



# 8<sup>TH</sup> MICROBIOME R&D & BUSINESS COLLABORATION CONGRESS: ASIA

## SINGAPORE

Lee Kong Chian School of Medicine, Nanyang  
Technological University, Singapore (Novena Campus)

7-8 May 2024



**JEROEN RAES**

Professor & Group Leader, Bioinformatics & Eco-Systems Biology Lab, Department of Microbiology & Immunology, Rega Institute, KU Leuven; Vice-Director, Vib Centre for Microbiology

The discovery of diverse microbiota has spurred new research, expanding our understanding of the microbiome's crucial role in health, disease, and prevention. The microbiome has gained increased attention for being recognized as a promising avenue to enhance human health. Researchers and industry players collaborate to bring microbiome discoveries to the market, presenting a unique investment opportunity. This, combined with large-scale collaborations and the sharing of sequencing data, establishes the microbiome as a significant force in science and medicine, essential for future interventions.

At the Raes lab, we actively contribute to this field by employing large-scale, next-generation sequencing, and innovative computational approaches. Our focus is on exploring the functionality and variability of the healthy human microbiome at the systems level. We delve into understanding alterations in the microbiome during disease, uncovering distinct gut flora types (enterotypes) independent of host factors. Our research extends to investigating the predictive capabilities of microbial markers for various intestinal diseases. Additionally, we pioneer the development of computational methods for analyzing (next-generation) sequence data and exploring community properties across diverse environments, including oceans and soil.

I am honoured to deliver the opening keynote address at the **8th Microbiome & R&D & Business Collaboration Congress: Asia**. This event aims to showcase groundbreaking research on microbiome and probiotics, and pledges to provide substantial insights and strategies for researchers and developers in transforming scientific discoveries into viable products.

I look forward to presenting the talk entitled **"Quantitative microbiome profiling in health and disease"** on the 7th of May 2024.

See you in Singapore!



Global Engage is proud to announce their 8th Microbiome R&D and Business Collaboration Congress Asia, which will take place in-person on the 7th and 8th of May 2024 in Singapore.

This conference is a rebranding of the Microbiome R&D and Business Collaboration and Probiotics & Prebiotics Congresses: Asia.

The revelation of the vast diversity within microbiota has driven research into new realms, expanding our comprehension of the microbiome's crucial role in health, disease, and prevention. This includes variations in microbial populations throughout the human body, influenced by environmental factors, immunological elements, and interplays among microbial species. Worldwide scientists and research institutions are continuously conducting cutting-edge research to deliver preventive treatments, cures, therapies, and supplements aimed at enhancing human health.

Run on multiple tracks across two days, this year's conference will feature over 45 leading scientists with talks focusing on the latest scientific advancements and business developments in the microbiome space. This will be accomplished through individual presentations, flash presentations and a panel discussion covering a range of topics, such as microbiome communities, the impact of the microbiome on health, disease, and the therapeutic sector, skin microbiome and cosmeceuticals, probiotics and prebiotics, brain health, as well as regulatory and business considerations, among others.

The revamped 2024 edition pledges to provide substantial insights into the primary challenges faced by researchers and product developers, along with strategies that will transform scientific discoveries into viable products. This event also acts as a platform to connect the community with investors in providing support towards commercialisation. There are numerous opportunities for attendees to expand your network within this rapidly growing field. Whether you aim to gain knowledge from leading scientists, showcase exciting research developments, or explore partnerships and funding opportunities in the industry, this conference is an event of utmost importance that you should not miss.

# CONFERENCE SYNOPSIS

## MICROBIOME IN HEALTH AND DISEASE

- Host-microbiota interactions - metabolic disorders / immunity
- Microbiota composition and impact on digestion
- Gut-brain axis
- Gastrointestinal disorders – IBD, IBS, colitis
- Early-life microbiome – prevention / treatment for allergies and diseases
- Vaginal microbiome and its importance on women and pregnancy

## SKIN MICROBIOME

- Skin microbiome & cosmeceuticals
- Skin health, wellbeing, and microbiome-associated skin diseases
- Skin immunology

## MICROBIOME THERAPEUTICS & BEYOND

- Bringing live biotherapeutic products (LBPs) to market – IP, regulation, GMP
- Pharmaceutical involvement in clinical advances and therapeutic development
- Investment, partnership/collaboration

## TECHNOLOGICAL ADVANCES AND STRATEGIES IN STUDYING MICROBIOME

- Multi-omics approaches, bioinformatics tools, microbiome analysis

## PRE-, PRO- AND POSTBIOTICS

- Role of probiotics, prebiotics and postbiotics in human health
- Imperatives for successful probiotic clinical trials
- Strain identification, designation and safety
- Efficacy and effectiveness of different strains on gut health
- Regulatory approaches for novel probiotics

## PERSONALISED NUTRITION

- Personalised nutrition, novel functional foods & fermentation
- Diet as a modulator of gut microbiota
- Influences of environment, nutrition and lifestyle on microbiome
- Case studies on metabolic disorders, gestational disease, allergy, etc.

## EVENT SPONSORS

### Platinum Sponsors



### Gold Sponsors



### Silver Sponsor



### Exhibitors & Content Sponsor



### Supporters



## MICROBIOME SPEAKERS



### JEROEN RAES

Professor and Group Leader, Bioinformatics and (Eco-)systems Biology Lab, Department of Microbiology and Immunology, Rega institute, KU Leuven; Vice-director, VIB Center for Microbiology



### ERAN ELINAV

Professor and Principal Investigator, Department of Immunology, Weizmann Institute of Science



### JOSEPH SUNG

Professor, Senior Vice President (Health & Life Sciences) and Dean, Nanyang Technological University



### JASON HARCUP

Chief R&D Officer - Beauty & Wellbeing, Unilever.



### NEERJA HAJELA

Head of Science and Regulatory Affairs, Yakult-Danone



### CELIA NING

Director, Nutrition Research Institute, Junlebao



### THOMAS DAWSON

Senior PI and Deputy Executive Director, A\*STAR Skin Research Labs



### NIRANJAN NAGARAJAN

Senior Group Leader, Genome Institute of Singapore, A\*STAR



### DENISE KELLY

Microbiome Investment Advisor, Seventure Partners



### SANG SUN YOON

Professor, Yonsei University and CEO, BioMe Inc



### ALEXANDER AKSENOV

Assistant Professor, University of Connecticut



### ANG QI YAN

Senior Scientist, Genome Institute of Singapore, A\*STAR



### JAMES MORTON

Consultant, Simons Foundation



### ADRIEN NIVOLIEZ

CEO, BiOSE Industrie



### SUNNY WONG

Associate Professor, Nanyang Technological University



### RATHA-KORN VILAICHONE

Professor of Medicine; Chief, Center of Excellence in Digestive Diseases, Thammasat University, Thailand



### KEIR NICHOLAS-HAIZELDEN

PhD Student, University of Liverpool



### JUN TERAUCHI

CSO, Metagen Therapeutics Inc



### ERIC HUANG CHUN-MING

Senior Scientific Advisor, Zymolo Inc



### TING FAN LEUNG

Professor, The Chinese University of Hong Kong



### HEMALI GUNT

Head of Clinical and Scientific Affairs, Burt's Bees



### JENNIFER FOUQUIER

Doctoral Candidate, The University of Colorado, Anschutz Medical Campus



### CHRISTOPHE LAY

Senior Team Leader, Gut Microbiology, Danone Nutricia



### REGINA KARIM

Global Senior Manager, Translational Science, H&H Group



### ARIELLE NGIN WAN NING

Regional Innovation Executive, Shiseido Asia Pacific



### WEI-KAI WU

Assistant Professor/ Research Physician, National Taiwan University Hospital



### PING HU

R&D Director Principal Scientist, Procter & Gamble Company, Corporate Function R&D, Discovery & Innovation Platform



### ALBERT DASHI

CSO and Co-founder, Sequential



### ANTONIO LC GOMES

Principal Scientist, Xbiome



### TAI L GUO

Professor, University of Georgia



### AARTHI RAVIKRISHNAN

Scientist, Genome Institute of Singapore, A\*STAR



### IRMA BERNADETTE S. SITOANG

Professor, University of Indonesia



### MARGARET J MORRIS

Professor, University of New South Wales



### JONATHAN LEE

Consultant, Assistant Professor and Chief Scientific Officer, National University Hospital, National University of Singapore, Asian Microbiome Library Pte Ltd



### CRISTIANO SABELLI

Scientific Affairs Director, Copan Italia



### GAN RENYOU

Principal Scientist, Singapore Institute of Food and Biotechnology Innovation (SIFBI), A\*STAR



### ELVINA PARLINDUNGAN

Scientist, A\*STAR



### PATRICIA CONWAY

CEO & Founder, PC Biome Pte Ltd and Visiting Professor, Singapore Centre for Environmental Life Sciences Engineering (SCELESE), Nanyang Technological University



### AMY LIN

Senior Principal Scientist, SIFBI, A\*STAR



### MARTIN PAGAC

Senior Scientist, DSM-Firmenich, Perfumery & Beauty



### TARUN CHOPRA

Director, Advanced Research, L'Oreal Research and Innovation



### KYLE YOUNG

Product Manager, ATCC



### ARNO BOUWENS

Director, Head of R&D, Perseus Biomics

90-MINUTE PRE-EVENT WORKSHOP

6<sup>TH</sup> MAY 2024 / 2:30-4:00 / ALOFT SINGAPORE NOVENA

SPONSORED BY



**Unlocking Potential: Academia-Industry Partnerships in the Microbiome Space**

In recent years, the microbiome has emerged as a promising frontier in biotechnology, with potential applications in various aspects of human health. This workshop aims to delve into the dynamics of academia-industry collaborations within this rapidly evolving field, highlighting successful partnerships that have yielded transformative technologies. This workshop is designed for researchers, industry professionals, and policymakers interested in exploring the potential of microbiome research and leveraging academia-industry partnerships to drive innovation in this rapidly evolving field.



**ALBERT DASHI**

Chief Scientific Officer,  
Sequential



**PATRICIA CONWAY**

CEO & Founder, PC Biome Pte Ltd and Visiting Professor,  
Singapore Centre for Environmental Life Sciences  
Engineering (SCELSE), Nanyang Technological University



**PINIDPHON  
PROMBUTARA**

Director of Commercial & Research Operation,  
Mod Gut Co., Ltd.




**VIDUTHALAI  
RASHEEDKHAN REGINA**

Research Director and Principal Research Fellow,  
SCELSE and L'Oreal-SCELSE Joint Laboratory


8:00-8:35	Registration / Refreshments
8:35-8:40	Global Engage Welcome Address
8:40-8:45	Conference Chair's Opening Remarks

8:45-9:15




**KEYNOTE ADDRESS:  
JEROEN RAES**  
Professor and Group Leader, Bioinformatics and (Eco-)systems Biology Lab, Department of Microbiology and Immunology, Rega institute, KU Leuven; Vice-director, VIB Center for Microbiology  
**Quantitative Microbiome Profiling in Health and Disease**  
Alterations in the gut microbiota have been linked to various pathologies, ranging from inflammatory bowel diseases and diabetes to cancer. Although large numbers of clinical studies aiming at microbiome-based disease markers are currently being performed, our basic knowledge about the normal variability of the human intestinal microbiota and its determining factors remains limited. Here, I will discuss our findings studying a large-scale study (Flemish Gut Flora Project; n=3400) of the gut microbiome variation in a geographically confined region (Flanders, Belgium), in which analysis of microbiome variability in health identified the primary parameters associated to microbiome composition. In this presentation, I will discuss our experiences in large-scale microbiome monitoring, show how the development of dedicated computational approaches can assist in microbiome analysis and interpretation, and which confounders are essential for inclusion in microbiome disease research. In addition, I will show how Quantitative Microbiome Profiling (QMP; Vandeputte et al. Nature 2017), which combines microbiomics with flow cytometry-based cell counts, is profoundly changing our view on gut microbiota variation and allowed the identification of an inflammation-associated, cross-disease enterotype. Leads from such QMP-based profiling are enabling the development of microbiome modulation strategies.

9:15-9:45




**KEYNOTE ADDRESS:  
JASON HARCUP**  
Chief R&D Officer – Beauty & Wellbeing  
**Microbiome: Developments in Skin and Adjacencies**  
As more is uncovered about the skin microbiome and how it is influenced by environment and lifestyle contexts, we consider adjacencies to other aspects of the human microbiome, and how these come together for holistic wellbeing

9:45-10:15




**ADRIEN NIVOLIEZ**  
CEO, BiOSE Industrie  
**The CMC Journey for a Live Biotherapeutic Product**  
Taking you on the complex LBP program journey and successfully delivering your GMP product through the clinic and into commercial production.



10:15-11:15	Morning Refreshments / Poster Presentations / One-to-One Presentations
-------------	--


MICROBIOME IN HEALTH & DISEASE

11:15-11:40



**SANG SUN YOON**  
Professor of Microbiology, Yonsei University College of Medicine and CEO, BioMe Inc  
**BM107, A Novel Butyrate-producing synbiotic system**  
We have pioneered an innovative system to circumvent the challenges of delivering butyrate for therapeutic purposes due to its noxious smell and rapid absorption in the small intestine which limits its effectiveness in the colon. Utilizing a food-grade bacterial strain, our system ingeniously produces butyrate directly in the colon by converting its precursor via enzymatic conversion. Preclinical studies in animals have robustly confirmed the generation of butyrate and its subsequent anti-inflammatory benefits. We anticipate our breakthrough to significantly advance the therapeutic delivery of butyrate for various diseases. Detailed results and potential implications will be presented.


11:40-12:05



**JAMES MORTON**  
Consultant, Simons Foundation  
**Multi-level Analysis of the Gut-brain Axis Shows Autism Spectrum Disorder-Associated Molecular and Microbial Profiles**  
Autism spectrum disorder (ASD) is a neurodevelopmental disorder characterized by heterogeneous cognitive, behavioural and communication impairments. Disruption of the gut-brain axis (GBA) has been implicated in ASD although with limited reproducibility across studies. Here, we developed a Bayesian differential ranking algorithm to identify ASD-associated molecular and taxa profiles across 10 cross-sectional microbiome datasets and 15 other datasets, including dietary patterns, metabolomics, cytokine profiles and human brain gene expression profiles. We found a functional architecture along the GBA that correlates with heterogeneity of ASD phenotypes, and it is characterized by ASD-associated amino acid, carbohydrate and lipid profiles predominantly encoded by multiple microbial species and correlates with brain gene expression changes, restrictive dietary patterns and pro-inflammatory cytokine profiles. We also show a strong association between temporal changes in microbiome composition and ASD phenotypes in the context of a fecal matter transplant.


SKIN MICROBIOME

11:15-11:40



**THOMAS L DAWSON JR**  
Deputy Executive Director and Senior Principal Investigator, A\*STAR Skin Research Labs  
**Lipid mediators in microbe-host Interaction**  
The gut microbiome has achieved near celebrity status, but the skin microbiome remains elusive and poorly investigated. Even today, most skin biome investigations focus on bacteria, despite multiple publications proposing a causative role for fungi in common skin disorders such as dandruff / seborrheic dermatitis, and exacerbation of wounds, atopic dermatitis, and eczema. Malassezia lipid metabolism is implicated in seborrheic dermatitis via release of irritating free fatty acids. However, as Malassezia are commensal, pathogenic, and likely mutualistic, we hypothesize their lipid metabolism is involved in more complex mycobiome host communication. Common language mediators across multiple kingdoms are oxygenated polyunsaturated fatty acids. Interestingly, these mediators in fungi and plants are referred to as "oxylipins", while in human and animal biology they are referred to as "eicosanoids". This has created research silos and led to poor inter-field communication and a lack of collaborative research on this crucial aspect of host/microbe interaction. We identify Malassezia signaling molecules on human skin, identifying the human skin "core lipidome". This work should provide a toolbox for further investigation of the role of the human microbiome in health and disease.

11:40-12:05



**ARIELLE NGIM WAN NING**  
Regional Innovation Executive, Shiseido Asia Pacific  
**Skin Microbiome Based Product Development for Sensitive Skin**  
Predominance of Cutibacterium over other genera was identified as a unique feature of sensitive skin microbiome in Japanese women, suggesting involvement of skin microbiome in the occurrence of sensitive skin in this population. In those sensitive skin, lower relative abundance of Staphylococcus epidermidis was also observed. As this was suspected to be responsible for sensitive skin phenotype, we developed our own prebiotic ingredient which supports the growth of S.epidermidis and the human test results will be reported.

12:05-12:35



**ARNO BOUWENS**

Director, Head of R&D, Perseus Biomics

**The Insights of Shotgun, the Price of 16S and the Speed of PCR: Optical Mapping Redefines Microbiome Profiling**



The discovery of biomarkers and therapeutic targets as well as routine testing require high volumes of high-quality data to fully tap into the microbiome's potential. Choosing between amplicon and shotgun sequencing involves a painful trade-off between depth of insight and cost, while both suffer from long time-to-result. We introduce DynaMAP, a sequencing-free, untargeted metagenomics method. It uses fluorocoding and optical mapping of metagenomic DNA to read out taxonomic barcodes. We present the DynaMAP performance validation data in comparison to sequencing and demonstrate its strain-level taxonomic resolution. We demonstrate that DynaMAP is particularly effective at strain/consortia tracking, as well as profiling complex microbiome samples in high taxonomic resolution. In summary, DynaMAP enables same-day microbiome profiling solutions in R&D, precision nutrition and diagnostic applications.

12:05-12:35



**IRMA BERNADETTE S. SITOANG**

Professor, University of Indonesia

**Profile of Skin Microbiome Among Different Grades of Acne Vulgaris and Normal Skin**



Acne has long been understood to have a complex physiological basis involving several main factors. Recent studies at the molecular and cellular level have found the role of skin microbiome dysbiosis characterized by alteration in the proportion of *C. acnes*, *Staphylococcus aureus* (*S. aureus*), *Staphylococcus epidermidis* (*S. epidermidis*), and other microorganisms between acne and normal skin. Furthermore, a better understanding of skin microorganism profile in AV is needed for developing targeted therapies for acne skin through this study by examining the skin microbiome in 36 participants with varying severity and normal skin.

12:35-1:40

Lunch / Poster Presentations / One-to-One Presentations

**MICROBIOME IN HEALTH AND DISEASE**

1:40-2:05



**ALBERT DASHI**

CSO and Co-founder, Sequential

**Advancing Women's Health: In-Vivo Microbiome Testing for Female Products**

Our study employs an in-vivo platform featuring advanced targeted next-generation sequencing and sampling techniques to assess the influence of female products on the vulva and vaginal microbiome. By exploring a spectrum of hygiene and personal care items, we will elucidate their specific effects on the richness, diversity, and stability of the vulva and vaginal microbial community. In our research we integrate laboratory insights with real-world scenarios, providing crucial evidence for product development. These findings will contribute to the formulation of female products that actively support the natural balance of the vaginal microbiome, promoting women's health and overall well-being. This condensed platform represents a significant leap in women's health research, providing a practical framework for microbiome testing that mirrors everyday conditions. The integration of advanced technologies, with a focus on real-world relevance, positions us at the forefront of efforts to enhance understanding and promote the health of the vulva and vaginal microbiome.

2:05-2:30



**MARGARET MORRIS**

Professor, University of New South Wales

**Divergent Impacts of Maternal Obesogenic Diet Versus Control on Maternal and Offspring Microbiome Development**

To explore the extent to which an obesogenic diet impacts maternal and offspring gut microbiota, we examined changes in gut microbiota composition across pre-pregnancy, gestation and lactation in rat dams fed either a high-fat, high-sugar Cafeteria (Caf) diet or Chow. Offspring were weaned onto chow diet. Caf diet consumption during pregnancy increased weight gain and adiposity and compromised maternal nursing behavior.  $\alpha$ - and  $\beta$  diversity measures in Caf-fed dams showed different trajectories across the progression of pregnancy, and more marked changes in Bacteroidetes and Firmicutes abundance were seen in Chow compared to Caf dams. Offspring born to Caf dams exhibited greater adiposity and plasma leptin at weaning and 14 weeks of age than those born to Chow dams. Maternal Caf diet induced clear differences in  $\beta$  diversity in weanlings but not  $\alpha$  diversity. At weaning SourceTracker analysis revealed similarities in the gut microbiota of Chow offspring and maternal gut microbiota in lactation, whereas Caf offspring were similar to the maternal gut microbiota during gestation. Maternal Caf diet exerted only marginal effects on gut microbiota composition in 14-week-old offspring consuming a healthy diet.

2:30-3:00



**KYLE YOUNG**

Product Manager, ATCC

**ATCC® NGS Standards: Addressing the need for Standardization in Microbiome Research**



The complexities involved in 16S rRNA and shotgun metagenomic analysis methods pose significant challenges for microbiome research. Significant biases can be introduced during sample preparation, DNA extraction, PCR amplification, library preparation, sequencing, or data interpretation. One of the primary obstacles in assay standardization is the limited availability of reference materials. To support this need, ATCC® developed NGS Standards from fully sequenced and characterized ATCC strains that were selected based on phenotypic and genotypic attributes or their prevalence in clinical or natural environments. To further enhance the use of NGS Standards and eliminate the bias associated with data analysis, we offer a data analysis module in collaboration with One Codex that provides simple output in the form of true-positive, relative abundance, and false-negative scores for 16S rRNA community profiling and shotgun metagenomic sequencing.

1:40-2:05

**SKIN MICROBIOME**



**TING FAN LEUNG**

Professor, The Chinese University of Hong Kong

**Deep Sequencing of Skin Microbes Reveals Novel Biomarkers and Treatment Targets for Eczema**

Microbes at different mucosal sites are a potent driver of immunological maturation. While there is rich evidence on early-life evolution of gut microbiome, the importance of microbiome at other body sites such as skin and airway is unclear. Our birth cohort revealed substantial temporal variations in skin microbiota during the first 12 months. Infants with persistent eczema had lower microbial biodiversity than those with transient eczema. Our metagenomics data revealed inverse relationship between eczema severity and microbial biodiversity as well as reciprocal relationship among different staphylococci on the skin. Early-phase clinical trials reported that the transfer of lantibiotic-producing coagulase-negative staphylococci suppressed *Staphylococcus aureus* growth and ameliorated eczema severity. In conclusion, the biodiversity and compositions of skin microbiota may be novel biomarkers and therapeutic targets for childhood eczema.

2:05-2:30



**PING HU**

R&D Director Principal Scientist, Procter & Gamble Company, Corporate Function R&D, Discovery & Innovation Platform

**Microbial Response to Therapeutic Ingredients and Applications for Consumer Product Innovation**

In recent years, the study of the human microbiome has emerged as a fascinating and promising field of research. The intricate relationship between microorganisms and human health has opened new avenues for therapeutic interventions and innovative consumer product development. This talk explores the microbial response to therapeutic ingredients and its implications for consumer product innovation. We will cover a few cases about how P&G uses RNASeq and metagenomics to examine the mechanism of microbial response to different therapeutic ingredients, develop a strategy for material selection, and credential a technical story for consumer product innovation.

2:30-3:00



**MARTIN PAGAC**

Senior Scientist, DSM-Firmenich, Perfumery & Beauty



**Menopause and Facial Skin Microbiomes**

Considerable efforts have been made to better understand the relationship between skin microbial community structures and chronological age. However, investigations into determining direct impacts of menopausal statuses, which are inherently linked to age, were neglected so far. With a steadily increasing life expectancy around the world, the rapidly growing population of postmenopausal women now lives one third of their lifetime in a state of estrogen deficiency. Hence there is an unmet need to expand our knowledge on the role of skin microbiome in postmenopausal health. Ultimately, microbiome-targeting interventions may provide valuable strategies to manage skin disorders associated with menopausal status.



3:00-3:25



**CHRISTOPHE LAY**

Senior Team Leader, Gut Microbiology, Danone Nutricia

**Early Life Nutrition and Its Relevance in the Past 1,000 Days: A Lifelong Microbial Journey Perspective**

The human gut microbiome is transmitted from one generation to the next. This transgenerational microbial inheritance occurs during pregnancy, during birth and during breastfeeding. Such vertical transmission contributes to educate our immature immune, metabolic and neurocognitive systems during foetal and early life, highlighting therefore the role of the microbiome in health and diseases. The first 1000 days of life is recognized as an important window to nurture child health and development, and an increasing body of evidence indicates that a compromised microbiome is a risk factor for the development of non-communicable diseases. Nutritional intervention could be harnessed as a means to reduce the disease risk associated with a compromised microbiome.

3:00-3:25



**HEMALI GUNT**

Head of Clinical & Scientific Affairs, Burt's Bees

**The Role of Microbiome in Lip Health**

We will review the latest research findings from clinical investigation on normal and dry lips of human subjects. Assessments of lip microbiome will be contrasted and compared between the two groups to determine its role in lip health. We will close with a preview of the relationship between the lip microbiome and lip surface protein. Evidence suggests the importance of this foundational understanding in predicting diseases and in developing appropriate care products.

3:25-4:25

Afternoon Refreshments / Poster Presentations / One-to-One Presentations

**MICROBIOME IN HEALTH AND DISEASE**

4:25-4:40



**EARLY CAREER RESEARCHER: ANG QI YAN**

Senior Scientist, Genome Institute of Singapore

**A Novel Bifidobacterium Longum Subspecies in the Gut of Bangladeshi Children Thrives During Weaning**

The gut microbiome plays a crucial role in infant health and development, yet it remains unclear how feeding practices and environmental factors influence microbiome development in infants from different geographic regions. We characterized the fecal microbiome and metabolome of 222 young children in Bangladesh, sampled at regular intervals over their first two years of life. We discovered a new subspecies of Bifidobacterium longum which was highly prevalent during the weaning phase when infants transition from mother's milk to solid foods, consistent with their genetic capacity for metabolizing both human milk and solid food substrates. We also identified a group of metabolites, including pipecolic acid, that were linked to this newly identified B. longum subspecies, shedding light on its role in the gut ecosystem. This discovery opens avenues for further research to understand how this B. longum subspecies and their metabolites contribute to infant health, growth and development.

4:25-4:40



**EARLY CAREER RESEARCHER: KEIR NICHOLAS-HAIZELDEN**

PhD Student, University of Liverpool

**Uncovering the factors of Staphylococcal fitness in the human skin microbiome**

The human skin is a rich environment home to a plethora of microorganisms which playing fundamental roles in maintaining homeostasis such as through pathogenic colonisation resistance and local immune system priming. Despite the human skin microbiome remaining less studied than the parallel gut microbiome, a growing body of research has identified this biome as a rich source of novel effector compounds relevant to both healthcare and commercial applications. The community structure of the human skin microbiome is interdependent on a variety of abiotic and biotic effectors, many of which are yet to be elucidated. Staphylococci are a prominent member of the human skin microbiome, present in almost all body sites and are associated with both beneficial and detrimental disorders. An understanding of how staphylococci interact in the skin environment is necessary for informing the development of novel treatment strategies and personal care products.

4:40-4:45



**FLASH TALK: AMY LIN**

Senior Principal Scientist, SIFBI, A\*STAR

**Unlock the Power of Dietary Fibre Structure Complexity in Shifting Gut Microbiota Toward Elevating Butyrate to Tackle Diet-Related Metabolic Diseases**

Diet-related metabolic diseases, pose significant challenges to the health care of the majority of Singapore population. Gut microbiome was found to significantly affect human health and overall well-being through enhancing immunity and producing beneficial metabolites. Despite the many factors that can influence human colonic microbiota composition, the influence of diet is particularly critical because most microorganisms in the gut require energy from the degradation of complex carbohydrates, especially dietary fibre (DF), for their growth. DF, which is the non-digestible component of food carbohydrates, serve as the major prebiotic source for the microbial community. It plays a pivotal role in modulating the richness and diversity of the gut microbiome and is fundamental for gut health. The high complexity of its structure is found to shift microbiota toward strains with high butyrate production and slow fermentation, which benefits in low bloating and sustained butyrate utilisation. The fermentation products short-chain fatty acids (SCFAs), particularly butyrate and propionate, carry many nutritional qualities, such as exerting anti-inflammatory effects, modulating the immune system, removing toxins & pathogens, boosting the epithelial cell barrier, and regulating glucose homeostasis & appetite. These factors are known to mitigate the pathogenesis of diverse metabolic diseases such as type II diabetes and obesity. Thereby, dietary fibre content and structure are indirectly influencing the onset and progression of various diseases. This relationship underlines the importance of a diet rich in various types of dietary fibres to support health. Although the importance of dietary fibre to tackle such disorders have been revealed through systematic and clinical trials, how different fibre sources are best utilized to manage these conditions, is a question that still need to be addressed. Here we propose a precision nutrition approach that exploits gut microbiota structure and diversity to anticipate human response to dietary fibre as a prodigious potential for food for health applications related to the prevention and control of diet-related metabolic diseases.

4:40-4:45

**FLASH TALK:**

Poster presenters and start-up companies will be provided with the opportunity to give a flash 4-minute overview of their work

4:45-4:50

**FLASH TALK:**

Poster presenters and start-up companies will be provided with the opportunity to give a flash 4-minute overview of their work

4:45-4:50

**FLASH TALK:**

Poster presenters and start-up companies will be provided with the opportunity to give a flash 4-minute overview of their work

MICROBIOME IN HEALTH & DISEASE



**JONATHAN LEE**

Consultant, Assistant Professor and Chief Scientific Officer, National University Hospital, National University of Singapore, Asian Microbiome Library Pte Ltd

**Translating Microbiome for GI diseases - A New Year's Resolution**

We have co-evolved with our gut microbiome over the years, which plays a critical role in normal development and function. This talk would highlight the importance of these missing members of our essential physiology, required for health maintenance and prevention of a wide range of gastrointestinal (GI) diseases. I would highlight our local microbiome studies in the fields of gastric and colorectal cancer, inflammatory bowel disease, liver cancer and non-alcoholic fatty liver disease.

4:50-5:15

SKIN MICROBIOME



**TARUN CHOPRA**

Director, Advanced Research, L'Oreal Research and Innovation

**Deciphering role of scalp microbiome in dandruff and health**

The human skin microbiome plays a critical role in maintaining skin health and function. Several clinical phenotypes are associated with an imbalance in the relative proportions of these microbiota including dandruff, which is characterized by abnormal flaking and irritation. Taxonomically, dandruff is associated with a higher incidence of Malassezia sp. and Staphylococcus spp., and a lower incidence of Cutibacterium sp., as compared to normal scalp. Anti-fungal treatments are very effective in controlling dandruff, but relapse is a chronic problem that requires the regular use of anti-dandruff products, highlighting the need to better understand this scalp concern. Particularly, it is not clear how the relative proportions of the microbial populations are either kept in balance on a healthy scalp, or what leads to a dysbalanced state, driving dandruff and seborrheic dermatitis. In this talk, I will speak about functional dissection of the scalp microbiome in dandruff and further describe how interaction dynamics between key microbiome members drive the Healthy and dandruff phenotypes of the scalp.

4:30-5:15

**50-MINUTE PANEL DISCUSSION:**

**Transitioning Microbiome Discoveries into Market Opportunities and Investment Landscape in Asia and Beyond**

This panel discussion focuses on:

- Exploring means to encourage emerging microbiome players expand their footprint in the market
- Evaluating ROI: Market potential, future outlook, effective investment strategies and investor perspective
- Assessing recent FDA approvals on biotech and investing in the microbiome
- Identifying challenges and risks (controls, standards, etc.) associated with transitioning microbiome discoveries into market opportunities



**DENISE KELLY** (Moderator)

Investment Advisor, Seventure Partners, UK



**JEROEN RAES**

Professor and Group Leader, Bioinformatics and (Eco-)systems Biology Lab, Department of Microbiology and Immunology, Rega institute, KU Leuven; Vice-director, VIB Center for Microbiology



**ALBERT DASHI**

CSO and Co-founder, Sequential



**JONATHAN LEE**

Consultant, Assistant Professor and Chief Scientific Officer, National University Hospital, National University of Singapore, Asian Microbiome Library Pte Ltd

5:15-6:05

6:05


End of Day 1 / Networking Drinks Reception / Group Photo / One-to-One Meetings



08:00-08:40	Registration / Refreshments
08:40-08:45	Conference Chair's Opening Remarks

GUT HEALTH & DISEASE

**8:45-9:15**



**KEYNOTE ADDRESS: JOSEPH SUNG**  
 Professor, Senior Vice President (Health & Life Sciences) and Dean, Nanyang Technological University, Singapore  
**What We Do Not Know About Using Microbiota as Therapeutics**

Fecal microbiota transplantation (FMT) has been used extensively in the treatment of various GI and extraintestinal conditions. Yet, there are still a lot of missing gaps in our knowledge in the gut microbiota and its behaviour. This includes undetected microbes, uncertain colonization, unclear mechanisms of action, uncertain indications, unsure long-term efficacy and side effects, among others. These unknowns may affect the therapeutic uses of FMT and the potentials and caveats of other related microbiota-based therapies. When used as an experimental therapy or last resort in difficult medical conditions, cautions should be taken against inadvertent complication. Research studies on the mechanism of action and the appropriate use of FMT in human warrant much more investigation. Robust scientific experiments and properly designed clinical studies are needed.


**9:15-9:40**



**DENISE KELLY**  
 Investment Advisor, Seventure Partners, UK  
**The Human Microbiome: Scientific Developments and Commercial Opportunities - An Investor Perspective**

Human body sites such as the gut, oral cavity, and skin are colonized with diverse microbial populations including bacteria, fungi, and viruses. The importance of these communities is profound, as they impact key physiological and pathophysiological processes throughout all life stages from birth to old age. DNA sequencing, multi-omics technologies applied to human clinical cohorts are identifying how microbes influence biological processes such as immunity and metabolism. The complexity of this data requires ML/AI to decipher key microbiome features associated with host response. These significant scientific and technical innovations are enabling microbiome-focused companies to develop a broad range of drug modalities from living bacteria to phage therapeutics. The recent FDA approval of donor derived fecal products has accelerated interest in developing rationally designed drugs for the treatment of diseases including inflammatory bowel disease and cancer. The presentation aims to highlight the scientific and commercial progress that will underpin the next wave of validated microbiome drugs.

**9:40-10:10**



**CRISTIANO SABELLI**  
 Scientific Affairs Director, Copan Italia  
**Reducing Bias in Sample Collection and Transport for Accurate Microbiome Analysis**


The last decade has seen a rapid increase in the number of microbiome studies, showing how our overall well-being is influenced by microorganisms residing in and on our bodies. While highlighting the importance of these microbial communities to our health, these studies not always result in overlapping findings due to the systemic bias that is introduced throughout the workflow. The very first key to all these studies is the accurate sampling and storage of samples until processing. Indeed, unrepresentative samples resulting from incorrect collection or compromised microbial constituents can be responsible for incorrect conclusions. In this presentation, advanced strategies for standardizing the preanalytical phase of microbiome studies are proposed.



10:10-11:10	Morning Refreshments / Poster Presentations / One-to-One Presentations
-------------	--

TOOLS AND STRATEGIES FOR MICROBIOME

**11:10-11:35**



**ALEXANDER AKSEKOV**  
 Assistant Professor, University of Connecticut  
**Mapping the Unknowns: Advanced Molecular Networking to Illuminate the Dark Metabolome**

Molecular networking is a powerful tool for discovering new molecules using mass spectrometry. Networking connects metabolites with structural similarities by leveraging similarities in fragmentation patterns. However, conventional molecular networking relies on arbitrary global spectral similarity thresholds, even though optimal connectivity is molecule class-specific. We present an advanced molecular networking approach utilizing unpruned full connectivity metabolite networks parsed using machine learning tools to determine naturally present "molecular communities." This enables preserving intra-community connectivity information and allows optimization of connectivity patterns for each metabolite class. We demonstrate how this method enables molecular discovery and significantly advances molecular networking, further unlocking the potential of mass spectrometry-based metabolomics. This strategy provides a powerful tool for mapping of complex metabolomes and natural product discovery.

PRE/PRO/POST-BIOTICS

**11:10-11:35**



**REGINA KARIM**  
 Global Senior Manager, Translational Science, H&H Group  
**Emerging Science of Postbiotics and the Market Trend**

The concept of postbiotics has gained significant traction in recent years, particularly following the publication of the postbiotics consensus by the International Scientific Association for Probiotics and Prebiotics (ISAPP). Postbiotics are defined as preparations of lifeless microorganisms and/or their components that confer health benefits to the host. The health effects associated with the administration of postbiotics include the regulation of the immune system, promotion of gut health, prevention of obesity, control of lipid metabolism and relief or prevention of symptoms related to chronic diseases. A key factor driving interest in postbiotics is their stability during industrial processes and storage. This characteristic allows postbiotics to be utilized in various food and supplement formats and facilitates widespread distribution without encountering challenges related to cold chain maintenance and temperature. Although clinical research indicates that integrating postbiotics into diets can contribute to promoting health, preventing, and treating diseases in both human and animal health, there is limited evidence in healthy populations. Another persisting challenge is the lack of regulatory incorporation of the term postbiotics by any government or international agency.

11:35-12:00



**NIRANJAN NAGARAJAN**

Senior Group Leader, Genome Institute of Singapore, A\*STAR  
**Deconstructing and Reconstructing Microbiomes and their role in AMR Transmission**

We live in a microbial world estimated to contain more than a million species, and yet humanity's adversarial relationship with microbes is shaped by a small fraction of pathogenic species and the pervasive use of antimicrobial agents. Efforts to eradicate microbes often have limited success, with disinfected environments being rapidly recolonized, and antibiotic treatment increasingly selecting for resistant pathogens. The global rise in antimicrobial resistance (AMR) rates for common pathogens (e.g. ESKAPE) is recognized as a pre-eminent threat to healthcare systems. As the range of effective antibiotics shrinks we approach a tipping point where no antibiotic works for a pathogen, putting at risk the lives of millions of vulnerable patients in hospitals worldwide. Already >1 million deaths/year are attributed to AMR, and by 2050 the UN projects that AMR will be responsible for more deaths every year than all cancers (>10 million deaths/year).

We need new approaches to track the transmission of antibiotic resistance across microbes and to understand how we can leverage ecological functions to reduce AMR reservoirs. We propose that the emerging field of genome-resolved metagenomics aided by long-read sequencing [1] can transform our ability to do microbial surveillance, and we showcase its application in tracking pathogens through hospital environments [2] as well as the gut microbiome [3]. In order to decipher how microbial communities assemble and can provide colonization resistance against pathogens, we have developed new microbiome modelling approaches that can provide mechanistic insights based on high-throughput metagenomic datasets [4, 5]. Together with other data mining approaches [6], we are now leveraging these to understand how microbiomes recover from the impact of antibiotics and how new classes of biotherapeutics can be developed to prevent the spread of antimicrobial resistant pathogens.

12:00-12:30

**30-Minute Solution Provider Presentation**  
 For sponsorship opportunities contact Reuben Raj  
[reuben@global-engage.com](mailto:reuben@global-engage.com)

MICROBIOME THERAPEUTICS & BEYOND

12:30-12:45



**EARLY CAREER RESEARCHER: JENNIFER FOUQUIER**

Doctoral Candidate, The University of Colorado, Anschutz Medical Campus

**EXPLANA: A user-friendly workflow for EXPLoratory ANALYSIS and feature selection in cross-sectional and longitudinal microbiome studies**

The potential for disease treatment through microbiome modification has led to an increase in longitudinal microbiome studies (LMS). Analytical objectives often include identification of features that relate to a response. Many challenges arise with data integration, compositional data, dimensionality reduction, categorical and numerical data, and the need for mixed-effects machine learning models for non-independent data. Additionally, LMS can be observational (measurements made over time, related to natural fluctuations) or interventional. Hence, feature changes can be calculated over time, for each subject, and these changes are dependent on different reference values. Thus, we developed a data-driven feature selection tool that includes preprocessing, data integration, calculation of differences if needed, mixed-effects Random Forests for feature selection, and methods to rank features and explain their impact on response. With one script, analysts obtain an .html report that includes figures, tables, and a description of methods for improved interpretation of complex results.

12:45-12:50



**FLASH TALK: GAN RENYOU**

Principal Scientist, Singapore Institute of Food and Biotechnology Innovation (SIFBI), A\*STAR

**Gut Microbiota-Mediated Innovation of Food Functional Ingredients**

Food functional ingredients like phytochemicals are overall with poor bioavailability and their beneficial functions can be largely dependent on gut microbiota-mediated biotransformation. Understanding the dynamic interactions of dietary phytochemicals with gut microbiota and underlying molecular mechanisms in humans can support the innovation of phytochemical's real bioactive metabolites as novel food functional ingredients and nutraceuticals by the strategy of gut microbiota biotransformation.

12:50-12:55

**FLASH TALK:**  
 Poster presenters and start-up companies will be provided with the opportunity to give a flash 4-minute overview of their work

12:55-2:00

Lunch / Poster Presentations / One-to-One Presentations

11:35-12:00



**CELIA NING**

Director, Nutrition Research Institute, Junlebao Dairy

**The Efficacy and Application of a Novel Probiotics Strains in Infant**

The first 1000 days of life are crucial for establishing a healthy gut microbiome, which ultimately impact long-term health outcomes. In recent years, the importance of early life nutrition in shaping a child's health and development has gained significant attention. Novel probiotics strains are being isolated and commercialized for a wide range of products, many of which are well studied on their benefits for infants. In this talk, a novel strain with accumulating safety and efficacy studies will be introduced. Hopefully, this talk will share some new insights for the application of probiotics in the infant nutrition market.

Key takeaways will be:

- The importance of probiotics for infant and young child's health
- The novel strain is safe and well tolerated by infant
- Infant supplementation with the novel strain can improve gut function
- Other achievements of Junlebao Dairy Group Co., Ltd. in probiotic research

12:00-12:30

**30-Minute Solution Provider Presentation**  
 For sponsorship opportunities contact Reuben Raj  
[reuben@global-engage.com](mailto:reuben@global-engage.com)

PRE/PRO/POST-BIOTICS

12:30-12:45



**EARLY CAREER RESEARCHER: AARTHI RAVIKRISHNAN**

Scientist, Genome Institute of Singapore, A\*STAR

**Gut Metagenomes of Asian Octogenarians Reveal Microbial Species Promoting Healthy Aging**

While rapid demographic changes in Asia are driving the incidence of chronic diseases related to aging, the limited availability of high-quality in vivo data hampers our ability to understand complex multi-factorial contributions, including gut microbial, to healthy aging. Leveraging the availability of a well-phenotyped cohort of community-living octogenarians in Singapore, we used deep shotgun metagenomic sequencing to do high-resolution taxonomic and functional characterization of their gut microbiomes (n=234). Species-level analysis identified a distinct age-associated shift in Asian gut metagenomes, characterized by a reduction in microbial richness, and enrichment of specific Alistipes species (e.g. Alistipes putredinis, Alistipes onderdonkii). Functional pathway analysis confirmed that these changes correspond to a metabolic switch in aging from microbial guilds that typically produce butyrate in the gut (e.g. Faecalibacterium prausnitzii, Roseburia inulinivorans) to alternate pathways that utilize amino-acid precursors. Extending these observations to key clinical markers helped identify >15 robust gut microbial associations to cardiometabolic health, inflammation, and frailty, including potential probiotics such as Parabacteroides goldsteinii and pathogenic species such as Dialister invisus, highlighting the role of the microbiome as biomarkers and potential intervention targets for promoting healthy aging.

12:45-12:50



**FLASH TALK: ELVINA PARLINDUNGAN**

Scientist, A\*STAR

**Exploring the Probiotic Potential of Lactic Acid Bacteria Strains Sourced from Asian Fermented Foods**

Lactic acid bacteria (LAB) are of great importance for food and health industries due to their technological and health beneficial properties. Due to their various benefits, LAB are used as functional food ingredients. However, not all LAB are probiotics and LAB should be evaluated for their probiotic attributes for potential future applications. In this project, untapped potential of novel LAB strains sourced from Asian Fermented Foods were explored.

12:50-12:55

**FLASH TALK:**  
 Poster presenters and start-up companies will be provided with the opportunity to give a flash 4-minute overview of their work



**KEYNOTE ADDRESS:  
ERAN ELINAV**

Professor and Principal Investigator, Department of Immunology, Weizmann Institute of Science, Israel  
**Host-Microbiome Interactions in Health and Disease**

The mammalian intestine contains trillions of microbes, a community that is dominated by members of the domain Bacteria but also includes members of Archaea, Eukarya, and viruses. The vast repertoire of this microbiome functions in ways that benefit the host. The mucosal immune system co-evolves with the microbiota beginning at birth, acquiring the capacity to tolerate components of the community while maintaining the capacity to respond to invading pathogens. The gut microbiota is shaped and regulated by multiple factors including our genomic composition, the local intestinal niche and multiple environmental factors including our nutritional repertoire and bio-geographical location. Moreover, it has been recently highlighted that dysregulation of these genetic or environmental factors leads to aberrant host-microbiome interactions, ultimately predisposing to pathologies ranging from chronic inflammation, obesity, the metabolic syndrome and even cancer. We have identified various possible mechanisms participating in the reciprocal regulation between the host and the intestinal microbial ecosystem, and demonstrate that disruption of these factors, in mice and humans, lead to dysbiosis and susceptibility to common multi-factorial disease. Moreover, we've recently uncovered that microbiome-associated compounds actively participate in regulation of the gut barrier function, as demonstrated in new human-relevant models of gut function. Furthermore, manipulation of this critical barrier function by administration of newly uncovered microbiome-modulating barrier stabilizers can prevent and treat a variety of microbiome-associated diseases, such as those impacting children with malnutrition. Collectively, understanding the molecular basis of host-microbiome interactions may lead to development of new microbiome-targeting treatments.

2:00-2:30



**KEYNOTE ADDRESS:  
SUNNY WONG**

Associate Professor, Nanyang Technological University, Singapore  
**Exploring the Gut Microbiome: A Link Between Obesity and Cancer Vulnerability**

This talk delves into the intricate relationship between the gut microbiome, metabolic conditions, and cancer risk. It explores how the composition and function of the gut microbiome contribute to chronic inflammation and metabolic dysfunction, fueling cancer development. The talk also highlights the direct impact of the gut microbiome on carcinogenesis through microbial metabolites, as well as its influence on systemic inflammation, hormonal regulation, and immune surveillance. Potential strategies to mitigate cancer risk by targeting the gut microbiome, such as probiotics, prebiotics, and fecal microbiota transplantation, are discussed. Attendees will gain an overview of current knowledge, research advancements, and future directions in unraveling the complex gut microbiome-metabolic conditions-cancer connection.

2:00-2:30

MICROBIOME THERAPEUTICS & BEYOND THE GUT



**JUN TERAUCHI**

Chief Scientific Officer, Metagen Therapeutics  
**FMT Based Microbiome Therapeutics Development in Japan**  
The clinical studies of Fecal Microbiota Transplantation (FMT) for ulcerative colitis have been conducted at

Juntendo University for almost 10 years with more than 200 patients' treatments. Based on these study data and outcomes, the pivotal study aiming to obtain official approval in Japan has started since 2023 by the collaboration between Juntendo University and Metagen Therapeutics (MGTx) under Advanced Medical Care Program B approved by the Ministry of Health, Labor and welfare in Japan. MGTX are trying to expand disease indications to other therapeutic areas, such as oncology and neurology. In this presentation, recent progress and future plans of FMT based microbiome therapeutics in Japan will be shared.

2:30-2:55



**ERIC HUANG CHUN-MING**

Senior Scientific Advisor, Zymolo Inc  
**Antioxidant-producing Electrogenic Bacteria as Bio-therapeutics**

Environmental electrogenic bacteria can utilize the process of extracellular electron transfer (EET) to transfer electrons from the bacterial cytosol to the extracellular space for the cycling of minerals and the degradation of biohazards. We have recently found that skin *Staphylococcus epidermidis*, which has functions like environmental electrogenic bacteria, can generate electrons as free radical scavengers, via a cyclophilin A-mediated pathway against ultraviolet (UV). Similarly, gut *Leuconostoc mesenteroides* yields tremendous electrons to reduce high-fat-diet (HFD)-induced formation of free radicals and decrease abdominal fat mass in mice. Gut *Lactobacillus plantarum* generated electricity to modulate the protein expression of gut tissue to enhance the epithelial colonization. Our previous studies have demonstrated that probiotic bacteria in skin or gut produced beneficial metabolites such as short-chain fatty acids. Here we highlight the role of electrons produced by bacteria in the human microbiome as novel therapeutics for treatments of skin and gut disorders.

2:55-3:20



**ANTONIO LC GOMES**

Principal Scientist, Xbiome  
**AI Implementation for Microbiome Secondary Metabolites Discovery and Therapeutics**

Natural products and their derivatives are an important source of therapeutics. The human microbiome is a large, mostly untapped source of small molecules. At Xbiome we use artificial intelligence and bioinformatics techniques to improve our ability to identify natural products with therapeutic potential, with particular interest in their synergistic potential in anti-tumor therapy.

3:20-3:45

PERSONALISED NUTRITION



**RATHA-KORN VILLAICHONE**

Professor of Medicine; Chief, Center of Excellence in Digestive Diseases, Thammasat University, Thailand  
**Interplay Role of Gut Microbiota in Pathogenesis and Management of GI Tract Diseases**

The human gut is complex microbial ecosystem composed of 100 trillion microorganisms. Gut microbiota plays dominant role in pathogenesis and therapy of many gastrointestinal (GI) tract diseases. Gut microbiota refers to the complex community of microorganisms including bacteria, viruses, and fungi living in GI tract. Key aspects of the pathogenesis including dysbiosis, inflammation, mucosal integrity and immune response. The current management including pre- pro and postbiotics, dietary modification, antibiotic, immunomodulators, fecal microbiota transplantation (FMT) and phage therapy. Understanding and recognition of interplay role between gut microbiota, host and GI tract diseases is a crucial aspect and need good quality future research. Personalized approaches or tailored therapy for unique microbiota composition for individual person are important for high quality and effective GI diseases management.

2:30-2:55



**WEI-KAI WU**

Assistant Professor/ Research Physician, National Taiwan University Hospital  
**Rediscovering Probiotics: From Functional Foods to Next-Generation Probiotics**

The link between gut microbiota, its metabolites, and human health is increasingly apparent, especially in relation to cardiometabolic diseases (CMD). Studies on allicin, found in raw garlic juice, demonstrate its positive effects on the gut microbiome, including reducing TMAO levels, enhancing microbial diversity, and increasing beneficial bacteria like *Akkermansia muciniphila* and *Faecalibacterium prausnitzii*. This suggests a novel preventative method for CMD. The evolving understanding of the gut microbiome's health impact has revived interest in probiotics. Traditional probiotics from fermented foods are now complemented by next-generation probiotics (NGPs) such as *Akkermansia muciniphila*, *Anaerobutyricum soehngenii*, and *Parabacteroides merdae*. These NGPs show potential in metabolism regulation, immune enhancement, and providing therapeutic benefits for obesity and cancer immunotherapy. We propose establishing a native strain biobank of NGPs, focusing on genetic and phenotypic profiling. We're exploring innovations like postbiotics and paraprobiotics to address the risks associated with live NGPs. Our research supports a holistic approach, combining functional foods and NGPs for personalized health solutions.

2:55-3:20



**PATRICIA CONWAY**

CEO & Founder, PC Biome Pte Ltd and Visiting Professor, Singapore Centre for Environmental Life Sciences Engineering (SCELSE), Nanyang Technological University  
**Single strains or multiple strains in a probiotic preparation -**

**Do we need more than one strain?**  
The field of probiotics is rapidly evolving and at times perhaps driven more by the marketing statements rather than the science. While there is evidence to support specific strains used in single strain preparation, there is an emerging trend for products to contain multiple strains in the one preparation, without evidence of efficacy of the combination. The objective of this presentation is to address the issue of whether more strains in a preparation makes it a "better probiotic" than a preparation based on a single strain. This question will be addressed by using two examples: (1) a clinical study in extremely preterm

3:20-3:45

3:20-3:45

Continued

3:20-3:45

infants in which a single strain dosage of Bifidobacterium was compared to a triple strain Bifidobacterium mix; (2) a study in adults in which two single strains of probiotic were compared. The infant study was carried out because evidence from systematic reviews suggests that multi-strain probiotics may benefit enteral nutrition more than single-strain probiotics in preterm infants. There are limited data on the effect of multi-strain probiotics on the microbiome and its metabolites, especially in extremely preterm infants. The infants were assessed in terms of the time taken for these extremely pre-term infants to reach full feed. It was shown that the time to full feed in the infants was similar between the single strain and the triple strain mix. In addition, both probiotics were effective in reducing dysbiosis (higher bifidobacteria and lower Gammaproteobacteria) and impacting on the microbiome metabolites, the short chain fatty acids. This study provides evidence that a single strain of an efficacious Bifidobacterium is as effective as a mixture of three strains of Bifidobacterium. The adult study compared a single strain of Lactobacillus fermentum to a Lactobacillus acidophilus for benefits on gut health in travellers. The incidence and severity of gut disturbances was assessed. There was a reduction in the incidence and severity of gut disturbances for those receiving the L. fermentum strain but not the L. acidophilus strain. This study provides evidence to support published literature that single strain of Lactobacillus can provide health benefits, and that it is specific for the strain of probiotic being used for a particular application. It is concluded that a single strain probiotic can be efficacious, but that the specific strain of probiotic being used will influence the outcome.

3:45

Closing Remarks / End of Day 2



## MAKING A POSTER PRESENTATION – CLOSING DATE 12<sup>TH</sup> APRIL 2024

Poster presentation sessions will take place in breaks and alongside the other breakout sessions of the conference. Your presentation will be displayed in a dedicated area, with the other accepted posters from industry and academic presenters.

We also issue a poster eBook to all attendees containing your full abstract, and you can share your poster as a PDF after the meeting if you desire (optional).

Whether looking for funding, employment opportunities or simply wanting to share your work with a like-minded and focused group, these are an excellent way to join the heart of this congress.

In order to present a poster at the forum, you need to be registered as a delegate. Please note that there is limited space available and poster space is assigned on a first-come-first-served basis (subject to checks and successful registration).

**NEW for 2024** – We have reserved a 10 minutes session in both tracks across two-days for non-vendor authors to present a flash presentation of their poster in order to showcase their work.

### Submission instructions

We will require the form (downloadable which can be downloaded from the website [www.global-engage.com/event/microbiome-asia](http://www.global-engage.com/event/microbiome-asia) to be submitted by 12<sup>th</sup> April 2024 to enter the competition. This is the formal deadline however space is another limiting factor so early application is recommended. Therefore please contact us with any questions you have as soon as possible.





### Optimize your microbiome workflow with the right standards

Your work is important—you don't have the time or resources to waste on culturing tens to hundreds of microbes.

Give yourself, your team, and your budget a break with ready-to-use controls from ATCC.

- ③ **Molecular standards** - Quantitative genomic and synthetic DNA and RNA representing hundreds of credible reference strains of relevant microbes.
- ③ **NGS standards** - Mock microbial communities available in a variety of formats and levels of complexity to challenge your assay standardization process.

**Visit us online at [www.atcc.org/ngs-standards](http://www.atcc.org/ngs-standards) to skip in vitro culturing and get straight to your assay and process development.**



**ATCC | Credible leads to Incredible®**

Authorized Distributor  
  
 Enabling Better Outcomes

©2024 American Type Culture Collection. The ATCC trademark and trade name, and any other trademarks listed in this publication are trademarks owned by the American Type Culture Collection unless indicated otherwise.