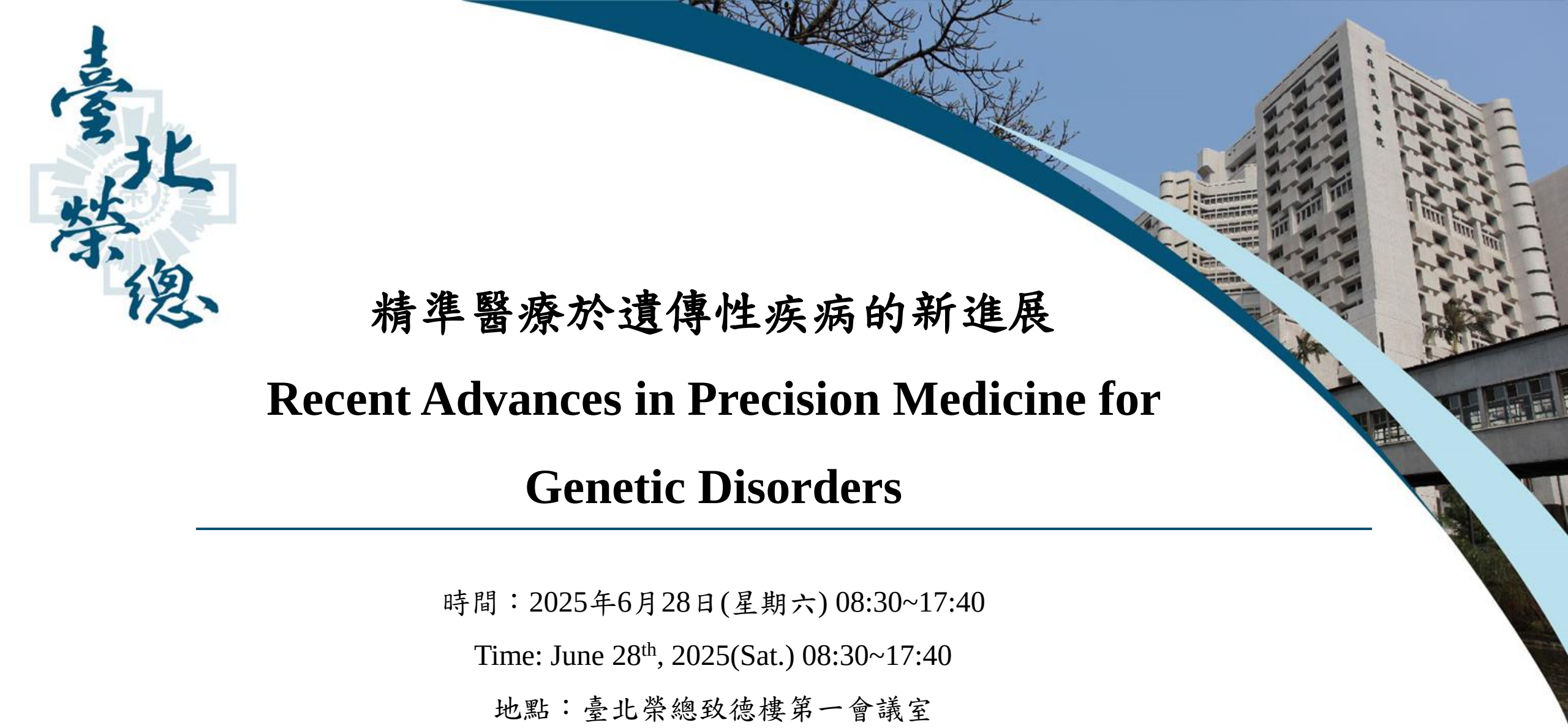

精準醫療於遺傳性疾病的新進展

Recent Advances in Precision Medicine for Genetic Disorders

時間：2025年6月28日(星期六) 08:30~17:40

Time: June 28th, 2025(Sat.) 08:30~17:40

地點：臺北榮總致德樓第一會議室

Rapid genome sequencing for genetic disease diagnosis and newborn screening

Stephen F Kingsmore

Rady Children's Institute for Genomic Medicine, San Diego, CA U.S.A

There are more than 10,000 single locus genetic diseases. Together they account for at least one third of neonatal intensive care unit admissions and at least one fifth of childhood hospitalizations. They are a leading cause of infant and childhood mortality and morbidity. For the past 15 years I have been part of teams that have pioneered the use of genome sequencing to identify children with these diseases and convert their management from empiric to precision medicine. I will review the results of these studies with respect to the unexpectedly high incidence of genetic diseases and unexpectedly high rate of improved outcomes. As genome-based diagnosis has come to be accepted as a first line test for ill children we have increasingly focused on genome-based screening for all children before symptom onset. I will review progress in this new area and suggest implications for public health worldwide.

Applications of a Rapid Real Time Analysis System for Whole Genome Sequencing to Clinicians.

全基因體定序即時分析系統在臨床上的應用

Dau-Ming Niu

牛道明

Institute of Clinical Medicine, National Yang Ming Chiao Tung University,Taipei, Taiwan, ROC

Department of Pediatrics, Taipei Veterans General Hospital,

國立陽明交通大學 臨床醫學研究所 及 臺北榮民總醫院 兒童醫學部

Rapid advances in genome research and sequencing technologies have made whole-genome sequencing (WGS) more affordable and clinically feasible. However, managing and analyzing the vast amount of WGS data remains a challenge. To address this, we have partnered with a bioinformatics company to develop Magic Bison, a real-time WGS analysis platform that integrates genomic analytics, cloud computing, big data processing, and artificial intelligence to enable fast and accurate diagnosis of genetic disorders.

Unlike conventional genetic tests, WGS is a lifelong resource. Magic Bison supports continuous reanalysis, enabling clinicians to generate updated insights as knowledge bases evolve. This dynamic feature enhances diagnostic precision and guides personalized treatment strategies throughout a patient's life. This presentation will share real-world clinical applications of Magic Bison for the rapid diagnosis of genetic diseases. Our collaboration has also led to the development of Strata Finder, an AI-driven algorithm within our system that evaluates WGS data for complex disease risks such as asthma, heart attacks (AMI), and strokes. Strata Finder has demonstrated accuracy rates of 96% or higher.

Beyond diagnostics, Magic Bison provides additional functionalities including pharmacogenomics profiling, constitution analysis, proactive health risk assessment, and HLA typing. The system enables real-time genomic analysis in NGS laboratories and is optimized for use in clinical settings, including outpatient follow-up visits, ensuring timely and informed decision-making. The platform features a user-friendly interface designed for healthcare professionals, with the goal of making WGS analysis accessible to general practitioners and paving the way for truly personalized precision medicine, prevention, and health.

Transforming Healthcare: The Role of Metabolomics in Clinical and Preventive Medicine.

醫療照護轉型:代謝體學在臨床與預防醫學的角色

Ming-Shi Shiao (retired)
蕭明熙(退休)
Department of Biomedical Sciences. Chang Gung University, Taoyuan, Taiwan, ROC
長庚大學 生物醫學系

Background: Metabolomics, a most recently developed omics in systems biology, has been applied in precision medicine. There are two major approaches in metabolomics-based research, untargeted and targeted metabolomics. By using liquid- and gas-chromatography-mass spectrometry (GC- and LC-MS) and nuclear magnetic resonance (NMR) spectroscopy as analytical tools for profiling of the whole low-molecular-weight (LMW) metabolites in biospecimens, untargeted metabolomics can be applied for hypothesis-generation. Targeted metabolomics, based on the presence of potential metabolite in identity and concentrations, may contribute to differentiating the study group into subgroups. The panel of potential metabolites, once validated, can be developed into biomarkers.

Methods: We have applied untargeted and targeted metabolomics to monitor the age-dependent cardiometabolic disease progression, namely metabolic syndrome, type 2 DM, cardiovascular disease (CVD), and heart failure. Extensive statistical analysis and mission-oriented databases allow us to gain better understanding in the landscape of these diseases.

Results and Discussion: Metabolomics enables precision medicine. A portfolio of biomarkers generated by targeted metabolomics may describe the interactions of multiple risk factors in disease progression even individualized treatment strategy. In the metabolomic study from metabolic syndrome to Type 2 DM and CVD, a portfolio of biomarkers including branched-chain amino acids (BCAAs), aromatic amino acids, and characteristic lipid metabolites have been reported. It involves energy metabolism, inflammation, and epigenomic risk factors. Coupling with other omics, metabolomics greatly promotes precision medicine.

From Gut to Health: Advances in Microbiota Research for Clinical and Preventive Medicine

從腸道到健康：微菌叢研究在臨床及預防醫學上的進展

Chun-Ying Wu

吳俊穎

Division of Translational Research, Taipei Veterans General Hospital, Taipei, Taiwan

台北榮民總醫院 轉譯研究科

This talk provides a comprehensive overview of recent breakthroughs in human microbiota research and their implications for clinical and preventive medicine. It begins with an introduction to the human microbiota as a "superorganism," emphasizing its vast genetic repertoire and role in maintaining host health. The talk explores the concept of gut dysbiosis and its role in contributing to a range of diseases, particularly through the gut-liver axis.

The presentation also discusses groundbreaking studies demonstrating the transmissibility of nonalcoholic fatty liver disease (NAFLD) through gut microbiota, including the role of specific bacteria such as *Klebsiella pneumoniae* and *Enterococcus faecalis*. Further, it examines the impact of environmental, dietary, and host genetic factors on microbiota composition and function. Special attention is given to multi-omics approaches, linking gut microbiota to metabolic syndrome, electrolyte levels, and viral infections such as HBV.

Finally, the presentation outlines the ongoing efforts of the National Human Microbiome Core Facility in Taiwan to develop a precision health framework through integrated microbiota platforms, including culturomics, fecal microbiota transplantation (FMT), metabolomics, and animal modeling. These efforts aim to translate microbiome science into personalized interventions and disease prevention strategies.

Integrating Precision Medicine, Multi-omics, and Digital Health: Crafting an Blueprint for Personalized Treatment

Chi-Ying Huang

黃奇英

Institute of Biopharmaceutical Sciences, National Yang Ming Chiao Tung University

陽明交通大學 生物藥學研究所

While high-throughput screens have revealed numerous anti-cancer compounds in cell lines, translating these findings to patient tumors remains a challenge due to genomic disparities. We introduce ADEPT—a deep learning framework combining an adversarial encoder with a transformer predictor—to bridge this gap by learning tumor-like mutation patterns from cell line data. ADEPT accurately predicts drug responses across cancer types and identifies clinically relevant biomarkers. Applied to triple-negative breast cancer, it highlighted repurposed drugs—including proteasome and HDAC inhibitors—with strong therapeutic potential and matched genetic markers. To elucidate mechanisms, we used GNINA and AlphaFold-based docking, followed by functional validation of predicted targets. An AI-driven pipeline further guided the search for optimized analogs with favorable drug-like properties, e.g. ADME-T, advancing the path from drug repurposing to precision oncology.

Newborn screening and treatment of Inherited Metabolic Diseases in Japan

Kimitoshi Nakamura

Department of Pediatrics, Kumamoto University Graduate School of Medical Sciences, Japan

Newborn screening has played a central role in the early detection and management of inherited metabolic diseases in Japan. Since its introduction in the 1970s, the scope of screening has continuously expanded. Today, using advanced methodologies such as tandem mass spectrometry (MS/MS), the program covers a wide range of amino acid disorders, organic acidemias, fatty acid oxidation disorders, and others. In some regions, pilot programs for lysosomal storage disorders and primary immunodeficiencies have also been implemented. These efforts have enabled the identification of affected infants before the onset of symptoms, allowing timely intervention and significant improvement in long-term outcomes.

Genetic analysis is indispensable for definitive diagnosis and further risk stratification. As a result of genetic analysis, it is possible to predict the onset time and complications, and begin the necessary treatment at the optimal period. However, confirmed diagnosis by genetic analysis has restrictions in terms of cost, time, and efficiency, and ethical consideration is also required. Therefore, it is important to carry out genetic analysis while conducting genetic counseling as necessary.

In addition to early diagnosis, treatment strategies have also evolved. Transplantation therapy and gene therapy are now becoming possible options for certain diseases, making the understanding of genetic background even more important. In this presentation, I will introduce the current status and recent advances in newborn screening and treatment of inherited metabolic diseases in Japan, and discuss the future directions for further improving patient care.

Optimizing Infantile Onset Pompe Disease Care: Rapid Diagnosis & Early Enzyme Replacement Therapy for Best Outcomes

Chia-Feng Yang[1], Ting-Wei Ernie Liao[1], Yen-Ling Chu[1], Li-Zhen Chen[1], Ling-Yi Huang[1], Yun-Ru Chen[1], Hui-Chen Ho[2], Shu-Min Kao[3], Yam-Jang Chen[1], Dau-Ming Niu[1,*]

[1]Department of Pediatrics, Taipei Veterans General Hospital, Taipei, Taiwan.
[2]Taipei Institute of Pathology, Neonatal Screening Center, Taipei, Taiwan
[3]The Chinese Foundation of Health, Neonatal Screening Center, Taipei, Taiwan

Background: Initiating enzyme replacement therapy (ERT) before severe and irreversible muscular damage occurs is crucial in infantile-onset Pompe disease (IOPD). This long-term follow-up study demonstrates our diagnostic and treatment strategies for IOPD and compares our clinical outcomes with those of other medical centers. Furthermore, we present a 24-month real-world experience of switching to avalglucosidase alfa in 40 patients diagnosed through Taiwan's newborn screening system.

Methods: In this long-term follow-up study, we analyzed the outcomes of very early ERT with short-term premedication hydrocortisone in patients with IOPD picked up from Taiwan nationwide newborn screening programme. Out of 1 628 539 infants screened between 1 January 2010 and 28 December 2024, 43 newborns had confirmed IOPD in Taipei Veterans General Hospital. The average age at ERT initiation was 10.06±4.17 days for patients with classic IOPD. Forty were regularly treated and monitored at our center. The average follow-up duration was 7.41±4.63 years. We compared the long-term treatment outcomes of our patients with those of other research groups and present a 24-month real-world experience of switching to avalglucosidase alfa

Results: Compared to patients in other studies, our patients exhibited better outcomes in multiple aspects. The switch in therapy led to further improvements in respiratory function, activity endurance, muscle strength and the levels of disease-specific biomarkers. This study highlights the potential benefits of very early treatment with short-term steroid premedication and switching ERT to avalglucosidase alfa in managing IOPD and offers a promising treatment strategy for long-term outcomes of IOPD.

Fabry Disease Update 2025

Raphael Schiffmann

Neurologist (clinic) at Texas Neurology, Dallas, Texas

Professor in the Department of Internal Medicine, Texas Christian University, Fort Worth, Texas

GLA gene variants: The categorization of *GLA* gene missense mutations has been complicated by the fact that some missense variants may fall into more than one category. For instance, the relatively common A143T variant may cause later-onset Fabry disease in some individuals but is a benign *GLA* variant in others. Therefore, testing α-galactosidase A activity in leukocytes of each individual male with the A143T variant is required to determine pathogenicity.

Disease pathophysiology: Efforts to mitigate the pathobiology of α-galactosidase A deficiency should differentiate between damaging (maladaptive) consequences and compensatory (adaptive) changes. Only the former may be modified to alleviate burden of disease.

Therapy: Current therapy leaves a significant unmet need, especially concerning cardiovascular complications and cardiological clinical outcomes. Non-Fabry-specific therapy is necessary and quite beneficial and must be utilized. Its contribution should be considered when trying to assess the net effect of Fabry-specific therapy. Enzyme replacement therapy (ERT) can be administered to patients independently of their *GLA* genotype, as it slows the decline of kidney function in most patients if initiated sufficiently early in the disease course. A novel ERT product, Elfabrio® (pegunigalsidase alfa-iwxj), has recently been approved in the US. It has a long circulating half-life and is likely less immunogenic. Galafold® (migalastat) has better tissue penetration than ERT, but its usefulness is restricted to patients with amenable missense *GLA* variants. However, it is important to realize that in a substantial proportion of common amenable mutations, migalastat increases α-galactosidase A activity level beyond the disease threshold and thus eliminates the metabolic disturbance that is at the center of Fabry disease. Novel allosteric non-inhibitory pharmacological chaperones are being developed for Fabry disease. Substrate reduction therapy is being tested but so far not in the best target patient population, using suboptimal endpoints. Liver-directed gene therapy is being developed using adeno-associated virus (AAV) that may have marginally greater benefits than ERT. Direct gene transduction of the affected organs such as the heart is most desirable but one such product has had significant safety problems. These limitations as well as concerns about poor utilization of gene therapy products post-regulatory approval in diseases that already have other approved efficacious therapies limit the enthusiasm about gene therapy in Fabry disease.

Biochemical Marker Evaluation in the Treatment of Fabry Disease Patients

治療法布瑞氏症相關生物標記之評估

Christiane Auray-Blais, LL.M., Ph.D.
Full Professor, Researcher
Department of Pediatrics, Division of Medical Genetics
Faculty of Medicine and Health Sciences
Université de Sherbrooke
Clinical Research Centre-CHUS
Sherbrooke, Quebec, Canada

Over the years, translational metabolomic research studies aiming at the discovery of Fabry disease biomarkers were devised using semi- and untargeted approaches with time-of-flight mass spectrometry. Various isoforms and analogs of globotriaosylceramide (Gb_3) and globotriaosylsphingosine (lyso-Gb_3), two glycosphingolipids, were discovered as part of these studies. Liquid chromatography tandem mass spectrometry methods were developed and validated for these biomarkers in urine and plasma specimens. Clinical applications for the evaluation of various treatments for Fabry disease, such as enzyme replacement therapy (ERT), chaperone therapy, and gene therapy will be presented. Results from the biomarker monitoring and longitudinal follow up of a 5-year gene therapy Fabry disease clinical trial in Canada will be presented. Additionally, the results from a biomarker research study for Fabry disease patients who switched from ERT to chaperone therapy (migalastat) will be revealed. Finally, the investigation of biomarkers for Fabry disease patients with a cardiac variant mutation in Taiwan will show the associations of specific analogs of lyso-Gb_3 with the left ventricular mass index (LVMI) and the Mainz Severity Score Index (MSSI). Fabry disease monitoring recommendations will be proposed: 1) plasma lyso-Gb_3 monitoring at treatment initiation or switch for longitudinal evaluation should be done at baseline and every 6 to 12 months; 2) considering the marked variability in the genotype and phenotype for Fabry disease patients, a complete biochemical profile of Fabry disease-related biomarkers in urine and plasma should be evaluated, for better monitoring and follow-up of treated patients as part of precision medicine.

Tissue and cell-based biomarkers of Fabry disease – Applications in clinical practice and clinical trials

Behzad Najafian

Department of Laboratory Medicine and pathology, University of Washington, U.S.A

Fabry disease is a rare X-linked lysosomal disease caused by a deficiency in alpha-galactosidase A (GLA), leading to the intracellular accumulation of glycosphingolipids and most prominently globotriaosylceramide (Gb3). Heterogeneity of the disease phenotype leads to major diagnostic and treatment challenges. The main sources of this heterogeneity are genotype (classic vs. later onset variants) and gender. Biomarkers help in accurate phenotype stratification which is necessary for precision medicine.

Diagnostic biomarkers are generally disease specific and do not necessarily inform about the phenotype at organ level. Fabry disease is a systemic condition with significant heterogeneity in complications not fully explainable by genotype. This signifies the roles of cell and tissue-based biomarkers in prognostication and precision medicine. Biopsies provide robust information on phenotype stratification, disease mechanisms and irreversible chronic injuries. A response to treatment, defined by cellular clearance from Gb3 inclusions, can be detected after ~6 months of enzyme replacement (ERT) or chaperone therapy in endothelial cells. Using unbiased quantitative electron microscopy, partial Gb3 clearance can be detected in podocytes after 6 months of chaperon therapy or one year of ERT. These methods are valuable tools for clinical endpoint assessments.

Recent advances in machine learning are underway to make such studies more readily available for both research and potentially in clinical grounds. For a life-long condition such as Fabry, non-invasive approaches that can be serially and safely implemented to detect early organ damage are critical for clinical guidance and treatment initiation. A combination of several modalities for cardiac (CMR, echocardiography, ECG, troponin, hs-cTnT, NT-proBNP), brain (MRI) and kidney (urine albumin, protein, GFR, podocyturia) complications together with general markers linked to the phenotype severity (e.g. plasma lyso-Gb3) is recommended. Further progress is needed to identify sensitive standardized non-invasive biomarkers that accurately reflect response to treatment and thereby can be used for precision medicine in patients with Fabry disease.

Immunological Challenges and Evolving Therapies in Fabry Disease: From Enzyme Replacement to Substrate Reduction Strategies

Professor Dominique P. GERMAIN, MD PhD
Division of Medical Genetics
University of Versailles and Paris-Saclay University
France
dominique.germain@uvsq.fr

Abstract:
Fabry disease is a rare, X-linked lysosomal storage disorder caused by mutations in the *GLA* gene, leading to deficient α-galactosidase A activity and accumulation of globotriaosylceramide (Gb3) and related glycosphingolipids. Enzyme replacement therapy (ERT), including agalsidase alfa, agalsidase beta, and the newer PEGylated formulation pegunigalsidase alfa, remains a cornerstone of treatment. However, ERT is frequently associated with immune responses, particularly the development of anti-drug antibodies (ADAs), which can be neutralizing and may reduce treatment efficacy. This immunogenicity is influenced by several factors, including *GLA* mutation type—especially null variants associated with absent endogenous enzyme production—and the administered dose, with higher doses possibly overcoming partial ADA-mediated inhibition. Infusion-related reactions are common and sometimes immunologically mediated, especially in antibody-positive patients.
Parallels with infantile-onset Pompe disease offer useful insights. In Pompe disease, ADA development is strongly influenced by the cross-reactive immunologic material (CRIM) status, with CRIM-negative patients being at highest risk. Immunomodulatory strategies, though mostly off-label, have been employed to prevent or attenuate ADA responses. These include methotrexate, corticosteroids, rituximab, and in some cases, proteasome inhibitors like bortezomib. Such protocols have shown efficacy in reducing ADA titers and improving clinical outcomes in high-risk patients, and their potential adaptation to Fabry disease deserves further exploration.
This presentation will also introduce substrate reduction therapy (SRT), which aims to decrease glycosphingolipid biosynthesis by targeting glucosylceramide synthase. Two oral agents are in advanced development. Lucerastat, a glucosylceramide synthase inhibitor iminosugar with promising preclinical and phase 1B data, failed to meet the primary endpoint (neuropathic pain reduction) in the phase III MODIFY trial, yet the ongoing open-label extension (MODIFY-OLE) has shown encouraging biomarker responses and stabilization of kidney function. Venglustat, a selective glucosylceramide synthase inhibitor, showed favorable biochemical outcomes in a phase II study (Deegan et al., *Mol Genet Metab*, 2020). Two randomized, placebo-controlled phase III trials—PERIDOT and CARAT—are currently ongoing to assess its clinical efficacy and safety. If approved by regulatory agencies, substrate reduction therapies may expand therapeutic options, especially for patients with limited ERT tolerance, immunogenic complications or infusion-associated reactions (IAR).

Current studies of Fabry disease in Taiwan

Yun-Ru Chen

Department of Pediatrics, Taipei Veterans General Hospital,

Fabry disease is an X-linked lysosomal storage disorder caused by mutations in the GLA gene, leading to globotriaosylceramide (Gb3) accumulation and multisystem involvement. Since 2008, we have conducted a nationwide newborn screening program in Taiwan, screening over one million newborns. A surprisingly high incidence of the IVS4+919G>A (IVS4) mutation has been observed, affecting approximately 1 in 1,400 males. This variant is associated with late-onset, predominantly cardiac Fabry disease. Our cohort data show that around 67% of IVS4-positive males and 35% of females over age 40 develop left ventricular hypertrophy. Gb3 accumulation and fibrotic changes were detected even before classic histopathological findings, suggesting that cardiac damage begins earlier than previously recognized. To address the therapeutic needs of this patient population, our team has been actively pursuing multiple treatment strategies. In collaboration with Dr. Cheng at Academia Sinica, we developed a novel small molecule for pharmacological chaperone therapy. This compound demonstrated comparable efficacy to Migalastat (GALAFOLD™) in restoring GLA enzyme activity in cellular models. Additionally, we have investigated RNA splicing modulation in partnership with Professor Hagihara at Kyoto University. Our studies showed that the splicing modulator RECTAS effectively corrected aberrant splicing caused by the IVS4 mutation in vitro. We also explored drug repurposing approaches using large-scale gene expression datasets, such as the Connectivity Map (CMap), to identify candidate compounds that modulate GLA or UGCG expression. Several promising agents have been identified for further preclinical evaluation. In the field of gene therapy, we utilized AAV8 and AAV9 vectors to deliver the GLA gene in G3Stg/GLAko mouse models. These studies demonstrated successful restoration of enzymatic activity and reduction of Gb3 accumulation, supporting the potential of AAV-mediated gene therapy for Fabry disease. Furthermore, given the high prevalence of the IVS4 mutation in Taiwan, we have developed a base editing strategy targeting the IVS4+919G>A mutation. Preliminary in vitro data show efficient correction of the mutant allele, indicating the feasibility of this approach as a genotype-specific therapeutic option. This presentation will summarize our key findings and potential therapies tailored to the unique Fabry genotype spectrum in Taiwan.

Mucopolysaccharidosis-now and future

黏多醣症-現在與未來

Hsiang-Yu Lin, Shuan-Pei Lin

林翔宇、林炫沛

Department Radiation Oncology, Lo-Tung Pohai Hospital, Yilan, Taiwan,

馬偕紀念醫院兒童遺傳學科

Taiwan launched its nationwide newborn screening (NBS) program for mucopolysaccharidoses (MPSs) in August 2015. By December 31, 2024, a total of 824,830 infants had been screened for MPS I; 713,933 for MPS II (including 371,388 males); 338,129 for MPS IVA; and 573,370 for MPS VI. Among these, 429 infants were referred for confirmatory testing: 13 for MPS I, 268 for MPS II, 124 for MPS IVA, and 24 for MPS VI. Confirmed diagnoses included 7 cases of MPS I, 14 of MPS II, and 10 of MPS IVA, with no confirmed cases of MPS VI. The prevalence rates were 0.85, 1.96 (3.77 for males), and 2.96 per 100,000 live births for MPS I, II, and IVA respectively. Notably, all confirmed cases were asymptomatic at the time of diagnosis.

The NBS program utilizes multiple diagnostic techniques, including LC-MS/MS enzyme assays on dried blood spots, tandem mass spectrometry analysis of urinary glycosaminoglycan-derived disaccharides, leukocyte enzyme activity measurement via 4-MU fluorometric assay, and Sanger sequencing for mutation detection.

Taiwan's MPS screening program is one of the largest worldwide and offers significant benefits. It reduces the average age of diagnosis from 4.2 years to just 0.2 years, employs precise biomarkers for accurate confirmation, and enables early treatments such as enzyme replacement therapy and hematopoietic stem cell transplantation, which can prevent irreversible symptoms. Additionally, the program has identified novel genetic mutations in Taiwanese infants, advancing understanding of MPS pathogenesis and improving diagnostic and therapeutic approaches.

Overall, Taiwan's NBS program has demonstrated high effectiveness in early detection, enhancing diagnostic accuracy and improving patient outcomes. Its success highlights the critical role of early screening for rare genetic disorders and provides a valuable model for other nations to follow.

Spinal Muscular Atrophy (SMA) - Now and Future

脊髓性肌肉萎縮症（SMA）— 現在與未來

Professor Yuh-Jyh Jong

鐘育志 教授

College of Medicine, Kaohsiung Medical University (KMU), Kaohsiung, Taiwan;

Department of Pediatrics, KMU Hospital, Kaohsiung, Taiwan

College of Engineering Bioscience, National Yang Ming Chiao Tung University, Hsinchu, Taiwan

高雄醫學大學 醫學院, 高雄醫學大學附設中和紀念醫院 小兒部,

國立陽明交通大學 工程生物科學學院

Spinal Muscular Atrophy (SMA) is a rare genetic neuromuscular disorder caused by mutations in the *SMN1* gene, leading to motor neuron degeneration and progressive muscle weakness. Historically, SMA was a leading genetic cause of infant mortality, with limited treatment options and poor long-term outcomes. However, the landscape of SMA care has transformed dramatically in recent years with the advent of disease-modifying therapies, including gene therapy (onasemnogene abeparvovec), antisense oligonucleotides (nusinersen), and oral splicing modifiers (risdiplam).

This presentation will discuss the current status of SMA diagnosis and treatment, highlighting the impact of newborn screening, early intervention, and multidisciplinary management on patient outcomes. We will also explore real-world evidence from Taiwan and other countries on treatment effectiveness, discuss challenges in access and equity, and examine emerging therapies in clinical trials. This comprehensive overview aims to provide insight into how science, policy, and coordinated care can continue to transform SMA from a fatal condition to a manageable chronic disease with hope for a better life.