5\textsuperscript{th} MICROBIOME R&D & BUSINESS COLLABORATION CONGRESS

4\textsuperscript{th} PROBIOTICS CONGRESS: ASIA

REGENT TAIPEI, TAIWAN
— 6 - 7 March 2019 —

Co-Hosts

National Central University

National Chiao Tung University

GLORIA

Global Research & Industry Alliance

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Global Engage is pleased to announce, as part of their worldwide microbiome series, the 5th Microbiome R&D and Business Collaboration Congress and co-located 4th Probiotics Congress which will be held on March 6-7, 2019 at the Regent Taipei, Taiwan. Co-hosted with the National Central University and National Chiao Tung University (GLORIA) of Taiwan, the congresses will bring together industry and academic delegates to discuss the latest microbiome research, the development of partnerships and commercial collaborations in this area and the expected growth of product pipelines.

Recent microbiome research has demonstrated the important role that communities of microorganisms play on human body. This area of research, associated with immunity and behavioural traits, is paramount in maintaining our health and keeping us away from disease. With numerous pre-clinical and clinical studies being conducted, microbiome is transitioning from a descriptive to a more mechanistic science. It is inevitable that microbiome is a promising prospect to improve human health, as it enables us to step forward and manipulate microbiota in a variety of ways. With the growing interest in the area, research experts and industry players are working together towards bringing microbiome discoveries to the market, making it an unprecedented investment opportunity alongside large-scale collaborations underway and sequencing data placed in the public domain. Due to this reason, microbiome is now set to make waves in the science and medical world as an essential prerequisite for future rational interventions.

Attracting over 300 delegates, the co-located meetings will promote comprehensive understanding and reciprocal benefits of the latest scientific and business developments in microbiome and probiotics. The 2-day interactive meeting will highlight cutting edge research and business case studies through expert presentations, and panel discussions exploring key issues in the subject area, an exhibition filled with solution providers showcasing their products and solutions, as well as networking breaks to promote interactions and business reach with fellow peers.

Having a diverged group of professionals interested in microbiome and probiotics, both scientific and industry talks will take place at this event. Topic areas to be addressed include microbiome in health and disease, skin microbiome, probiotics and brain health amongst others as well as the regulatory issues associated with these areas of research. It is hoped that the meetings will further develop the microbiome and probiotics research, as well as foster more collaborations and commercialisation of the areas in Asia.
MICROBIOME DISCOVERIES
- Latest updates on the microbiome movement in Asia and across the globe
- Tools and techniques for studying microbiome
  - Metagenomics
  - Sequencing method / bioinformatics

MICROBIOME IN HEALTH AND DISEASE
- Relationship between obesity and metabolic disease
- Inflammation
- Gut-brain axis
- Enteric infection/microbiome pathogen interactions
- Case studies such as IBD, diabetes, obesity, colitis
- Antibiotics resistance
- Infant gut microbiome

MICROBIOME-BASED THERAPIES
- Drug delivery
- Faecal microbiome transplant
- Biomarker / Clinical Development

OUTSIDE THE GUT
- Skin microbiome
  - Strategies and tools for studying skin microbiome
  - Case studies on acne, eczema, atopic dermatitis, wound health & cosmetic applications
- Women’s health
  - Host-interactions, vaginal microbiome, preterm birth and pregnancy progression
- Gut-brain axis
- Oral and respiratory microbiome research

COMMERCIALISATION OF MICROBIOME AND PROBIOTICS
- Developing business relationships between academia & pharma
- Collaborations/partnerships – the global scope of microbiome research/structuring successful collaborations
- Bringing live microbial products to market – IP, regulation, GMP
- Pharmaceutical involvement and therapeutic development
- Probiotic strain identification, designation and safety

PROBIOTICS R&D
- Strain discovery
- Gut-pathogen interactions
- Role of probiotics in IBS management
- Antibiotic exposure & multidrug resistance
- Role of probiotics as anti-diarrhoeal agents
- Efficacy and effectiveness of different strains
- Biocontrol of gut pathogens with probiotics
- Probiotics and the gut-brain axis
- Probiotics and skin
- Probiotics and allergy / disease
- Food and fermentation

PAEDIATRICS
- Milk-oriented microbiota
- Atopic eczema
- Probiotic and trial safety in infant populations
- A role for probiotics in malnutrition and the developing world

WOMEN’S HEALTH
- Reducing the recurrence of urogenital infections in women
- Probiotics in bacterial vaginosis
- Vaginal microbiome

REGULATION AND PRODUCT DEVELOPMENT
- Examining the probiotic market in the Asia-Pacific region
- Safety and QC
- Strain identification, designation and safety
- IP, regulation and GMP perspective
- Clinical trials and health claim substantiation
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CONFIRMED SPEAKERS

JACK GILBERT
Faculty Director, The Microbiome Center and Professor, Department of Surgery, University of Chicago, USA | Founder, The Earth Microbiome Project and Co-Founder, American Gut Project

MARK MORRISON
Chair and Professor, Microbial Biology and Metagenomics, University of Queensland Diamantina Institute, Australia

NICOLE ROY
Principal Scientist and Science Team Leader, AgResearch, New Zealand

BAOLI XU
Principal investigator and Director of Microbial Genome Research Center, The Institute of Microbiology and Chinese Academy of Sciences, China

CÉCILE CLAVAUD
Project Leader, Research and Innovation Skin Microbiome Unit, L’Oreal, France

YUNN HWEN GAN
Associate Professor, National University of Singapore, Singapore

JQ LIU
Principal Scientist, Procter & Gamble, Singapore

TZEHAU LAM
Senior Scientist, Procter & Gamble, Singapore

CHRISTOPHE LAY
Senior Scientist, Gut Microbiota, Danone Nutricia Research, Singapore

MARGARET MORRIS
Professor and Head of Pharmacology, University of New South Wales, Australia

LARRY WEISS
CEO and Founder, Persona Biome

YI-BING LIN
Vice Chancellor, University System of Taiwan, National Chiao-Tung University, Taiwan

JACQUES RAVEL
Professor, Microbiology and Immunology and Associate Director for Genomics, Institute for Genome Sciences, University of Maryland School of Medicine, USA

FELICE N JACKA
Professor and Director, Food and Mood Centre, IMPACT SRC, Deakin University, Australia and President, International Society for Nutritional Psychiatry Research

HAZEL MITCHELL
Professor, University of New South Wales, Australia

SHAHRUL RAZID
Dean, Faculty of Agricultural and Food Sciences, University Putra Malaysia

NIRANJAN NAGARAJAN
Senior Group Leader, Genome Institute of Singapore, Singapore

NIKLAS LARSSON
Research Director, Probi AB, Sweden

JAMES CHU
CEO of GLORIA, National Central University, Taiwan

JOHN COMMON
Principal Investigator, Skin Research Institute of Singapore (SRIS), Singapore

YOSHIHISA YAMASHITA
Professor and Chairperson, Section of Preventive and Public Health Dentistry, Division of Oral Health, Growth and Development, Kyushu University Faculty of Dental Science, Japan

DEV MITTAR
Lead Scientist and Head of R&D ATCC, USA

CHUN-MING ERIC HUANG
Chair Professor, Department of Biomedical Sciences and Engineering, National Central University, Taiwan

ELIANA MARINO MORENO
Principal Research Fellow and Immunology and Diabetes Laboratory Head, School of Biomedical Sciences, Monash University, Australia

WEI-LI WU (Chair)
Assistant Professor, Department of Physiology, College of Medicine, National Cheng Kung University, Taiwan

UMA DEVI A/P PALANISAMY (Chair)
Associate Professor, Monash University, Malaysia

NIKLAS LARSSON
Research Director, Probi AB, Sweden
CONFIRMED SPEAKERS

ANDERS HENRIKSSON
Principal Application Specialist, DuPont Nutrition & Health, Australia

NAGENDRA SHAH
Professor, Functional Food, Hong Kong University, Hong Kong

JOHAN VAN HYLCKAMA VLIEG
Vice President Microbiome & Human Health Innovation, Chr. Hansen A/S, Germany

MING-JU CHEN
Professor, Department of Animal Science and Technology, National Taiwan University, Taiwan

YING-CHIEH TSAI
Professor, Institute of Biochemistry and Molecular Biology, National Yang-Ming University, Taiwan

HANNA SIDJABAT
Honorary Fellow and Chief Investigator, University of Queensland Centre for Clinical Research, Australia

GWANG PYOKO
Professor, School of Biological Sciences, Seoul National University, Korea

YASUHIRO KOGA
President, Japanese Society for Probiotic Science

JIN-ZHONG XIAO
General Manager, Next Generation Sequencing Institute, Morinaga Milk, Japan

GREGORY LAMBERT
CEO, TargEDys, Netherlands

PATRICIA CONWAY
Visiting Professor, Nanyang Technology University (NTU), Singapore

REBECCA SLYKERMAN
Clinical Neuropsychologist and Senior Research Fellow, University of Auckland, New Zealand

TOH MINGZHAH
Research Fellow, Food Science & Technology Programme, Department of Chemistry, National University of Singapore

LEE YEONG YEH
Professor of Medicine & Consultant of Gastroenterology, Hepatology & Internal Medicine, Universiti Sains Malaysia

JIN-SENG LIN
Director, Culture Collection and Research Institute Synbio Tech Inc., Taiwan
**KEYNOTE PRESENTATION:**

**JACK GILBERT**
Faculty Director, The Microbiome Center and Professor, Department of Surgery, University of Chicago, USA/ Founder, The Earth Microbiome Project and Co-Founder, American Gut Project

**Invisible Influence: The Microbiome and Human Health**
The human microbiome is quickly being recognized as a dynamic part of the human ecosystem, and research is starting to demonstrate that using ecology to understand this ecosystem has profound benefits for patient wellness. The immune system controls our interaction with the microbial world, and yet the microbial communities in our bodies are central to modulating the immune response. Changes in the human microbiome have substantial influence on atopy, neurological disorders, metabolic disorders, and a range of complex conditions and disease states. We will discuss evidence of these mechanisms of interaction and how we have started to disturb the delicate balance of the immune-microbe equilibrium, impacting the development and function of our immune systems. Central to this disturbance is the distance we have placed between our children and the microbial world, which has been demonstrated to have a substantial influence on their physiological, immunological, neurological and even endocrinological development. Applying new strategies to identify how the microbial ecosystem correlates with diseases states and treatment efficacy through Microbiome-Wide Association Studies (MWAS) is altering the trajectory of precision medicine, and providing a new framework for facilitating patient care.

**KEYNOTE PRESENTATION:**

**CHUN-MING ERIC HUANG**
Chair Professor, Department of Biomedical Sciences and Engineering, National Central University, Taiwan

**Microbiome Banking and Editing with Electro-biotics**
A commercial stool bank by collecting human gut microbiota is available in the market. Efforts from our group are devoted to establish a “Skin Microbiome Bank” for development of novel skin probiotics and/or prebiotics. The microbes within a human microenvironment may compete with each other for the same carbon source of fermentation. Microbiome editing by targeting individual bacterial species in the microbiome using bacteria-specific carbon source is our strategy to restore a health-associated microbiome after dysbiosis. The conjugates of carbohydrates and polymers provide unique carbon sources (prebiotics) for specific skin probiotic bacteria. Our recent results have demonstrated that skin bacteria can yield electricity during the bacterial fermentation. By using electrogenic bacteria, we develop new technology derived from the concept of probiotic-prebiotic-postbiotic-“electrobiotic”. Next-generation sequencing (NGS), although it is a new approach to biomarker identification, may not be able to dynamically detect the dysbiotic microbiome. We here introduce the technology of “electrobiotic” for profiling and monitoring the skin dysbiosis in real time.

**GLOBAL ENGAGE WELCOME ADDRESS AND MORNING CHAIR’S OPENING REMARKS:**

**REBECCA SLYKERMAN**, Clinical Neuropsychologist and Senior Research Fellow, University of Auckland, New Zealand

**JOHAN VAN HYLCKAMA VLIEG**
Vice President, Microbiome & Human Health Innovation, Chr. Hansen A/S, Germany

**Microbes matter more than ever – Innovation in probiotics in the microbiome era**

**SOLUTION PROVIDER PRESENTATION:**

**SENIOR REPRESENTATIVE**
Winclove

Title TBC

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Tel: +603 2117 5193
Dietary tools for shaping the gut microbiome

There is a substantial pool of data on the gut microbiome, which plays a crucial role in human health and disease. The gut microbiome is composed of trillions of microorganisms that inhabit the intestines, and it has been linked to various health conditions, including obesity, inflammatory bowel disease, and type 2 diabetes. The gut microbiome is influenced by a variety of factors, including diet, genetics, and lifestyle. Recently, there has been growing interest in using dietary tools to modulate the gut microbiome in order to improve health outcomes.

For example, prebiotics are dietary fibers that are selectively fermented by the gut microbiota, leading to increased production of short-chain fatty acids (SCFAs) and functional metabolites. SCFAs are known to have beneficial effects on gut health, including improving gut barrier function and reducing inflammation. Similarly, probiotics are live microorganisms that, when administered in adequate amounts, confer a health benefit on the host. Probiotics have been shown to enhance immune function, reduce inflammation, and improve gut barrier function.

In conclusion, the gut microbiome is a complex ecosystem that is highly influenced by dietary factors. By using dietary tools, such as prebiotics and probiotics, we can modulate the gut microbiome to promote health and prevent disease.

References:
### Microbiome in Health & Diseases

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<tr>
<td>12:40-13:10</td>
<td><strong>BAO LI XU</strong>&lt;br&gt;Principal investigator and Director of Microbial Genome Research Center, The Institute of Microbiology and Chinese Academy of Sciences, China</td>
<td><strong>Title TBC</strong></td>
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<td>13:10-14:10</td>
<td><strong>YUNN HWEN GAN</strong>&lt;br&gt;Associate Professor, National University of Singapore, Singapore</td>
<td><strong>Factors affecting gut colonization and pathogenesis of hypervirulent Klebsiella pneumoniae, the causative agent of liver abscesses disease</strong>&lt;br&gt;Hypervirulent Klebsiella pneumoniae is an emerging cause of community-acquired pyogenic liver abscesses in parts of Asia such as South Korea, Singapore, Taiwan and Hong Kong. Hypervirulent isolates are generally hypermucoviscous with the possession of a large virulent plasmid encoding demonstrating effects of a range of dietary components on composition of the gut microbiome. This presentation will elaborate on:&lt;br&gt;• The effects of different dietary proteins on the composition of gut microbiota, as well as reported health benefits of the such proteins.&lt;br&gt;• The role of human milk oligosaccharides in establishing an optimal microbiota early on in life, and&lt;br&gt;• Probiotics, which may deliver significant benefits even in the presence of a well-established gut microbiome.</td>
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### Skin Microbiome

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<td>12:40-13:10</td>
<td><strong>NIRANJAN NAGARAJAN</strong>&lt;br&gt;Senior Group Leader and Associate Director, Genome Institute of Singapore, A*STAR, Singapore</td>
<td><strong>Skin Microbiome and Eczema</strong></td>
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### R&D - Food & Diseases

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<td>12:40-13:10</td>
<td><strong>NIKLAS LARSSON</strong>&lt;br&gt;Research Director, Probi AB, Sweden</td>
<td><strong>Probi Osteo® protects against bone loss at lumbar spine in healthy early postmenopausal women</strong>&lt;br&gt;In a recently conducted clinical study, Probi Osteo®, a combination of three probiotic bacteria from Probi, was shown to reduce the bone loss at lumbar spine in a population of early post-menopausal women. Bone health was measured as bone mineral density at lumbar spine by dual energy X-ray absorptiometry. It was shown that intake of the probiotic product for 12 months resulted in significantly less bone loss as compared to placebo (p&lt;0.05). The difference between the groups was even more prominent in women with osteopenia and those with less than 6 years from the start of menopause.</td>
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### Luncheon / Poster Presentations / One-to-One Meetings

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contribute also to reinforce the skin barrier function (tight junctions, elicitation of antimicrobial peptides) and repair. Thus it is essential to understand how its disequilibrium contributes to skin conditions as for example scalp condition. Dandruff is one of the most common scalp conditions, affecting approximately half of adult population worldwide. This inflammatory chronic disorder is related to skin barrier disruption, epidermal cellular proliferation and differentiation, as well as shifts in sebum composition. It has been frequently associated with yeasts from Malassezia genus, which are also members of the healthy cutaneous microbiome. However, the microbial role has not been elucidated yet, and the etiology of the disorder remains incompletely understood. We used sanger and next-generation sequencing (NGS) to analyze bacterial and fungal microbiota associated with skin from normal and dandruff subjects. Microbial shift in bacterial and fungal communities were observed in lesional and in non-lesional sites from dandruff subjects, suggesting that dandruff is related to a systemic process that is not restricted to the site exhibiting clinical symptoms. Our recent studies on dandruff scalp microbiota provides new perspectives for the understanding of this disorder, establishing steps toward a broader view of scalp health and the role of the microbiome in the symptom development.

Disequilibrium contributes to skin conditions as for example scalp condition. Dandruff is one of the most common scalp conditions, affecting approximately half of adult population worldwide. This inflammatory chronic disorder is related to skin barrier disruption, epidermal cellular proliferation and differentiation, as well as shifts in sebum composition. It has been frequently associated with yeasts from Malassezia genus, which are also members of the healthy cutaneous microbiome. However, the microbial role has not been elucidated yet, and the etiology of the disorder remains incompletely understood. We used sanger and next-generation sequencing (NGS) to analyze bacterial and fungal microbiota associated with skin from normal and dandruff subjects. Microbial shift in bacterial and fungal communities were observed in lesional and in non-lesional sites from dandruff subjects, suggesting that dandruff is related to a systemic process that is not restricted to the site exhibiting clinical symptoms. Our recent studies on dandruff scalp microbiota provides new perspectives for the understanding of this disorder, establishing steps toward a broader view of scalp health and the role of the microbiome in the symptom development.

Nutritional intervention could be harnessed as a mean to reduce the disease risk associated with a compromised microbiome. In Singapore and many parts of the world, K1 and K2 capsular types are the predominant hypervirulent isolates. In Klebsiella induced liver abscess (KLA), colonization by the bacteria is believed to precede translocation from the intestines to the liver. However, factors which predispose and facilitate the colonisation in the gut are not clearly defined. In our oral infection mouse model with a K1 capsular type, hypervirulent K. pneumoniae, we examine the role of probiotics administration after antibiotics treatment, as well as the role of capsule and fucose usage for efficient gut colonization. I shall discuss our results on each of these aspects as well as other factors that could contribute to the ability of the bacteria to establish an intestinal niche.

The results on each of these aspects as well as other factors that could contribute to the ability of the bacteria to establish an intestinal niche.
JOHN COMMON
Institute of Molecular Biology, A*STAR, Singapore
Skin microbiome signatures in health and disease correlate with host immunity and microbial virulence
The skin is a challenging ecosystem to study meta-omics due to the low amount of biomass that can be recovered, which limits downstream techniques that are currently feasible on human subjects. We have recently been using metagenomics to investigate microbial communities present on the skin of atopic dermatitis patients to better understand shifts in community diversity and microbial functional characteristics. We can identify skin microbiome dermotypes that stratify groups of AD patients and observed that these groups correlate with host immunity and microbial virulence.

JIN-SENG LIN
Director, Culture Collection and Research Institute, SYNBIO TECH INC., Taiwan
Microbiome, Probiotics and Exercise Performance
The human gut harbors a vast array of microorganisms that significantly affect host nutrition, metabolic function, gut development, and maturation of the immune system and epithelial cells. Recent studies also shown that gut microbiota may have a key role in controlling the oxidative stress and inflammatory responses as well as improving metabolism and energy expenditure during intense exercise. Then modifying the microbiota through the use of probiotics could be a promising tool to improve exercise performance and energy availability. In this study we examined the effects of L. plantarum TWK10 (LP10) supplementation on exercise performance, physical fatigue, and gut microbial profile. Male Institute of Cancer Research (ICR) strain mice were divided into three groups (n = 8 per group) for oral administration of LP10 for six weeks at 0, 2.05 X 10^8, or 1.03 X 10^9 colony-forming units/kg/day, designated the vehicle, LP10-1X and LP10-5X groups, respectively. LP10 significantly decreased final body weight and increased relative muscle weight (%). LP10 supplementation dose-dependently increased grip strength (p < 0.0001) and endurance swimming time (p < 0.001) and decreased levels of serum lactate (p < 0.0001), ammonia (p < 0.0001), creatine kinase (p = 0.0118), and glucose (p = 0.0151) after acute exercise challenge. The number of type I fibers (slow muscle) in gastrocnemius muscle significantly increased with LP10 treatment. In addition, serum levels of albumin, blood urea nitrogen, creatinine, and triacylglycerol significantly decreased with LP10 treatment. Long-term supplementation with LP10 may increase muscle mass, enhance energy harvesting, and have health-promotion, performance-improvement, and anti-fatigue effects.
Psoriasis is a chronic immune-mediated inflammatory skin disease that affects about 2% of the world’s population. It arises in genetically predisposed individuals. Both the skin and the gut microbiome influence the development and function of immune system. Studies on the cutaneous microbiome show a trend toward an increased relative abundance of Streptococcus and a decreased level of Propionibacterium in patients with psoriasis compared to healthy controls. In the gut microbiome, the ratio of Faecalibacterium prausnitzii and Escherichia Coli (F:E index) was perturbed in psoriatic individuals compared to healthy controls. Modulating the gut and skin microbiota can be beneficial in psoriasis.
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<td>08:55-09:00</td>
<td><strong>KEYNOTE PRESENTATION:</strong> JUN WANG (Reserved)</td>
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<td>CEO, iCarbonX, China</td>
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<td>09:00-09:30</td>
<td><strong>KEYNOTE PRESENTATION:</strong> YASUHIRO KOGA</td>
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<td>President, Japanese Society for Probiotic Science</td>
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<td>Prevention of periodontal diseases by an oral probiotic strain, Lactobacillus salivarius TI2711 (LS1)</td>
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<td>The susceptibility of the host, the presence of pathogenic bacteria and the absence of “beneficial bacteria” are the main etiological factors of periodontal diseases. We have isolated Lactobacillus salivarius TI2711 (LS1) as an oral probiotic strain. Porphyromonas gingivalis is considered a major pathogenic bacterium causing periodontal diseases. LS1 completely killed P. gingivalis in a co-culture system at an input ratio of one to one-million. In a clinical study where subjects were daily administered 2x10⁹ CFU LS1 for 4 weeks, the number of P. gingivalis in the subgingival plaque decreased to about one-tenth after 4-week-treatment.</td>
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<td>09:30-10:00</td>
<td><strong>SPONSORED PRESENTATION:</strong> JIN-ZHONG XIAO</td>
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<td>Director, Next Generation Sequencing Institute, Morinaga Milk, Japan</td>
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<td>Insight into the reason of being of Bifidobacterium in human gut</td>
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<td>Bifidobacterium is one of the major members of the human intestinal microbiota which comprises thousands of bacterial species. The genus Bifidobacterium has been known to contain &gt; 60 species/subspecies. Some of these bifidobacteria species are typical inhabitants of the human gut (designated as human-residential bifidobacteria, HRB) whereas others naturally colonise the guts of other animals (designated as non-HRB). This presentation will make some insight into the reason of being (how and why) of Bifidobacterium inhabiting the human gut, based on our new findings from genotypic and physiological studies.</td>
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<td>10:00-10:30</td>
<td><strong>SPONSORED PRESENTATION:</strong> FELICE N JACKA</td>
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<td>Professor and Director, Food and Mood Centre, IMPACT SRC, Deakin University, Australia and President, International Society for Nutritional Psychiatry Research</td>
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<td>The therapeutic potential of diet and the gut microbiota in brain and behaviour</td>
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<td>With mental disorders the leading source of disability globally, the identification of new targets for prevention and management is imperative. A rapidly emerging field of research suggests that the microbiome-gut-brain axis is of substantial relevance to mood and behaviour. Similarly, unhealthy diet has recently emerged as a significant correlate of and risk factor for depression. This presentation will address the evidence for the gut microbiota as a key factor mediating the link between diet and mental illnesses and focuses on the potential of gut-focused interventions for the prevention and treatment of such disorders. The development of new technologies is affording a better understanding of how diet influences gut microbiota composition and activity and how this may, in turn, influence mental illness. New evidence is also pointing to the utility of diet in influencing mental health. Although in its early stages, the emerging field of research focused on the human microbiome suggests an important role for the gut microbiota in influencing brain development, behaviour and mood in humans. The recognition that the gut microbiota interacts bi-directionally with other environmental risk factors, particularly diet, suggests promise in the development of interventions targeting the gut microbiota for the prevention and treatment of mental health disorders.</td>
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<td><strong>PANEL DISCUSSIONS:</strong> A Step to Commercialisation: Building a Microbiome Network between Academics and Industry for Microbiome Discovery Efforts</td>
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<td>JACK GILBERT</td>
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<td>Faculty Director, The Microbiome Center and Professor, Department of Surgery, University of Chicago, USA / Founder, The Earth Microbiome Project and Co-Founder, American Gut Project</td>
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<td>11:35-12:10</td>
<td><strong>PANEL DISCUSSIONS:</strong> Towards Preventive Measures: Exploring the Current Market Trends and Regulatory Approach on Probiotics Use in Asia</td>
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<td>Morning Chair’s Opening Remarks: Lee Yeong Yeh, Professor of Medicine &amp; Consultant of Gastroenterology, Hepatology &amp; Internal Medicine, Universiti Sains Malaysia</td>
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ALTERATION in the production of microbial associated with altered gut microbiota or T2D and many inflammatory diseases are strongly linked.

The globally rising incidence of T1D and T2D and many inflammatory diseases are strongly linked.

**Diet and Gut Microbiota in Diabetes**

**Fighting Fire with Fiber: The role of**

Monash University, Australia

**Dietary modulation of the gut microbiome and behaviour – can we intervene?**

Our work has demonstrated that rats fed an obesogenic, cafeteria style diet consistently show deficits in hippocampal dependent memory tasks, and reduced diversity of their gut microbiome compared to control rats. Such behavioural deficits were independent of weight differences, as rats consuming diets high in saturated fat or high in sugar, for just two weeks, had impaired spatial memory even while consuming similar amounts of energy as control rats on a regular diet. We found that the memory deficits were associated with changes in the gut microbiota composition and genes related to inflammation in the hippocampus, which is a key brain region for memory and learning. More recently we have investigated whether the bacteriostatic antibiotic, minocycline, which is reported to exert anti-inflammatory effects, can modulate spatial memory. Again, the cafeteria diet produced persistent deficits in spatial memory (novel place recognition) that were prevented by minocycline cotreatment. Of interest, chow rats treated with minocycline performed worse than those treated with vehicle. Faecal microbiota alpha diversity was reduced by both cafeteria diet and minocycline, but these reductions were not associated with changes in the gut microbiota composition and genes related to inflammation on the novel place task. However, abundances of specific OTUs within Bacteroides and Lactobacillus were associated with place task performance. Together, studies such as these suggest the gut microbiota could play a causal role in regulating behaviour. Current experiments are exploring the impact of faecal transfer on memory performance in rats consuming the obesogenic diet.

**The vaginal microbiota: Translating microbiome science to novel therapies, a path forward**

The vaginal microbiota forms the first line of defence against sexually transmitted infection (STIs). Population-based surveys of the bacteria inhabiting the vagina have shown that several kinds of vaginal microbiota exist, that differs in bacterial composition and abundance. Further, in some women, these communities are dynamic and can change over short period of time, while in other, they are highly stable and do not change. The impact of both composition and dynamic of the vaginal microbiota on women’s health and the susceptibility to diseases is becoming clearer through the application of modern genomic technologies, ecological principles and in vitro modelling. Our understanding of the interactions between the vaginal microbiota, the host and diseases has grown and now affords the rationale selection of consortium of bacteria, mimicking beneficial vaginal microbiota that could form the basis of novel and personalised strategies to maximize a woman’s first line of defence, and women’s health in general. Translational research and well-powered clinical trials are desperately needed to validate these approaches. Manipulation of the vaginal microbiota has the potential to change the way clinicians approach women’s health and preventive care, as well as empower women to protect themselves.

**Shaping body weight through manipulating gut microbiome with probiotics**

Shaping body weight through manipulating gut microbiome with probiotics

Surprisingly, two kefir probiotics, Lactobacillus plantarum APS1 (APS1) and L. kefiranofaciens M1 (M1), exhibited completely opposite results in anti-obesity. APS1 manipulated the gut microbiome's obesity-associated

**Microbiome and Diet**

**Microbiome Outside the Gut**

**Probiotics – Health & Diseases**

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Short-chain fatty acids (SCFAs). SCFAs are produced in the large bowel through bacterial fermentation of dietary fiber and play an important role in maintaining gut mucosal integrity and a balanced gut microbiota ecology. SCFAs, particularly acetate and butyrate, show beneficial immunomodulatory effects contributing to the prevention of inflammatory and autoimmune diseases. A change in diet towards processed food, high in fat and meat protein, can significantly alter the composition of gut microbiota and adversely affect the intestinal immune system that can lead to metabolic dysfunction. The gut microbiota produces short chain fatty acids (SCFAs), which have been reported to exert a wide range of anti-inflammatory benefits. We showed that alterations in diet and gut microbial ecology underlie the pathogenesis of type 1 diabetes (T1D). In the non-obese diabetic (NOD) mouse, we found high concentrations of bacterial metabolites acetate and butyrate in blood and faeces correlated with protection from disease. We employed specialised high-acetate- and butyrate-yielding diets, which also significantly increased number of Tregs, reduced the frequency and number of auto-reactive CD8+ T cells, correlated with changes in intestinal microbial composition and diversity and improved gut epithelial integrity.

High amount-producers of ALD in vitro, no information is available regarding oral microbiota profiles related to ALD production. The salivary microbiota from 100 healthy males were classified into two types of communities (A and B) using 16S rRNA gene sequencing. ALD production was significantly higher in the type A community, while relative abundance of Neisseria species was significantly lower in this type community. Even if adjusted for alcohol drinking and total amounts of salivary bacteria, the subjects with type A microbiota exhibited a significantly higher ALD production, as compared with those with type B microbiota. In addition, the relative abundance of Neisseria was negatively correlated with the acetaldehyde production (P = 0.001). We concluded that the salivary microbiota from South-East Asia, containing about 60 % resistant starch. The Asian region also offers plentiful herbs and spices that are available in Asia. An interesting source is sago starch, which is derived from palm (Metroxylon sagu) indigenous plants that are available in Asia. An interesting source is sago starch, which is derived from palm (Metroxylon sagu) indigenous to South-East Asia, containing about 60 % resistant starch. Some in vitro and in vivo studies have demonstrated the ability of sago starch to increase numbers of Lactobacillus and Bifidobacterium. Studies on the effects of resistant starch on the glycemia index, insulin responses, and satiety have been continuously progressing, proving its role as a functional food. The Asian region also offers plentiful herbs and spices that are used as traditional medicines since ancient times. Most are due to their bioactive compounds i.e. polyphenols or flavonoids. Most polyphenols are of low bioavailability, where their influence on health may be either through intestinal absorption or interaction with colonic microbiota. Root of turmeric (Curcuma longa) is widely used as condiment in Asian food as well as a traditional remedy in Chinese and Indian Ayurvedic medicine. The curcuminoid are metabolised by colonic microbiota, modulating the bacterial population and their metabolic activity.

Metabolites, followed by regulation of lipid metabolism, enhancement of energy expenditure and inhibition of appetite. The specific hepatic metabolites induced by the APS1-manipulated gut microbiome also contributed to the amelioration of hepatic steatosis. While, M1 showed a reversed mechanism leading to higher body weight gain and body fat than their HFD counterparts. Our findings highlighted a possible microbiome and metabolome that contributed to shape the body weight and suggested that probiotics could serve as a potential therapy for modulating physiological function and downstream of the microbiota.
LARRY WEISS  
CEO and Founder, Persona Biome  
How can we talk about health care when we don’t understand health and we don’t care?  
The emerging science of the microbiome is still in its infancy yet it is the driving force behind a transformative scientific revolution. What lies ahead will have broad implications for us as scientists, our companies and academic institutions, our health, and perhaps for our survival. It is worth reflecting on where we are today, how we got here, what we have learned so far, and the limitations of our methods and of our vision. I will discuss what we are learning about our biological past by studying the microbiota of minimally impacted hunter-gatherers in the Amazon and how it is challenging our deeply held ideas about human health that may inform our path forward.

DEV MITTAR  
Lead Scientist and Head of R&D ATCC, USA  
Development and evaluation of site-specific standards for gut, skin, oral, and vaginal microbiome studies  
The human microbiome is a rapidly growing field of research with the potential to become one of the most important tools for personalized health and precision medicine. To date, a significant body of work has been performed on the human gut microbiome to evaluate its species composition and influence on physiology; this research has led to additional studies on microbiomes localized at other sites on the human body (e.g., skin, oral, vaginal). However, a predominant limitation in these site-specific microbiome studies is the lack of appropriate and relevant standards to control the technical biases introduced throughout the metagenomics workflow. To address this, ATCC has developed a set of genomic and whole cell mock microbial communities from fully sequenced and characterized ATCC strains that represent species found in the oral, skin, gut, or vaginal microbiome. To further enhance the use of these standards and eliminate the bias associated with data analysis, we have also collaborated with One Codex to develop data analysis modules that provide simple output in the form of true-positive, relative abundance, and false-negative scores for 16S rRNA community profiling and shotgun metagenomics sequencing.

LEE YEONG YEH  
Professor of Medicine & Consultant of Gastroenterology, Hepatology & Internal Medicine, Universiti Sains Malaysia  
Effects of environment insults on gut-brain axis and using probiotics for its restoration  
The use of probiotics can relieve gut symptoms and psychological disturbance through restoration of microbial balance and the gut-brain axis. Recent research has shown an intricate relationship between host gut wall and luminal microbiota environment which is critical in maintaining gut health and psychological well-being. Some factors have been shown to affect gut microbiota, but environment is probably most important, for example, diet rather than genes has been shown to be the primary determinant of gut enterotype and obesity in Asian populations. Disruption of a stable microbiota composition (dysbiosis) due to an environmental insult from e.g. major flood, typhoon and air pollution; common disasters in the Asian region, can lead to gut-brain axis disturbance in the form of irritable bowel syndrome and anxiety. Thus, this presentation aims to discover the effects of environment insults on gut-brain axis and how probiotics can possibly be used in such conditions.

HANNA SIDJABAT  
Honorary Fellow and Chief Investigator, University of Queensland Centre for Clinical Research, Australia  
Probiotics for newborn babies: potential benefit to reduce the burden of neonatal sepsis  
Probiotics types such as Lactobacilli and Bifidobacteria have been used for infants who have sepsis can be treated without any side effect. However, if the infants are in late stage of sepsis, probiotics can not be helpful outcome. The motility and maturity of gastric tract in neonatal can be improved by using probiotics. In this presentation, I will focus on the clinical trial applications of probiotics for newborn. There are several benefits of using probiotics for newborn babies: 1) The intestinal barrier resistant can be increased against the bacteria that crossing barrier and spread their poison. 2) modification the host reaction according to production of microbe; 3) mucosal response for IgA can be increased. 4) Anti-inflammatory such as Cytokines production can be raised. However, the benefit of probiotic activities relies on the dose in specific period time and on the species of bacterial strains.

TOH MINGZHAN  
Research Fellow, Food Science & Technology Programme, Department of Chemistry, National University of Singapore  
Interactions between probiotic bacteria and yeasts: Potential applications in probiotic foods  
The health-promoting properties conferred by probiotics are contingent on the number of live microorganisms present in their delivery system at the point of consumption. As such, it is crucial that probiotic food products contain high levels of viable probiotic cells after manufacturing, and that adequate amounts are maintained throughout the distribution chain until it reaches the consumers. Various intrinsic and extrinsic factors can negatively influence the survival of probiotics in foods during production and storage, thereby diminishing the efficacy of the beneficial microorganisms. Recent studies have demonstrated that the co-existence of yeast and probiotic bacteria could enhance the viability of the latter under elevated temperature and acidic conditions. Therefore, the use of yeasts as an adjunct culture in probiotic foods could potentially improve the functional properties of these products. In this presentation, the effect of yeasts on the growth of probiotic bacteria in different food matrices, and their survival at low pH conditions will be discussed. In addition, the implications of mixed yeast-bacteria fermentation on the organoleptic qualities of foods will also be covered.
MAKING A POSTER PRESENTATION

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 with your full abstract in and 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.

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