5th Microbiome R&D & Business Collaboration Congress

4th Probiotics Congress: Asia

Regent Taipei, Taiwan
6-7 March 2019

Co-Hosts

National Central University
National Chiao Tung University

www.global-engage.com
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.
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SPONSORS & EXHIBITORS

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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’Oréal, France

YUAN 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 SARBINI
Dean, Faculty of Agricultural and Food Sciences, Universiti Putra Malaysia

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

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

JAMES CHU
CEO of GLORIA, National Central University, Taiwan

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

NIKLAS LARSSON
Research Director, Probi AB, Sweden

6TH MICROBIOME R&D & BUSINESS COLLABORATION CONGRESS / 4TH PROBIOTICS CONGRESS: ASIA 2019
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 SYKERMAN
Clinical Neuropsychologist and Senior Research Fellow, University of Auckland, New Zealand

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

LEE YEOONG 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
### Registration & Refreshments

**08:00-08:50**

### MICROBIOME

#### 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.

#### SOLUTION PROVIDER PRESENTATION:

**SENIOR REPRESENTATIVE**
Winclove
Title TBC

### PROBIOTICS

#### KEYNOTE PRESENTATION:

**Invitation Out**

#### SPONSORED PRESENTATION

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Email: reuben@global-engage.com
Tel: +603 2117 5193
## 10 MINUTE OPENING FROM THE TAIWANESE MINISTRY:

Title TBC

### MICROBIOME IN HEALTH & DISEASES

**Chair:** Wei-Li Wu, Assistant Professor, Department of Physiology, College of Medicine, National Cheng Kung University, Taiwan

**Chair:** Hok Bing Thio, Head Residency program & Vice Chair, Department of Dermatology, Erasmus University Medical Center, Netherlands

**Chair:** Hok Bing Thio, Head Residency program & Vice Chair, Department of Dermatology, Erasmus University Medical Center, Netherlands

### MICROBIOME R&D

**Nicole Roy**
Principal Scientist and Science Team Leader, AgResearch, New Zealand

*The COMFORT cohort: Identifying biomarkers for gut-brain axis relevant to functional gut disorders*

The links between food, gut function and comfort, and brain function are at the forefront of nutritional research. Irritable Bowel Syndrome (IBS) is a functional gut disorder characterised by chronic or recurrent abdominal discomfort mostly associated with changes in gut habit in the absence of a detectable organic cause. Several central and peripheral mechanisms initiate perturbations in gut motor and sensory functions and lead to IBS symptoms. Peripheral molecules, and associated pathway dysfunctions and altered tissue metabolism, are important to better define functional gut disorders. In a case-control study, individuals with functional gut symptoms (cases) or asymptomatic (controls) undergoing colonoscopy were recruited. Demographics, symptoms score, psychological score and dietary records were recorded. Metabolomics of biological samples, shotgun metagenomics sequencing of faecal samples and quantification of plasma neurotransmitters and bacterial metabolites were carried out to identify microbial and host factors and gain mechanistic insights into functional gut disorders.

### R&D - FOOD

**Nagendra Shah**
Professor, Functional Food, Hong Kong University, Hong Kong

*Challenges of synthesizing gamma-aminobutyric acid (GABA) in milk by a novel strain of Lactobacillus brevis NPS-QW-145 isolated from Korean kimchi*

In this study, several GABA-producing LAB isolates have been isolated from naturally fermented foods such as Korean kimchi. Previous screening methods are time-consuming and inefficient. In the present study, we have developed a novel screening and identification method for GABA-producing LAB from Korean kimchi. Acid treatment was applied to screening procedure to obtain acid-tolerant LAB isolates, and then a simple identification of GABA-producing LAB based on release of gas by these bacteria has been developed. The amount of GABA produced by LAB isolates at various monosodium glutamate (MSG) concentrations and incubation time in MRS medium was quantified by HPLC. Genetic identification of high GABA-producing LAB was carried out by both 16S rRNA gene and glutamate decarboxylase gene. Nine potential GABA-producing LAB isolates were selected by observing gas release during fermentation. The conversion ability of MSG into GABA for all nine LAB isolates was 100% (supplementation level 10 g/L MSG, incubation time 24 h), over 80% (supplementation level 30 g/L MSG, incubation 48 h), over 60% (supplementation level 50 g/L MSG, incubation time 72 h) and over 50% (supplementation level 70 g/L MSG, incubation time 72 h). These nine LAB isolates were genetically identified as Lactobacillus brevis by 16S rRNA gene and confirmed by glutamate decarboxylase gene.

### 10:45-11:50 Morning Refreshments / Odd-Numbered Poster Presentations / One-to-One Meetings

**Yi-Bing Lin**
Vice Chancellor, University System of Taiwan, National Chiao Tung University, Taiwan

*Application of Artificial Intelligence to Earth Microbiome*

**Hazel Mitchell**
Professor, University of New South Wales, Australia

*Title TBC*

**Anders Henriksson**
Principal Application Specialist, DuPont Nutrition & Health, Australia

*Dietary tools for shaping the gut microbiome*

There is a substantial pool of data...
BAOLI XU  
Principal investigator and Director of Microbial Genome Research Center, The Institute of Microbiology and Chinese Academy of Sciences, China

**Title TBC**

14:10-14:35

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

**Title TBC**

14:10-14:35

Skin microbiome has positive impact on several aspects of human health, such as innate immune response modulation and protection against pathogens. Microorganisms interact with host keratinocytes and innate immune system, stimulating the secretion of antimicrobial peptides, free fatty acids, cytokines and chemokines, which might lead to adaptive immune responses. The skin microbiota

14:35-15:00

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

**Factors affecting gut colonization and pathogenesis of hypervirulent Klebsiella pneumoniae, the causative agent of liver abscesses disease**

Hypervirulent Klebsiella pneumoniae is an emerging cause of community-acquired pyogenic liver abscess 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:

- The effects of different dietary proteins on the composition of gut microbiota, as well as reported health benefits of the such proteins.
- The role of human milk oligosaccharides in establishing an optimal microbiota early on in life, and
- Probiotics, which may deliver significant benefits even in the presence of a well-established gut microbiome.

14:35-15:00

NIRANJAN NAGARAJAN  
Senior Group Leader and Associate Director, Genome Institute of Singapore, A*STAR, Singapore

**Skin Microbiome and Eczema**

14:35-15:00

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

**Microbiota-Gut-Brain Axis, Psychobiotics and Neuropsychiatric Disorders**

Psychobiotics, a class of probiotics with psychotropic activities via the gut-brain axis. Lactobacillus plantarum PS128 is a novel psychobiotic, which normalized depression-like behaviors in early life-stressed mice and improved locomotion in Parkinson’s disease-like mice. In a 4-week, randomized,
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 increasing body of evidence indicate that a compromised microbiome is a risk factor for the development of non-communicable diseases. Nutritional intervention could be harnessed as a mean to reduce the disease risk associated with a compromised microbiome.

Conversely, intestinal niche.

The ability of the bacteria to establish an as other factors that could contribute to results on each of these aspects as well
gut colonization. I shall discuss our of capsule and fucose usage for efficient antibiotics treatment, as well as the role of probiotics administration after 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.

K1 capsular type, hypervirulent K.

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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.

"rmpA and iron siderophores such as aerobactin. 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."

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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.

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To date, there is limited evidence on the microbial basis of body odor in teenagers and kids. Even though human sweat is odorless, bacterial growth and decomposition of specific odor precursors in it is believed to give rise to body odor in humans. While mechanisms of odor generation have been widely studied in adults, little is known for teenagers and kids who have distinct sweat composition from immature apocrine and sebaceous glands, but are arguably more susceptible to the social and psychological impact of malodor. We integrated information from whole-microbiome analysis of multiple skin and multiple time points to perform the largest metagenome-wide association study to date on malodor. Correlations between odor intensity and the relative abundance of specific bacteria and the associated metabolic pathway will be presented. The results showcase the power of skin metagenomics to study host-microbial co-metabolic interactions, identifying distinct pathways for odor generation from sweat in kids and teenagers, and highlighting key enzymatic targets for intervention.

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Clinical trials have shown that PS128 is a feasible and insignificant effects. These results showed that PS128 is a feasible and natural intervention for alleviating symptoms of neuropsychiatric disorders.

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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.
08:30-08:55 | Refreshments

08:55-09:00 | KEYNOTE PRESENTATION:
JIN-ZHONG XIAO
Director, Next Generation Sequencing Institute, Morinaga Milk, Japan

Insight into the reason of being of Bifidobacterium in human gut

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 > 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.

10:00-10:30 | SPONSORED 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

A Step to Commercialisation: Building a Microbiome Network between Academics and Industry for Microbiome Discovery Efforts

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.

10:30-11:35 | Morning Refreshments / Poster Presentations / One-to-One Meetings

11:35-12:10 | PANEL DISCUSSIONS:
Towards Preventive Measures: Exploring the Current Market Trends and Regulatory Approach on Probiotics Use in Asia
**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 performance 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**

Interestingly, two kefir probiotics, Lactobacillus bulgaricus and L. kefiranfaciens (M1), exhibited completely opposite results in anti-obesity. APS1 manipulated the gut microbiome’s obesity-associated

**Therapies, a path forward**

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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 immunity 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.

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COMPANY SHOWCASE
Prebiotics: An Asian Perspective
DEAN SHAHRUL RAZID SARBINI
Associate Professor, Faculty of Agricultural and Food Sciences, Universiti Putra Malaysia

The Asian region being the largest and most populous continent on earth, signifies most diverse biological resource provides plentiful source of indigenous plants as prebiotic. This study will look at prebiotic 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 Bifidobacteria. 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 curcumoid are metabolised by colonic microbiota, modulating the bacterial population and their metabolic activity.

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COMPANY SHOWCASE
Postnatal depression and anxiety affect a woman’s risk of ongoing psychological problems and relationship with her baby. We conducted a randomised, double-blind, placebo-controlled trial of the effect of Lactobacillus rhamnosus HN001 in 423 New Zealand women. Results showed a significant reduction in postnatal depression and anxiety symptoms. There is pre-clinical evidence suggesting the gut microbiome is involved in developmental outcomes in childhood. Longitudinal cohort studies of children followed from birth through childhood suggest early antibiotic exposure is associated with poorer neurocognitive outcomes. The area of probiotic supplementation for improved neurocognitive outcomes is emerging. Early trials have not consistently found beneficial effects of probiotics and research is continuing to answer question about the role that antibiotics and probiotics play in childhood neurodevelopment.

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COMPANY SHOWCASE

5TH MICROBIOME R&D & BUSINESS COLLABORATION CONGRESS / 4TH PROBIOTICS CONGRESS: ASIA 2019
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 microbiome standards for gut, skin, oral, and vaginal microbiome studies.

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.
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.

In order to present a poster at the congress 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). We charge an admin fee of $50 to industry delegates to present, that goes towards the shared cost of providing the poster presentation area and display boards, guides etc. This fee is waived for those representing academic institutions and not for profit organisations.
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