PCR-confirmed category 4 or 5 COVID-19 patients between 2020 and 2023 who also had positive mycology cultures or serology. Patients with positive fungal tests more than 90 days after their initial COVID-19 diagnosis were excluded. *Results:* Among 5,075 PCR-positive COVID-19 patients, 23 (0.45%) met the criteria. Of these, 15 (65.2%) had candidiasis, seven (30.4%) aspergillosis, and one (4.3%) *Exophiala* fungaemia. No mucormycosis cases were identified. The male-to-female ratio of IFDs was 2.8:1, with ages ranging from 26 to 77 years (mean 59.6). The interval between COVID-19 diagnosis and positive fungal test ranged from 3 to 38 days, averaging 12.6 days for candidiasis and 16 days for aspergillosis (difference not statistically significant). Only acute kidney injury was significantly linked to candidiasis. Common factors across all cases included indwelling vascular catheters (95.7%), ICU admission (91.3%), mechanical ventilation (87%), lung diseases (65.2%), and kidney impairment (60.9%), poorly controlled diabetes (34.8%), and liver impairment (26.1%). Overall mortality was 91.3% (100% for aspergillosis and *Exophiala* fungaemia, 86.7% for candidiasis). *Discussion:* Though IFD prevalence in COVID-19 patients is low, its high morbidity and mortality make it a critical concern. Early identification of risk factors may help reduce its occurrence and improve outcomes.

**M41: Efficacy of hydrogen peroxide fumigation in reducing indoor fungal load: dematiaceous fungi exhibit greater resistance than hyaline fungi**

Mohd Nizam Tzar[1], Hamidah Yusoff[1], Siti Zubaidah Abdul Karib[2], Rosidah Ramli[2], Mohd Hafidzul Jasman[2]
*[1]Department of Medical Microbiology and Immunology, Faculty of Medicine, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia; [2]Department of Medical Education, Faculty of Medicine, Universiti Kebangsaan Malaysia, Kuala Lumpur, Malaysia*

*Introduction:* Sick-building syndrome (SBS) encompasses symptoms such as respiratory complaints, eye irritation, and allergies linked to indoor environmental factors, including biological contaminants like fungi and bacteria. Hydrogen peroxide fumigation is increasingly used for indoor microbial control due to its safety and broad-spectrum efficacy. This study evaluated the effectiveness of hydrogen peroxide fumigation in reducing indoor fungal and bacterial contamination in an 18-floor building. *Materials & Methods:* Thirty-eight Sabouraud dextrose agar plates were placed at 38 sites across the building prior to hydrogen peroxide fumigation. Air sampling was conducted before and after fumigation to assess microbial growth. Fungal isolates were identified phenotypically and molecularly where possible. Changes in microbial load and fungal species diversity were analysed. *Results:* Before fumigation, 32 of 38 sites showed fungal growth, with ten locations harbouring three or more fungal species. Post-fumigation, 28 sites still yielded fungal isolates, though overall microbial counts significantly decreased, particularly bacteria, which were completely eliminated. Hyaline moulds were significantly reduced, whereas dematiaceous moulds showed relative resistance, likely due to melanin-mediated protection. Several medically important fungi were identified, raising concerns about occupant health. *Discussion:* Hydrogen peroxide fumigation effectively reduces indoor microbial burden but does not provide a permanent solution to SBS, as fungi, especially dematiaceous species, may persist or recolonize. Comprehensive indoor air quality management including ventilation, humidity control, and regular cleaning is essential. Future studies should incorporate molecular identification and clinical symptom correlation to better understand health impacts and optimise mitigation strategies.

**MM42: The Double-Pronged Threat of Corynebacterium striatum Bacteraemia: From Native Valve Endocarditis to Acute Cerebrovascular Infarction**

Siti Khairani Mohd Hafiz Ngoo[1], Yuhin Karina Yusoff[3], Faizah Mustapha[3], Fadzilah Mohd Nor @ Ghazali[1,2]
*[1]Department of Medical Microbiology & Parasitology, Faculty of Medicine, Universiti Teknologi MARA, Sg. Buloh Campus, Selangor, Malaysia; [2]Medical Microbiology Unit, Department of Clinical Diagnostic Laboratories, Hospital Al-Sultan Abdullah, Universiti Teknologi MARA, Bandar Puncak Alam, Selangor Malaysia; [3]Microbiology Unit, Department of Pathology, Hospital Selayang, Selangor, Malaysia*

*Introduction: Corynebacterium striatum* is a non-spore-forming Gram-positive rod, often regarded as a skin commensal, but it is increasingly recognised as a true pathogen, especially in immunocompromised patients. This case report highlights the diagnostic challenge faced by clinicians and microbiologists in distinguishing contamination from true infection. *Case Report:* A 61-year-old gentleman with underlying bilateral urolithiasis presented with abdominal pain and persistent fever for one week despite oral antibiotics. He was initially diagnosed with right pyelonephritis and started on intravenous (IV) amoxicillin-clavulanic acid after blood and urine cultures were taken. Despite treatment, his condition worsened with a reduced Glasgow Coma Scale (GCS) score. CT brain revealed an acute ischemic stroke in the right posterior cerebral artery (PCA) territory. Antibiotics were escalated to piperacillin-tazobactam. Blood cultures later grew Gram-positive bacilli identified as *Corynebacterium striatum.* A repeat blood culture two days later again grew *Corynebacterium striatum* with a similar antibiotic susceptibility profile. Persistent bacteraemia prompted an echocardiogram, which revealed mitral valve vegetation, leading to a switch to IV vancomycin. As his neurological status declined, a lumbar puncture was performed, but cerebrospinal fluid (CSF) cultures showed no growth. Vancomycin was continued with dose adjustments based on therapeutic levels. Despite completing six weeks of treatment, the patient showed minimal improvement and was discharged home with residual disability. *Discussion:* The decision to treat *C. striatum* infection should consider the patient's clinical history, immune status, presence of invasive procedures or indwelling devices, and supporting laboratory and imaging evidence to determine its significance as a true pathogen rather than a contaminant.

**MM43: Co-infection or Coincidence? The Clinical Significance of HHV-6 Detection in Streptococcus pneumoniae Meningitis: A Case Report**

Muhammad Zaki Amali Basiron[1,2], Amizah Othman[1], Siti Asma' Hassan[2], Syazwani Mohd Tajuddin[2]
*[1]Microbiology Unit, Department of Pathology, Hospital Sultanah Bahiyah, Kedah, Malaysia; [2]Department of Medical Microbiology & Parasitology, School of Medicine, Universiti Sains Malaysia, Kelantan, Malaysia*

*Introduction:* Co-infections of bacterial and viral meningitis are rare in paediatric population, but the rising use of highly sensitive NAATs can complicate interpretation when multiple pathogens are detected. *Case report:* A previously healthy 3-month-old girl presented with an 11-day history of fever (without rash), irritability, and recurrent vomiting. Physical examination revealed a bulging fontanelle with increased head circumference. Laboratory tests showed hyperleukocytosis and elevated CRP. Blood culture confirmed *Streptococcus pneumoniae*, serotype 14 via latex agglutination. Lumbar puncture revealed clear cerebrospinal fluid (CSF) with lymphocytic pleocytosis, elevated protein, and low glucose (with concomitantly elevated plasma glucose). Multiplex PCR of the CSF was also positive for *Streptococcus pneumoniae* (CT value 17.3) and concurrently detected human herpesvirus 6 (HHV-6) (CT value 21.9). The patient developed a left frontal subdural effusion and sinus thrombosis, necessitating burr hole drainage and anticoagulation. She completed 14 days of cefotaxime 330mg q6h and C-penicillin 825000u q6h. The patient improved without seizures or focal neurological deficits and was stable at discharge and follow-up. *Discussion:* Despite HHV-6 detection, clinical and CSF findings supported bacterial meningitis, confirmed by blood culture. HHV-6 likely represented latent infection. Co-infections may cause severe neurological symptoms due to blood-brain barrier disruption or viral reactivation from immune dysregulation. Most congenital HHV-6 infections stem from chromosomally integrated viruses (ciHHV-6) and are asymptomatic. *Conclusion:* Accurate differentiation between bacterial and viral meningitis requires integrating clinical and laboratory data to guide effective antimicrobial therapy and optimise outcomes.

**MM44: A Case of Unsuspected Disseminated Tuberculosis in an Immunocompetent Host: A Diagnostic Challenge**

Fadia Sharmin Fauzi[1,2], Nur Izati Mustapa[1]
*[1]Department of Pathology, Hospital Sungai Buloh, Selangor, Ministry of Health Malaysia; [2]Medical Microbiology & Parasitology Department, Faculty of Medicine, Universiti Teknologi MARA, Sg. Buloh Campus, Selangor*

*Introduction: Mycobacterium tuberculosis complex* causes Tuberculosis (TB) which primarily infect the lungs and occasional disseminated infection especially among high-risk individuals with HIV, diabetes mellitus, immunosuppression and children below 5 years. This is a rare case of disseminated tuberculosis in a middle-aged immunocompetent female presenting with pulmonary tuberculosis, Pott's disease, tuberculous aortitis and multiple lymph nodes involvement in thorax and abdomen. *Case Report:* A 42-year-old female with underlying hypertension presented to the emergency department complaining of lower back pain for 1 month with no history of recent fall or trauma. She was treated as having a mechanical back and was referred to the surgical department as an outpatient. US abdomen done 4 months later revealed collection at the lumbar region. A CT thorax-abdomen-pelvis found bilateral psoas collection with extension to subligamentous epidural collection and bilateral subphrenic collection. Also seen, periaortic collection and periaortic aortitis with possible communication with left lower lobe bronchioles resulting in left lower lobe collapse consolidation; multiple lung nodules and liver hypodensities with pregastric, mediastinal and peritoneal nodes enlargement. Further history revealed 15kg weight loss within 6 months with intermittent episodes of night sweat. Sputum for geneXpert detected a 'trace' of *Mycobacterium tuberculosis*. Intensive phase anti-tuberculosis therapy of isoniazid, rifampicin, ethambutol and pyrazinamide was initiated. Percutaneous drainage of psoas collection was done, and samples sent for MTB culture grew *Mycobacterium tuberculosis*. An imaging done 4 months later revealed a smaller psoas collection. *Discussion:* This case emphasises the importance of maintaining high suspicion for tuberculosis in TB prevalent countries even in low-risk patients with unusual presentation. Role of rapid MTB PCR in providing a prompt diagnosis of tuberculosis was able to guide clinicians with the treatment decision.

**MM45: Mycelial Menace: A Fusarium Horror in the Haematologic Shadows**

Shing Yieng Chiew[1], Norashikin Samsudin[2], Athirah Mohammad[1], Nurnabilah Zainuddin[1], Alisa Hanum Arba'eni @ Arbaen[1]
*[1]Department of Pathology, Hospital Umum Sarawak, Sarawak, Malaysia; [2]Department of Pathology, Faculty of Medicine & Health Sciences, Universiti Malaysia Sarawak, Kota Samarahan, Malaysia*

*Introduction:* Fungal infections are potentially fatal, particularly in immunocompromised individuals. While yeast infections remain the predominant cause of fungaemia in patients with malignancies, the incidence of mould infections is rising and warrants greater clinical attention. This report presents a case of disseminated fusariosis in a patient with acute myeloid leukaemia. *Case report:* A 42-year-old woman with no known comorbidities presented with fever and vomiting for one day, accompanied by dizziness and loss of appetite lasting one week. Full blood count revealed pancytopenia with profound neutropenia. Subsequent laboratory tests confirmed a diagnosis of acute myeloid leukaemia. Induction chemotherapy was initiated. She experienced persistent temperature spikes and developed multiple painful erythaematous papules on the extremities, unresponsive to multiple courses of broad-spectrum antibiotics and antifungal therapy. Two sets of repeated blood cultures, initially misreported as yeast-like cells in the preliminary Gram stain, were later identified as *Fusarium solani* species complex through microscopic examination of the isolate. The antifungal therapy was promptly adjusted to a combination of amphotericin B lipid complex and voriconazole. She showed clinical improvement after two weeks of antifungal combination therapy. *Discussion: Fusarium* may mimic yeast on Gram stain; therefore, we emphasise the importance of communicating clinical presentations and suspected diagnoses, especially for malignancy-related infections, to laboratory personnel to ensure vigilant screening for hyphae. Molecular testing is less feasible at some centres; thus, microscopic examination serves as a rapid, cost-effective diagnostic tool for genus-level identification of *Fusarium*, which is often sufficient to guide prompt and appropriate management in most clinical settings.

**MM46: A fatal Chromobacterium violaceum sepsis in infant with suspected chronic granulomatous disease**

Norashikin Samsudin[1,2], Siti Hafsyah Mohd Hariri[2], Zeehaida Mohamed[2]
*[1]Department of Pathology, Faculty of Medicine & Health Sciences, Universiti Malaysia Sarawak, Sarawak, Malaysia; [2]Department of Medical Microbiology and Parasitology, School of Medical Sciences,Universiti Sains Malaysia, Kelantan*

*Introduction: Chromobacterium violaceum* is a saprophytic, Gram-negative bacilli that produces a distinctive violet pigment and is often regarded as a contaminant. Although it is rarely pathogenic in humans, significant infections have been reported - disproportionately high in individuals with chronic granulomatous disease (CGD), a genetic condition characterised by the inability of neutrophils to perform adequate oxidative metabolism during phagocytosis of catalase-producing bacteria. *Case report:* A 5-month-old term boy presented to the emergency department with fever and post-feeding vomiting for two days. He had a history of prolonged hospitalisation for four months due to multiple infections and was suspected to have autosomal recessive CGD. Intubation was commenced due to poor perfusion and unresponsiveness. Blood culture obtained in the emergency department grew *Chromobacterium violaceum* identified by the VITEK 2 system with an excellent identification score. The isolate was susceptible to gentamicin, amikacin, ceftazidime, cefepime, imipenem, and meropenem. Despite active intervention, his condition further deteriorated, and he succumbed to severe decompensated septic shock on the same day. The diagnosis of CGD was subsequently confirmed by a dihydrorhodamine (DHR) flow cytometric test result that became available posthumously. Genetic counselling was arranged for his parents. *Discussion: Chromobacterium violaceum* can cause fulminant, life-threatening infection in CGD patients, particularly infants. Despite prompt intervention, rapid deterioration and fatality are significantly high in this vulnerable group. This case highlights the importance of early parental counselling and consideration of definitive therapy, such as haematopoietic stem cell transplantation.

**MM47: Beyond the Usual Route: A Case of Postpartum Gonococcaemia in the Absence of Genital Symptoms**

Norashikin Samsudin[1], Nurnabilah Zainuddin[2], Nurhafizah Hatta[2], Alisa Hanum Arba'eni @ Arbaen[2], Shasheila Mohd Daud[3], Sue Marie Cheng Kian Pei[4], Arlizan Baizura Ariffin[1], Madzlifah Ahadon[1]

*[1]Department of Pathology, Faculty of Medicine & Health Sciences, Universiti Malaysia Sarawak, Sarawak, Malaysia; [2]Department of Pathology, Sarawak General Hospital, Sarawak, Malaysia; [3]Department of Obstetrics and Gynaecology, Faculty of Medicine & Health Sciences, Universiti Malaysia Sarawak, Sarawak, Malaysia; [4]Department of Obstetrics and Gynaecology, Sarawak General Hospital, Sarawak, Malaysia*

*Introduction: Neisseria gonorrhoeae* is a Gram-negative diplococci associated with sexually transmitted infections, that typically infects the urethral, endocervical, rectal and pharyngeal mucosa. In women, gonococcal infections are often asymptomatic, which predisposes them to a higher risk of developing disseminated gonococcal infection (DGI). Here, we report a case of postpartum *Neisseria gonorrhoeae* bacteraemia, also known as gonococcaemia. *Case report:* A 21-year-old woman at term presented during active phase of labour, with one-day history of productive cough with greenish sputum. Delivery was complicated with postpartum haemorrhage secondary to uterine atony. Two hours post-delivery, she developed a sudden onset of fever with chills and rigors. Generalized skin petechiae were noted. She was empirically treated with intravenous cefuroxime for maternal pyrexia secondary to upper respiratory tract infection. Blood culture grew *Neisseria gonorrhoea*, and antibiotic therapy was escalated to ceftriaxone for a five-day course. Vaginal and throat swab cultures were negative. Biohazard screening was unremarkable, and her husband was referred for screening. Her baby was assessed for possible perinatal infection, but no evidence of infection was found. She recovered uneventfully and was discharged on day nine of admission. *Discussion:* Early recognition and targeted antimicrobial therapy are crucial in managing gonococcaemia, particularly during pregnancy and postpartum period. This is to prevent DGI, maternal morbidity and neonatal infection. This case highlights the need for a holistic approach including sexual health education, partner screening and neonatal assessment of perinatal infection by *Neisseria gonorrhoea* and with possible re-testing in patients if symptoms recur.

**MM48: Simultaneous Detection of plasmid mediated mcr-1 to mcr-5 Genes: Optimisation of a Multiplex PCR Analysis for Colistin Resistance Testing**

Rohaidah Hashim[1], Nadia Syahirah Suhaimi[1], Nur Asyura Amdan[1], Aisya Nazura Azman[1], Kerlina Sakudat[1], Nursaedah Zion[1],

*[1]Bacteriology Unit, Infectious Disease Research Centre, Institute for Medical Research, National Institute of Health, Selangor, Malaysia*

*Introduction:* Colistin, known for their effectiveness against gram-negative bacteria, often regarded as a last resort antibiotic, especially for treating infections caused by carbapenems resistant Enterobacterales. Identification of plasmid-borne gene, mcr-1, in Enterobacteriaceae strains from clinical and veterinary samples, marked a significant development in antimicrobial resistance. This discovery sparked global concern due to its ability for rapid spread. Its variants (mcr-2 to mcr-10) have later been reported imposing renewed scientific focus on colistin resistance. Detection of mcr-1 and its variants is crucial. Nevertheless, to this date there is no commercially available kit that is able to characterise the genes. The aim of this study is to develop a multiplex PCR assay enabling simultaneous detection of mcr-1 to mcr-5 for clinical use. *Materials & Methods:* Primers for all five target genes were individually designed, validated, and subsequently combined into a single multiplex PCR assay through adjusting the concentrations of PCR components, harmonizing annealing temperatures, and fine-tuning cycling parameters to ensure robust and specific amplification of all target genes in a single assay. *Results:* The final multiplex PCR assay demonstrated clear, distinct bands for each gene, with no cross-reactivity or nonspecific amplification, indicating high specificity and efficiency. *Discussion:* The successful development of this multiplex PCR assay marks a significant step toward improving the detection of colistin resistance. By enabling the simultaneous detection of mcr-1 to mcr-5, this assay addresses a critical gap in current diagnostic and surveillance capabilities, particularly in Malaysia, where existing data on mcr genes prevalence have been inconsistent and fragmented.

**M49: Intracranial Haemorrhage in Paediatric Systemic Lupus Erythaematosus: A Diagnostic and Therapeutic Challenge**

Nur Diyana Mohd Shukri[1,2], Syazwani Mohd Tajudin[1,2], Noor Suryani Mohd Ashari[1,2], Nurul Khaiza Yahya[1,2]

*[1]Department of Immunology, School of Medical Sciences, Universiti Sains Malaysia, Kelantan, Malaysia*

*Introduction:* Paediatric systemic lupus erythematosus (SLE) is a rare condition impacting approximately 15-20% of SLE patients. Studies revealed that early-onset SLE frequently presents with atypical features, follows a more severe disease course, and is linked to poor prognosis. Neuropsychiatric lupus is a recognised complication. However, intracranial haemorrhage remains an uncommon and potentially fatal presentation, posing diagnostic and therapeutic challenges. *Case report:* A previously healthy 10-year-old girl presented with high-grade fever, red petechiae spots over the face, neck and bilateral lower limbs and persistent bleeding over spontaneous tooth extraction prior to admission. She was initially worked up for acute leukaemia in view of pancytopenia. However, the laboratory investigations showed severe thrombocytopenia, normocytic anaemia, positive antinuclear antibodies, elevated anti-dsDNA antibodies, and normal complement levels. Computed Tomography of the brain revealed a spontaneous right frontal bleed with bilateral subdural haemorrhage. She fulfilled the EULAR/ACR 2019 criteria for SLE. *Discussion:* Intracranial haemorrhage in paediatric SLE is relatively rare and may occur due to immune thrombocytopenia, central nervous system vasculitis, or antiphospholipid syndrome. Diagnosis requires a high index of suspicion, particularly when SLE has not been previously diagnosed. Neuroimaging is essential for early identification of haemorrhagic events, while immunological and haematological investigations are pivotal in confirming the underlying autoimmune aetiology. This case underscores the critical role of comprehensive laboratory evaluation in the diagnosis and management of atypical presentations of paediatric SLE. A timely laboratory assessment enabled the prompt initiation of immunosuppressive therapy, which may have helped reduce the risk of long-term neurological sequelae.

**MM50:High-resolution HPV genotyping uncovers genotype-specific trends**

Sarah, Abdul Halim, Norlelawati A Talib, Nurdiyana Mohamed
*Department of Pathology and Laboratory Medicine, Kulliyyah of Medicine, International Islamic University Malaysia, Pahang, Malaysia*

*Introduction:* Human papillomavirus (HPV) is a circular, double-stranded DNA virus with genotype-specific oncogenic potential. Given the differential oncogenicity of individual genotypes, precise molecular typing is essential for genomic surveillance, risk stratification, and evaluation of vaccine efficacy across populations. *Material and Methods:* A total of 3,814 cervical specimens were retrospectively analysed from patients attending Sultan Ahmad Shah Medical Centre, SASMEC@IIUM between 2018 and 2024. Genomic DNA was extracted and subjected to multiplex real-time PCR-based genotyping. Specimens collected from 2018 through February 2024 were tested using the Anyplex™ II HPV28 Detection assay, while those from March 2024 onward were processed with the Allplex™ HPV28 Detection kit (Seegene, Inc.). Both platforms utilise proprietary TOCE™ (Tagging Oligonucleotide Cleavage and Extension) and DPO™ (Dual Priming Oligonucleotide) technologies, enabling high-specificity, high-throughput simultaneous detection of 28 HPV genotypes in a single reaction. *Results:* HPV DNA was identified in 8.6% of cases. High-risk (HR) genotypes dominated the landscape, with HPV-52 (11.4%), HPV-66 (9.5%), and HPV-18 (8.0%) being the most prevalent. HPV-18 demonstrated consistent annual detection, whereas HPV-52 showed an incremental rise in prevalence from 0.8% in 2019 to 1.3% in 2024, indicating potential genotype replacement or selective pressure effects. Low-risk genotypes such as HPV-6 and HPV-11 were less commonly detected. *Conclusion:* This study illustrates the diagnostic value of multiplex molecular platforms in delineating genotype-specific HPV trends. The emerging increase in HPV-52 prevalence highlights the need for sustained molecular monitoring to guide regional vaccination strategies and refine diagnostic algorithms.

**MM51: RSV Takes the Lead: Post-COVID-19 Shift in Viral Respiratory Infections in a Malaysian Tertiary Hospital**

Nurul Izzati Abdul Aziz[1,2], Rinni Damayanti[1], Hasni Mahayidin[2], Zamberi Sekawi[2], Rosni Ibrahim[2]
*[1]Department of Pathology, Hospital Sultan Idris Shah, Serdang, Selangor, Malaysia; [2]Department of Medical Microbiology, Faculty of Medicine and Health Sciences, Universiti Putra Malaysia, Serdang, Selangor, Malaysia*

*Introduction:* Movement restrictions during the COVID-19 pandemic suppressed the circulation of respiratory viruses. However, a resurgence with altered viral patterns occurred post-restrictions. The recent study aimed to determine viral aetiologies, and associated risks among patients with severe acute respiratory infections (SARI) in the post-COVID-19 era. *Material and Methods:* A retrospective cross-sectional study was conducted at Hospital Sultan Idris Shah, from January to June 2023, including 389 SARI patients tested via PCR for Influenza A/B, Respiratory Syncytial Virus (RSV), and SARS-CoV-2. Demographic and clinical data were extracted from the hospital record. *Result and Discussion:* Among 389 patients, 38% tested positive: RSV (23.4%) was predominant, followed by influenza (12.3%) and SARS-CoV-2 (4.1%). The majority were aged between 0–5 years old. The majority (89.9%) were given antibiotics, while only 16.8% received antivirals and severe outcomes were observed in 14.1% of cases. Significant associated risks include exposure to sick contacts (AOR = 1.79, $p = 0.025$), the need for ventilatory support (AOR = 1.86, $p = 0.029$) and non-invasive ventilation (AOR = 2.89, $p = 0.007$), reduced white cell count (WCC) (AOR = 0.88, $p < 0.001$) and antiviral therapy (AOR = 5.26, $p < 0.001$). *Conclusion:* In the post-COVID-19 era, RSV emerged as the leading viral cause of SARI, predominantly in young children. Statistically significant associations include exposure to sick contacts, need for respiratory support, and reduced white cells. As viral predominance in most cases, it is crucial to promote the judicious use of empirical antibiotics in patients with SARI to prevent unnecessary use and resistance.

**MM52: Enhanced Tuberculosis Diagnosis through Combined Rapid Mycobacterium tuberculosis (MTB) PCR and Culture: Diagnostic Agreement and Clinical Utility**

Lee Chai Chen[1], Mohd Firdaus Che Mat[1], Mahani Roslan[1], Adibah Che Mohamad[1], Tan Yee Ling[1], Izlyn Zalikha Annisa Nor Rasidi[1], Chandralegga Chandrasekharan[1], Alisha Nur Emilia Balqis Abdul Rahman[1], Khoo Jo Lynn[1], Norziha Zainul Abidin[1], Nurul Atiqa Mohd Yuseri[2], Yew Oi Fong[2], Masita Arip[1,2,3]
*[1]Molecular Diagnostics Laboratory, Sunway Medical Centre, Petaling Jaya, Selangor Darul Ehsan, Malaysia; [2]Microbiology Department, Sunway Medical Centre, Petaling Jaya, Selangor Darul Ehsan, Malaysia; [3]Allergy and Immunology Research Centre, Institute for Medical Research, National Institutes of Health, Ministry of Health Malaysia, Setia Alam, Selangor, Malaysia*

*Introduction:* Tuberculosis caused by the bacterium *Mycobacterium tuberculosis* (MTB) remains a major global public health challenge. Accurate and timely diagnosis is crucial for effective disease control as well as patient management. Although both culture and rapid PCR are established diagnostic tools, relative comparison of their concordance and complementary roles in clinical practice remains limited. This study evaluates agreement between rapid MTB PCR and MTB culture, highlighting their combined utility in routine diagnostics. *Materials & Methods:* A retrospective study was conducted from 2018 to 2024, involving 1,201 patients with paired rapid MTB PCR test and MTB culture results. Patients ranged in age from less than 5 to 100 years, with females accounting for 55% (median age 56 years) and males 45% (median age 60 years). Confirmation of rifampicin resistance by both PCR and culture-based drug susceptibility testing (DST) was also examined. Diagnostic agreement was calculated using Cohen's Kappa coefficient. Sensitivity, specificity, positive predictive value (PPV), and negative predictive value (NPV) were also assessed with 95% confidence intervals (CIs). Sample size was sufficient to provide adequate statistical power (≥90%) to differentiate clinically significant differences in diagnostic performance measures. *Results & Discussion:* The MTB/RIF PCR test demonstrated high agreement with MTB culture with a Cohen's Kappa of 0.86 (95% CI: 0.82–0.90), indicating strong inter-method reliability. Sensitivity was 98.7% (95% CI: 97.2–99.4), specificity 94.6% (95% CI: 93.1–96.0), PPV 81.0% (95% CI: 76.4–85.6), and NPV 99.7% (95% CI: 98.8–99.9). Of the total, 214 rifampicin-resistant cases identified by PCR, concordance with culture-based DST was high (Kappa = 0.95; 95% CI: 0.91–0.98). Subgroup analysis showed that specificity was slightly lower in smear-negative patients. However, the negative predictive value (NPV) is consistently high in all subgroups, indicating strong reliability in ruling

out TB. The PPV was lower than NPV and most likely reflects the overall prevalence of TB among the test population. *Conclusion:* Combination of rapid MTB PCR with MTB culture optimises diagnostic routines by enabling rapid organism detection, viability confirmation, and drug resistance profiling. The high accuracy, strong agreement, and excellent NPV make rapid PCR an appropriate frontline diagnostic tool, especially for application in high-burden TB facilities.

**MM53: Beyond the Rash: Blood Culture Detection of Meningococcal Meningitis in an Infant with Culture-Negative CSF**

Susilahwati Muhammad[1], Nursyahirah Afiqah binti Mohammad[1], Siti Hafsyah Mohd Hariri[2]
*[1]Department of Pathology, Hospital Tawau, Sabah, Malaysia [2]Department of Medical Microbiology and Parasitology, School of Medical Sciences, Universiti Sains Malaysia, Kelantan, Malaysia*

*Introduction:* Meningococcal meningitis is a life-threatening condition in infants that may present atypically. While rash is a classical sign, its absence should not exclude the diagnosis. Culture-negative CSF adds further diagnostic complexity, highlighting the need for robust microbiological support. *Case report:* A 5-month-old immunized boy presented with seizures following three days of fever and one day of cough. He demonstrated neck stiffness and uprolling of the eyeball but no rash. Multiple seizures occurred throughout admission, required intravenous diazepam and phenytoin. CECT brain revealed no radiological signs of meningitis. Subsequent lumbar puncture was performed, revealed low CSF glucose and elevated protein, strongly suggestive of bacterial meningitis; however, CSF culture was negative. Blood culture isolated *Neisseria meningitidis*, sensitive to ceftriaxone, penicillin and ciprofloxacin. He was treated with IV C-penicillin for a week and high-dose IV cefotaxime for 14 days but was discharged against medical advice due to financial constraints and defaulted follow-up. Serotyping for *Neisseria meningitidis* was sent to the Institute for Medical Research(IMR), the result was non-typeable. *Discussion:* This case highlights a diagnostic challenge of meningococcal meningitis presenting without rash and with both negative CSF culture and non-contributory imaging. Despite the absence of radiological findings, clinical signs and CSF biochemistry supported meningitis. Blood culture was essential for pathogen identification. The non-typeable result further underscores limitations of conventional serogrouping. Molecular diagnostics such as multiplex PCR could have improved pathogen detection in this culture-negative case.

**MM54: Molecular characterisation of unclassified hepatitis C genotypes in Malaysia**

Sharifah Aina Afzan Syed Aminuddin, Nurul Asshikin Ruslan, Jeyanthi Suppiah, Rozainanee Mohd Zain
*Virology Unit, Infectious Research Disease Centre (IDRC), Institute for Medical Research, National Institute of Health, Setia Alam, Shah Alam, Selangor, Malaysia*

*Introduction:* Hepatitis C virus (HCV) is a quasispecies and its high genetic diversity has led to the emergence of eight genotypes and a large number of subtypes in limited geographical areas. In the era of pan-genotypic Direct Acting Agents (DAA), HCV genotypes still have important values in epidemiology and management of patients. In addition, it is important to address the limitations of the current commercial HCV genotype assays in the market in detecting certain genotypes of HCV. The study aimed to characterise the unclassified HCV genotypes from the commercial assays. *Materials & Methods:* 59 undetermined genotypes HCV were subjected to RNA extraction and PCR amplification based on the in-house newly developed method. The in-house assay is targeted at the 5'-UTR region of HCV genome. The amplified products were then subjected to Sanger sequencing. Results were analysed using the Standard Nucleotide BLAST and plotted for phylogenetic trees to further assess the HCV genotypes. *Results:* 50/59 (84.8%) samples were successfully amplified and sequenced. 9 samples were unable to amplify for the target region. All samples are identified as HCV genotype 1a, 3a/e/k and 6n/f/xe. *Discussion:* Unclassified HCV genotypes can be genotyped with the newly developed Sanger sequencing assay. The assay can be performed to overcome the limitations of the current commercial assay for HCV genotyping.

**MM56: UTILITY OF ECP IN ENDOTYPING OF ALLERGIC DISEASES: A T2 BIOMARKER PERSPECTIVE FROM A NATIONAL ALLERGY LABORATORY**

Husna Ahmad, Ying Yi Kim, Nurul Rahim, Kamalia Kamarudin
*Allergy Unit, Institute for Medical Research, National Institute of Health, Ministry of Health, Malaysia*

*Introduction:* Identifying type 2 (T2) inflammation and its mediators is crucial for allergic diseases endotyping in the era of precision medicine. Eosinophilic cationic protein (ECP) is a functional marker of eosinophil activation, directly involved in the inflammatory pathways of allergic diseases. Although ECP is an established test, its testing has been underutilised. This study reviews the clinical utility of ECP testing. *Materials & Methods:* Between 2020 and 2024, a total of 108 ECP test requests were received, and the clinical summaries with ECP levels were analysed. *Results:* Nineteen samples (16.7%) were rejected due to poor sample quality, while 89 underwent ECP testing (Immunocap Phadia). Requests were from patients with uncontrolled symptoms of bronchial asthma (BA) (n=27, 30.3%), BA-COPD overlap (n=2, 2.2%), atopic dermatitis (AD) (n=10, 11.2%), allergic rhinitis (AR) (n=25, 28%), allergic conjunctivitis (AC) (n=1, 1.1%), food allergy (FA) (n=1, 1.1%), chronic spontaneous urticaria (CSU) (n=15, 16.9%), and other skin diseases (bullous pemphigoid (n=3), drug hypersensitivity(n=2) (5.6%) and hypereosinophilia (n=3, 3.3%). Elevated ECP levels (normal <15 µg/L) were observed in 55 patients (61.1%). These included patients with BA (63.0%), BA-COPD (100%), AD (55.6%), AR (64.0%), CSU (40%) and all patients (100%) with AC, FA, and hypereosinophilia. *Discussion:* ECP, though an older test, holds renewed clinical value as a biomarker of eosinophil-driven T2 inflammation. Its elevation is most notable in patients with respiratory allergies, AD, CSU and hypereosinophilic states, highlighting its role in allergic diseases endotyping and personalised treatment strategies. However, high sample rejection rate calls for better adherence to sampling procedures.

**MM57: Sustained Virological Response and Its Predictive Factors in Chronic Hepatitis C Patients at Hospital Kuala Lumpur**

Noralwani Badarol Hisham[1,2], Nur Izzati Kamal Roslan[3], Niazlin Mohd Taib[2], Mazriza Madon[1], Norita Zainol[1], Zamberi Sekawi[2], Siti Norbaya Masri[2]

*[1]Microbiology Unit, Department of Pathology, Hospital Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia; [2]Department of Medical Microbiology, Medicine and Health Science Department, Universiti Putra Malaysia, Selangor, Malaysia; [3]Pharmacy Department, Hospital Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* Direct-acting antivirals (DAA) provide a promising approach to hepatitis C elimination, achieving high efficacy and safety for sustained virological response (SVR). We aim to investigate the SVR among chronic hepatitis C patients treated with DAA and its predictive factors. *Materials & Methods:* The retrospective cohort study included 335 chronic hepatitis C patients treated with DAA from 2020 until 2023 at Hospital Kuala Lumpur. We assessed the SVR at least 12 weeks after treatment discontinuation by quantifying hepatitis C RNA using RT-PCR. Odds ratios from a logistic regression test were analysed to identify significant predictors of SVR. *Results:* Overall, the treatment effectiveness rate is 89% (298 out of 335) (95% CI: 85.1-92.1), with deaths classified as failures to achieve SVR. For patients with virological outcomes, 96.4% (298 out of 309) (95% CI: 93.7-98.2) achieved SVR. The significant independent predictor of treatment failure was non-compliance with DAA (adjusted OR: 68.3, 95% CI: 16.3-285.0, p>0.001) and factors linked with cirrhosis, which include treatment regimen with sofosbuvir/ velpatasvir (versus sofosbuvir/daclatasvir) (aOR: 6.1, 95% CI: 1.4-26.5, p=0.015), MELD 3.0 score between 10 to 15 as compared to score less than 10 (aOR: 4.6, 95% CI: 1.1-18.2, p=0.031), genotype 3 (aOR: 4.5, 95% CI: 1.1-17.6, p=0.031), and increased total bilirubin level (aOR: 1.1, 95% CI: 1.0-1.1, p=0.003). *Discussion:* The findings highlight the effectiveness of DAA in achieving SVR in patients with chronic hepatitis C. Adhering to treatment and ensuring early diagnosis and intervention to prevent the progression of advanced liver disease are crucial for achieving successful outcomes.

**MM58: Five-Year Performance Analysis of Exclusive Fluorescence-Based Acid-Fast Bacilli Microscopy: A Single Laboratory's Experience (2020-2024)**

Norhidayah Kamarudin[1], Wan Husna Barakah[2], Nurdiyana Mohamed[1],

*[1]Department of Pathology and Laboratory Medicine, Kulliyyah of Medicine, International Islamic University Malaysia, Kuantan, Pahang, Malaysia;[2]Department of Pathology and Laboratory Medicine, Sultan Ahmad Shah Medical Centre@International Islamic University Malaysia, Kuantan, Pahang, Malaysia*

*Introduction:* Tuberculosis (TB) remains a major public health concern. Its effective control depends on accurate detection of acid-fast bacilli (AFB). Many diagnostic laboratories rely on conventional staining methods without or in combination with fluorescence staining. This study aims to evaluate the performance of fluorescence microscopy as the sole method for AFB detection through participation in the external quality assurance (RCPA QA) program. *Materials & Method:* A retrospective analysis was conducted on 40 smears received between 2020 and 2024. Each smear was stained with auramine-O and analysed solely by fluorescence microscopy. The diagnostic agreement analysis between the submitted and expected results was performed. A semi-quantitative scoring method (2 = exact match, 1 = ±1 grade difference, 0 = ≥2 grade difference) was used to derive an internal performance index against the peer group mode. *Results:* 39/40 (97.5%) results were concordant, with one minor discordance reported. The overall exact matches were at 67.5% (27/40) with acceptable grade variation of ±1 at 30% (12/40). A 100% concordance was recorded for surveys conducted in 2020, 2021, 2022, and 2024. All negative smears were correctly identified. An internal performance score against the peer group mode was at 85%, with 70% (28/40) exact matches and 30% (12/40) with ±1 grade difference. *Discussion:* Our experience demonstrates that using fluorescence microscopy exclusively for AFB detection is both effective and reliable. It consistently delivers high diagnostic accuracy with a high internal performance score, indicating a strong concordance with peer consensus. The single minor discordant result was later reassessed and found to align with the expected result. These findings suggest that the discrepancy was due to interpretive variability rather than a systematic error. Despite this, our findings reinforce the method's viability and dependability within an EQA framework.

**MM59: Distribution of Hepatitis C virus genotypes among cirrhotic liver disease patients in sixteen government hospitals across Malaysia**

Norita Zainol[1], Nur Hidayah Mas'od[2], Yuet Ying Loo[3],

*[1]Department of Pathology, Hospital Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia*

*Introduction:* The Ministry of Health, Malaysia, started implementing DAA (Direct Acting Antiviral) in 2017 and the success rate is over 90% and some studies reporting up to 97%. DAA treatment failure is partly attributed by specific genotypes, notably genotype 3, which exhibits lower responsiveness.The objective of the study is to study common genotypes in Hepatitis C population especially with cirrhotic liver disease in Malaysia. *Materials & Methods:* A retrospective observational study was used to examine the distribution of HCV genotypes across 16 state government hospitals from 2022 to 2024 to guide elimination strategies. A total of 2,399 plasma samples with viral loads ≥1,000 copies/mL were analysed using the Roche cobas® 4800 system for genotyping (1–6, subtypes 1a/1b). *Results:* Genotype 3 dominated (63.23%), consistent with Southeast Asian trends, followed by genotype 1 (23.21%). Genotypes 5 and 6 were absent, while genotypes 2 (0.25%, n=6) and 4 (0.08%, n=2) appeared sporadically. Indeterminate (3.7%, n=90) and invalid results (8.79%, n=211) were also observed. Sarawak contributed the highest sample volume (16.88%), followed by Selangor (13.92%) and Perak (10.80%). Demographically, males comprised 85% (n=2,045) of cases. Ethnic distribution revealed genotype 3 predominance across all groups: Malays (40%, n=967), Chinese (8.5%, n=204), Indians (4.1%, n=99), and other minorities (10.4%, n=250). *Discussion:* These findings underscore genotype 3's endemicity in Malaysia, aligning with regional patterns, and highlight disparities in HCV burden among states, ethnic and genders. The absence of genotypes 5–6 suggests limited circulation, while indeterminate results may reflect emerging variants or technical limitations. The study supports the needful of strengthening genotypes surveillance to monitor potential shift in genotype distribution and improving of genotyping assays to

reduce indeterminate or and invalid assays ensuring reliable treatment guidance. Genotype guided DAA strategies are important as primary therapeutic focus in cirrhotic patients.

**MM60: Kodamaea ohmeri Strikes the Vulnerable: A Rare Case of Fungemia in an Elderly Immunocompromised Host**

Hui Shan Chua[1], Saarah Huurieyah Wan Rosli[2]
*[1]Microbiology Unit, Department of Pathology, Ampang Hospital; [2]Faculty of Medicine &amp, Health Sciences, Universiti Sains Islam Malaysia*

*Introduction: Kodamaea ohmeri*, formerly known as *Pichia ohmeri*, is an emerging opportunistic fungal pathogen increasingly reported among immunocompromised individuals. Historically used in the food industry, its identification as a human pathogen has become more frequent, particularly in fungemia and catheter-related infections. *Case report:* We report a case of a 71-year-old male with diabetes, hypertension, and end-stage renal disease secondary to plasma cell leukaemia (oligosecretory IgG kappa) on chemotherapy and dialysis via right internal jugular catheter presented with *Clostridium difficile* colitis, confirmed by GDH and toxin assays. He later developed hypovolemic shock. Concurrent hospital-acquired pneumonia required escalation to intravenous Meropenem. Blood cultures yielded *K.ohmeri*, identified via MALDI-TOF MS (score 2.30). Despite initiation of antifungal therapy with intravenous Micafungin followed by Fluconazole, the patient deteriorated and died from respiratory failure related to underlying conditions. *Discussion: K.ohmeri* infection is rare but increasingly recognised in patients with haematological malignancies, indwelling catheters, or immunosuppressive therapy. Proper identification is essential, as misidentification with *Candida* species was common before the advent of MALDI-TOF MS. Though echinocandins and Amphotericin B show good *in-vitro* activity, Fluconazole susceptibility varies, and treatment response is often unpredictable. *Conclusion:* Clinicians and microbiologists must remain vigilant of *K. ohmeri* as an emerging cause of invasive fungal infections with high morbidity and mortality in immunocompromised patients. Early detection using advanced diagnostic tools and individualised antifungal therapy are key to improving patient outcomes.

**MM61: Six Years of HIV-1 Diagnostic Data in Infants Born to HIV-Positive Mothers in Malaysia (2019–2024)**

Fatin Amirah Suib, Izan Shahrina Adam, Nuramera Nazua Zarul Akmar, Wilhelmina William, Emmanuel Tiagaraj Aroldoss, Khayri Azizi Kamel, Rozainanee Mohd Zain
*Virology Unit, Infectious Disease Research Centre, Institute for Medical Research, National Institute of Health.*

*Introduction:* Polymerase Chain Reaction (PCR) based diagnostic testing is essential for the timely detection and treatment of Human Immunodeficiency Virus (HIV) in infants born to HIV-positive mothers. This study examines demographic, regional, and treatment-related trends in HIV-1 detection in Malaysia over a six-year period. *Methods:* We retrospectively analysed 1,695 valid PCR test records of infants born to confirmed HIV-1 positive mothers from 2019 to 2024. Data included infant gender, ethnicity, region of origin, test results, and Zidovudine (AZT) prophylaxis status. *Results:* Among the tested infants, 40 (2.36%) were HIV-1 positive. Gender distribution was nearly equal, with 51.1% male and 47.2% female. Ethnic prevalence was highest among Malay infants (27.5%), followed by foreign-born (25.0%) and Bumiputera infants from Sabah and Sarawak (25.0%). Regionally, East Malaysia had the highest proportion of HIV-positive cases (37.5%), followed by the Central Peninsular (32.5%). Notably, 20.0% (8 out of 40) of HIV-positive infants had no recorded AZT prophylaxis, while only 7.5% (3 out of 40) received full prophylaxis. In contrast, 32.7% (541 out of 1655) of HIV-negative infants had complete coverage. However, the substantial number of missing records (828 out of 1695) could introduce potential discrepancies in the analysis. *Discussion:* Despite a low HIV-1 detection rate, transmission persists, particularly in underserved communities and those without complete AZT prophylaxis. Higher prevalence among foreign-born and marginalised infants suggests disparities in healthcare access. Improving documentation, treatment adherence, and outreach programs is crucial. Strengthening healthcare equity and follow-up systems can enhance infant HIV prevention and reduce transmission rates in Malaysia.

**MM62: Unmasking Hidden Colistin Resistance: Leveraging Explainable AI to Decipher Genomic Predictors in Acinetobacter baumannii UPM_HSAAS_Ab14**

Noof Bani Khaled[1 *], Choo Yee Yu[2], Narcisse Mary Sither Joseph[1,3], Rosni Ibrahim[1,3], Tengku Zetty Maztura Tengku Jamaluddin[1,3], Syafinaz Amin-Nordin[1,2,3]
*[1]Department of Medical Microbiology, Faculty of Medicine and Health Sciences, Universiti Putra Malaysia, Selangor, Malaysia; [2]Institute of Bioscience, Universiti Putra Malaysia, Selangor, Malaysia; [3]Hospital Sultan Abdul Aziz Shah (HSAAS), Universiti Putra Malaysia, Selangor, Malaysia.*

*Introduction:* Colistin resistance in *Acinetobacter baumannii* is a major global health concern, particularly with the absence of known genetic markers. This study investigated a clinically resistant isolate to colistin by using artificial intelligence (AI) to uncover potential hidden genomic factors. *Materials & Methods:* Fifty-five multidrug-resistant (MDR) *A. baumannii* clinical isolates underwent phenotypic colistin susceptibility testing via broth microdilution. Whole genome sequencing (WGS) was performed, and annotated genomic features were analysed using Random Forest and support vector machine (SVM) models. SHAP (SHapley Additive exPlanations) values were used to interpret feature importance and rank contributions to resistance. *Results:* Among the isolates that were examined, 54 (98.2%) were susceptible to colistin. Phenotypic resistance was shown by one isolate strain UPM_HSAAS_Ab14 (1.8%) (MIC = 4 µg/mL). WGS analysis revealed the absence of known colistin resistance genes, such as *mcr, pmr*A/B, and *lpx*ACD. Machine learning models demonstrated robust predictive performance, with Random Forest achieving 92.7% accuracy and 94.1% sensitivity, and SVM yielding 91.0% accuracy and 91.2% sensitivity. SHAP interpretation identified a hypothetical protein (+0.42), an intergenic region (+0.36), and a mobile element near an ORF (+0.28) as positive predictors of resistance. In contrast, conserved housekeeping genes were consistently associated with susceptibility based on their negative contribution in SHAP analysis. *Discussion:* The results demonstrate how explainable AI is effective in exposing elusive genomic

contributors to resistance. The integration of AI with WGS offers a robust approach for the early detection of resistance, facilitating the development of diagnostics and informing treatment strategies for challenging drug-resistant pathogens.

**MM63: When Typhoid Skips the Gut: Salmonella Typhi Presenting as a Submental Abscess**

Wan Husna Barakah Meor Jamaludin[1], Norhidayah Kamarudin[1], Ahmad Aizzuddin Abd Rahni[2], Nurdiyana Mohammed[1]
*[1]Department of Pathology and Laboratory Medicine, Sultan Ahmad Shah Medical Centre @IIUM, Kuantan Pahang, Malaysia; [2]Integrated Wound and Stoma Care Unit, Sultan Ahmad Shah Medical Centre @IIUM, Kuantan Pahang, Malaysia.*

*Introduction:* Salmonella enterica serovar Typhi typically causes enteric fever, with bacteraemia and gastrointestinal involvement. Isolation from extraintestinal sites such as soft tissue abscesses is rare. We report an unusual case of *Salmonella* Typhi isolated from a submental abscess in a patient with no gastrointestinal symptoms. *Case report:* A 61-year-old man with underlying uncontrolled diabetes mellitus presented with painful anterior neck swelling for 2 weeks, associated with odynophagia. Examination revealed a fluctuant 7x7 cm submental mass, erythematous with necrotic patch and pus discharge. Pus and tissue cultures yielded pure growth of Gram-negative rod, non-fermenter, positive for O, H and Vi antigen confirmed as *Salmonella* Typhi. The isolate was susceptible to ampicillin, ceftriaxone, trimethoprim-sulfamethoxazole and ciprofloxacin. He was treated successfully with a combination of surgical drainage and intravenous ampicillin-sulbactam for 10 days. *Discussion:* Extraintestinal infections due to *Salmonella* Typhi are uncommon and often associated with predisposing conditions such as diabetes mellitus or immunosuppression. In such cases, haematogenous dissemination from an unrecognised or asymptomatic bacteraemia may seed distant tissues. The absence of gastrointestinal symptoms in our patient highlights the potential for *Salmonella* Typhi to present atypically, complicating clinical diagnosis. This rare case of *Salmonella* Typhi in a submental abscess broadens the clinical spectrum of extraintestinal salmonellosis and highlights the importance of microbiological testing in head and neck infections. Prompt culture, targeted antimicrobial therapy, and appropriate surgical intervention remain essential to achieve favourable outcomes.

**MM64: From ice to rainforest: preliminary lichens antibacterial properties against multidrug-resistant organisms**

Aisyah Syakirah Shahari[1], Navindra Kumari Palanisamy[1,2], Nurul Alimah Abdul Nasir[4], Che Puteh Osman[5], Jerzy Smykla[6], Ivan Parnikoza[7,8], Beata Krzewicka[9], Fadzilah Mohd Nor[1,2,3 *]
*[1]Institute of Medical Molecular Biotechnology (IMMB), Universiti Teknologi MARA, Sungai Buloh Campus, Selangor, Malaysia. [2]Department of Medical Microbiology & Parasitology, Faculty of Medicine, Universiti Teknologi MARA, Sungai Buloh Campus, Selangor, Malaysia. [3]Integrative Pharmacogenomics Institute (iPROMISE), Level 7, Ff3, Faculty of Pharmacy, Universiti Teknologi MARA, Puncak Alam, Selangor, Malaysia. [4]Department of Pharmacology, Faculty of Medicine, Universiti Teknologi MARA, Sungai Buloh Campus, Selangor, Malaysia. [5]Faculty of Applied Sciences, Universiti Teknologi MARA, Shah Alam Campus. Selangor, Malaysia; [6]Department of Biodiversity, Institute of Nature Conservation, Polish Academy of Sciences, Poland; [7]State Institution National Antarctic Scientific Centre of Ukraine, Ministry of Education and Science of Ukraine, Ukraine; [8]Institute of Molecular Biology and Genetics, National Academy of Sciences of Ukraine; [9]W. Szafer Institute of Botany, Polish Academy of Sciences, Poland.*

*Introduction:* The emergence of multidrug-resistant (MDR) bacteria including methicillin-resistant *Staphylococcus aureus* (MRSA) and *Acinetobacter baumannii* (MDRAB) poses a critical threat and creates an urgency for alternative antimicrobial agents. Lichens, known for their unique secondary metabolites, offer promising antimicrobial potential. This study evaluates the antibacterial activity of lichen crude extracts from Antarctica and Malaysia against MDR organisms. *Materials and Methods:* Crude extracts from five Antarctic and one Malaysian lichen species were screened against 14 clinical MDR isolates (7 MRSA, 7 MDRAB). Extraction was performed using acetone and methanol through maceration. Antibacterial activity was assessed via the Kirby-Bauer disc diffusion method. Extracts were further purified by solid-phase extraction (SPE) and analysed by LC-MS. *Results and Discussion:* Acetone and methanol extracts showed significant antibacterial activity against MRSA, while activity against MDRAB was limited. Among acetone extracts, the Antarctic lichen *Cladonia deformis* showed the highest activity (12–21 mm inhibition zones), followed by the Malaysian *Cladonia rudis* (16–18 mm). All Antarctic lichens, except *Usnea aurantiaco-atra*, inhibited MRSA. Limited MDRAB activity was observed in *Umbilicaria antarctica*, *Usnea antarctica*, and *C. deformis*. Methanol extracts displayed moderate to strong MRSA activity (9–20 mm), but no activity against MDRAB. *Conclusion:* Lichen crude extracts, particularly from *Cladonia deformis* and *C. rudis*, demonstrated promising antibacterial effects against MRSA. Ongoing LC-MS analyses are focused on non-targeted metabolite screening, highlighting the need for targeted MS/MS to confirm specific metabolites that possess antibacterial properties. These findings support the potential of lichen-derived compounds as alternative strategies to combat antimicrobial resistance.

**MM65: From Gold Standard to New Benchmark: National Parasite Centre Validates PCR for Helminth Detection**

Norafandi Mohd Noor[1], Sia Chew Guan[1], Rayuwani Mohamad Kamal[1], Suhaila Md Hanapiah[2], Kayalvilee Laechimanan[2]
*[1]Department of Pathology, Hospital Sibu, Sarawak, Malaysia; [2]Department of Pathology, National Cancer Institute, Malaysia*

*Introduction:* Helminth infections still remain a health burden in Malaysia especially in the Borneo region. Although stool microscopic examination (FEME) is still the standard diagnostic test, its sensitivity is low especially with low levels of infection or mixed infections. PCR as a diagnostic test is more sensitive and specific than a stool microscopic examination. The present study assessed the accuracy and the incremental value of helminth PCR testing; it is carried out at two national parasitology laboratories, Hospital Sibu and the National Cancer Institute (IKN). *Material and Methods:* Both stool FEME and multiplex helminth PCR targeting *Strongyloides* spp, Ancylostoma spp, Hymenolepis spp, *Necator americanus*, *Taenia* spp, and *Trichuris trichiura* were performed on 20 stool samples. PCR testing was done independently by Hospital Sibu and IKN. Microscopy was considered the gold standard. The following diagnostic values (sensitivity (Sn), specificity (Sp) and inter-laboratory concordance were tested. *Results:* True positives and true negatives were 7 and 12, respectively out of 20 samples evaluated by stool FEME. One case was PCR-positive but microscopy-negative, which could represent a false positive, or an earlier/subclinical infection not detected on

microscopy. There were no false negatives. The estimated values of helminth PCR sensitivity and specificity were 100 and 92.3%, respectively. Agreement (%) between PCR results from Hospital Sibu and IKN was 95.0%. The PCR was shown to be able to identify mixed infections, undetectable under standard microscopy. *Discussion:* Helminth PCR showed high sensitivity and good specificity and high inter-laboratory agreement. The assay's capability of detecting mixed and low-density infections emphasises its clinical relevance to increasing diagnostic yield beyond that which is possible with stool microscopy only. Beyond potential bias in this retrospective analysis, larger sample size, improvement of DNA extraction, and standardisation of enrichment protocols could improve diagnostic accuracy in future prospective studies. Up-scaling helminth PCR application would enhance national parasite surveillance and case detection protocols.

**MM66: In silico prediction and in vitro validation of quorum quencher–derived therapeutic peptides**

Deepa Anbazhagan[1], Tang Yin Quan[2]
*[1]Department of Microbiology, International Medical School, Management and Science University, Shah Alam, Malaysia; [2]School of Biosciences, Faculty of Health and Medical Sciences, Taylor's University, Selangor Darul Ehsan, Malaysia*

*Introduction:* The escalating global threat of antimicrobial resistance necessitates the discovery of novel therapeutic strategies. Antimicrobial peptides (AMPs), particularly those derived from natural proteins, offer promising alternatives due to their broad-spectrum activity and safety profile. Quorum sensing (QS), a microbial communication mechanism mediated by lactone-containing molecules, plays a vital role in virulence regulation. Disruption of QS via quorum quenching (QQ) enzymes such as lactonases provides a potential antimicrobial strategy. *Materials & Methods:* This study employed an *in-silico* approach to design short AMPs (10 amino acids) derived from lactonase sequences. Using AntiCP, peptide modifications were guided by amphipathicity, hydrophobicity, and cationic properties. The pharmacological properties of these peptides were predicted using ToxinPred (toxicity), IAMPE (antimicrobial potential), and HemoPI (haemolytic activity). Peptide structures were modeled using the PEP-FOLD3 de novo structure prediction tool. Promising AMP candidates were selected for synthesis and *in vitro* evaluation. *Results:* Several lactonase-derived peptides displayed favourable *in silico* profiles: high predicted antimicrobial activity, low haemolytic potential, and minimal toxicity. Structural modelling confirmed the formation of amphipathic α-helices, a characteristic feature of potent AMPs. *In vitro* assays for validation of the antimicrobial activity against Gram-negative and Gram-positive bacteria, with select peptides would demonstrate low cytotoxicity and haemolysis. *Discussion:* This study highlights the potential of lactonase-derived short AMPs as novel therapeutics. By targeting QS mechanisms while maintaining selective toxicity profiles, these peptides offer a dual-action approach which includes direct antimicrobial effects and quorum sensing disruption. Further optimisation and *in vivo* testing may position these AMPs as candidates for future antimicrobial development.

**We would like to thank the Director General of Health Malaysia for his permission to publish these abstracts.**