5TH MICROBIOME R&D & BUSINESS COLLABORATION CONGRESS

4TH PROBIOTICS CONGRESS: ASIA

SATELLITE MEETING: TAIWAN MICROBIOME CONGRESS

REGENT TAIPEI, TAIWAN

6-7 March 2019

Co-Hosts

National Central University

National Chiao Tung University
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.

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

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

DAR-BIN SHIEH
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MING-JU CHEN
Professor, Department of Animal Science and Technology, National Taiwan University, Taiwan and President, Taiwan Association of Lactic Acid Bacteria

YASUHIRO KOGA
President, Japanese Society for Probiotic Science

HANNA SIDJABAT
Honorary Fellow and Chief Investigator, University of Queensland Centre for Clinical Research, Australia
### 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
- Biocore 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
CONFIRMED SPEAKERS

WEI-LI WU
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JQ LIU
Principal Scientist, Procter & Gamble, Singapore

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

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Fernwood Foundation Research Fellow, Deakin University, Australia

CUONG D TRAN
Senior Research Scientist, CSIRO, Australia
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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.

Building an evidence base for the clinical and mechanistic effects of a probiotic supplement for allergy
Aberrant regulation of immune activity by the microbiome is considered a key driver for the increasing prevalence of allergic rhinitis (AR). While modulation of the microbiome through probiotic supplementation may have clinical benefit for AR, there is a need for supplement-specific clinical and mechanistic evidence before guidelines on the use of probiotics for AR can be issued. A key weakness in probiotic research identified by regulators is the lack of a systematic clinical development process to build evidence for the use of probiotic supplementation in disease. The aim of this study was to develop early phase clinical and mechanistic evidence to guide human clinical research on a multi-species supplement for AR (Ecologic® AllergyCare, Winclove Probiotics, The Netherlands). Physician confirmed AR patients consumed one sachet of 2 g freeze-dried multi-species probiotic supplement containing five bacterial strains twice daily for eight weeks. Utilising a Simon Two-Stage design, the primary outcome measure for a clinical benefit was a reduction in the mini-Rhinoconjunctivitis Quality of Life index of 0.7 of a scale-step. For the study to be considered a success ≥10 patients were required to experience a clinically beneficial response. A total of 40 participants completed the study. There were 25 participants (63%, 49-76%, P<0.001; mean, 95% confidence interval, P-value) out of 40 participants that had a clinically meaningful response to treatment based on assessment of mRQLQ. Significant reductions in symptom scores and overall AR severity was observed and there was a trend for a reduction in the frequency of allergy related medication. Nasal mucosa and blood samples collected pre- and post-supplement from a cohort of responders and non-responders were subsequently analysed for immune gene expression using Nanostring digital immune gene expression profiling to investigate inflammatory mechanisms mediating the beneficial effects of supplementation. Unsupervised hierarchical cluster analysis discriminated responders and non-responders in blood and nasal lysate at baseline, with HLA-C and ET5 >1.5-fold higher (p<0.01) in peripheral blood in responders. There was a significant difference (p=0.03) in Th-1 cell score abundance between the groups from pre- to post-supplementation. Overall, the beneficial clinical effects of supplementation on AR warrant continued clinical investigation in phase 3 trials. AR responders to this probiotic supplement may have a T-cell mediated inflammatory endotype.
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 can 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.
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.

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 with lesser relative abundance of Neisseria species were independently associated with high ALD production, in spite of the high ALD production capacities of Neisseria species.

alleviating symptoms of neuropsychiatric disorders.

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University System of Taiwan, National Chiao Tung University, Taiwan
Application of Artificial Intelligence to Earth Microbiome

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.

ANDERS HENRIKSSON
Principal Application Specialist, DuPont Nutrition & Health, Australia
Dietary tools for shaping the gut microbiome
There is a substantial pool of data 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.
prominent in women with osteopenia and those with less than 6 years from the start of menopause.

healthy microbiome may potentially lead to obesity, autism or allergy development besides other current issues in infant health and development. HMOs are now available as ingredients for infant and general nutrition.

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. HMOs are now available as ingredients for infant and general nutrition.

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.

The human gut microbiota may have a key role affecting host nutrition, metabolic function, and protection against pathogens. Probiotics and Exercise Performance

The definition of probiotics specifies that it is a preparation of live microorganisms. However, studies have been presented using killed preparations and there are clearly benefits and reduced infection risk with killed preparations. This study explored the use of a killed bacterial preparation on colorectal cancer tumours. It has previously been shown that a preparation of heat inactivated Clostridium sporogenes can negatively impact on the growth of HCT116 and CT26 colorectal cancer cells in culture. It was therefore of interest to examine the impact of this preparation of heat inactivated C sporogenes on tumours in vivo. Using immunocompetent BALB/c mice, the preparation was tested for its impact on subcutaneously induced tumours. The preparation was found to exert a direct anti-tumour effect as observed by a decrease in the CT26 tumour volume and an improved survival rate of the mice. One group of mice with induced tumours and then treated with the preparation, and hence had reduced tumours, were re-challenged with an additional subcutaneous injection of the CT26 cells in the alternative flank. Tumours did not develop in these mice, indicative of a protective immune response. It was concluded that the heat inactivated C. sporogenes has the potential to be developed as a direct anti-tumour agent.
are generally hypermucoviscous with the possession of a large virulent plasmid encoding 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.

stimulating the secretion of antimicrobial peptides, free fatty acids, cytokines and chemokines, which might lead to adaptive immune responses. The skin microbiota 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.

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, and the data showed that LP10 significantly decreased final body weight and increased relative muscle weight (%). LP10 supplementation dose-dependently increased grip strength and endurance swimming time and decreased levels of serum lactate ammonia, creatine kinase and glucose after acute exercise challenge. Long-term supplementation with LP10 may increase muscle mass, enhance energy harvesting, and have health-promotion, performance improvement and anti-fatigue effects.
corresponding patterns of divergence over space and time. To study common HAI-associated pathogens that were typically present at low abundances, a combination of culture enrichment and long-read nanopore sequencing was used to obtain thousands of high contiguity genomes (2347) and closed plasmids (2944), a significant fraction of which (>30%) are not represented in current sequence databases. Leveraging these high quality assemblies for characterizing resistance gene combinations and plasmid architectures revealed the dynamic nature of hospital environment resistomes and its untapped reservoirs. Phylogenetic analysis identified multiantibiotic resistant clonal strains as being more widely disseminated and stably colonizing across hospital sites. Further genomic comparisons with clinical isolates across multiple species supports the hypothesis that multidrug resistant strains can persist in the hospital environment for extended periods of time (>8 yrs) to opportunistically infect patients. These findings highlight the importance of characterizing antibiotic resistance reservoirs in the hospital environment and establishes the feasibility of systematic genomic surveys to help target resources more efficiently for preventing HAI.

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.

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.
Microbial taxa that differed between IBS and control phenotypes and the control subjects, with major perturbations in amino acid, bile acid and lipid metabolism. Metabolomic profiles differed significantly between the IBS samples were measured using shotgun metagenomics. Plasma metabolites were measured using LC-MS metabolomics, while 205 fecal samples were measured using shotgun metagenomics. Plasma metabolomic profiles differed significantly between the IBS phenotypes and the control subjects, with major perturbations observed in amino acid, bile acid and lipid metabolism.

Microbial taxa that differed between IBS and control participants included Megasphaera, Blautia, and Bilophila. Canonical correlation analysis revealed associations (r>0.5) between numerous plasma lipids (e.g. diacylglycerolipids, triacylglycerolipids, and phosphatidylethanolamines) with Blautia and a group of unclassified Lachnospiracae. These two taxa were a major component of the microbiome, collectively accounting for >25% of the community. Similarly, correlations (r>0.7) were observed between plasma lipids and
microbial genes involved in lipid and carbohydrate metabolism, including glyoxylate and dicarboxylate metabolism, and glycerolipid metabolism. Our results highlight links between major members of the fecal microbiome, in both composition and function, with the plasma metabolome in an IBS cohort. Integrated multi-omic analyses can reveal potentially critical mechanistic differences between subjects of different GI status.

**POSTER PRESENTATIONS**

**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.

**POSTER COMPETITION – CLOSING DATE 8TH FEBRUARY 2019**

1. Submit your entry prior to the closing deadline (1 entry per person)
2. One winner from each Congress will be selected by the judge(s)
3. The winners of the poster presentation will be given a 15-minute speaking position on the conference agenda and notified in advance of the meeting
4. The judge(s) will make the decision based on the abstract(s) submitted
5. The winners will receive a certificate from the organisers
6. Representatives from solution provider organisations are not eligible to enter the competition but are welcome to present posters at the meeting as normal

**Poster space is limited so early submission is recommended**
The digestive anatomy of humans can be described as a combinatorial system, where the large intestine provides a facultative afterburner: housing a mixture of microbes that can utilise both endogenous secretions as well as food components escaping proximal (host-mediated) digestion and absorption. In engineering terms, this site functions as a plug-flow digester with microbial activities and ecosystem functions affected by a combination of nutrient availability and transit time. To date, the overwhelming amount of knowledge about diet x microbiome interactions has been generated by snapshot analyses, that is, by using extracts prepared from collected stool samples. By doing so, understanding the temporal changes in the microbiome during food digestion and transit remain limited in scope. Additionally, our knowledge of the mucosa-associated microbial communities, especially those of the upper gastrointestinal tract, are also underdeveloped; and perhaps, it can be considered the forgotten gut microbiome. For these reasons, innovations in sample collection, microbiota analysis and integration of the data with other clinical measures are all required if the promise and opportunities attributed to "microbiome research" are to be translated into gastrointestinal health and well-being. Here, I will present an overview of the "Brisbane approach" to building a conceptual framework of the role of the gastrointestinal microbiota in digestion, and their role in the clinical manifestations of digestive diseases. Our collective goal is to better predict and shape the impacts of the gut microbiota via the concepts of nutritional ecology: the study of how the nutrient milieu and its variations across temporal and spatial scales affects gut microbiota structure-function relationships. Continued progress needs to be made in these areas if the nutritional ecology of the gut is to be better managed, to restore and/or sustain gut homeostasis and resilience, and to reduce the social and economic burdens of digestive diseases and disorders.

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 2x10^9 CFU LS1 for 4 weeks, the number of P. gingivalis in the subgingival plaque decreased to about one-tenth after 4-week-treatment.

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.
The vaginal microbiota is considered to be dominated by lactobacilli; although cultural and ethnic variations exist. The most common Lactobacillus species are L. crispatus, L. gasseri and L. jensenii. L. iners is also commonly observed but the species has been suggested to have a dual role; both in health and disease. Bacterial vaginosis (BV) is a common condition that affects most women at some stage. BV is characterised by reduced levels of vaginal lactobacilli and an over growth of e.g. Gardnerella vaginallis and Atopobium vaginae. This imbalance is used in diagnosis with the so-called Nugent-score. Probiotic lactobacilli have been investigated as an adjunct to antibiotic treatment and shown to be successful. However, most studies have investigated the effect of vaginally applied probiotics. Here, I report on the development of the vaginal microbiota following antibiotic treatment for BV and the oral use of probiotics in BV. Two-week consumption of a combination of L. rhamnosus HN001 and L. acidophilus La-14 by healthy women, resulted in vaginal colonisation in 85% of the women. Interestingly, colonisation still increased in the week after consumption was stopped. In vitro studies have shown that both strains and in particular L. acidophilus La-14 produce hydrogen peroxide; an important antimicrobial involved in the stabilisation of a healthy vaginal microbiota. Both strains were also shown to inhibit the growth of G. vaginalis and A. vaginae in vitro and prevented experimental vaginosis in mice. In a subsequent human study, 40 women with borderline BV, as judged by Nugent-score of 4-6 and vaginal symptoms were randomised to receive either probiotic treatment or placebo for 15 days. In the probiotic group, Nugent-score improved to below 3 (no BV) with no change in the placebo group. Symptoms of itching and vaginal discharge also improved significantly in the probiotic group. As a complementary treatment to antibiotics for BV, the administration of L. acidophilus La-14 and L. rhamnosus HN001 was observed to improve recovery rate and reduce recurrence of BV. The combination of L. acidophilus La-14 and L. rhamnosus HN001 is beneficial in the management of BV.
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 microbiota 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.

advances in Genomic sequencing technologies have significantly improved our ability to measure and identify microbes in, on and around us. This has led to a rapid expansion in our understanding of the role of the microbiome in human physiology in health & disease. As a unique body niche, the skin is home to a characteristic combination of microbial species that have pretty much taken over any available real estate on the body. The skin microbiome shows significant diversity of taxonomy across different regions of the skin as well as between individuals. Evolving scientific consensus has started to consider this skin microbiome as an integral part of the skin physiology. Understanding the relationship among microbes and between microbe and skin biology is important to drive our understanding of skin beauty & health thereby driving product innovations with a very different lens. Strategies to translate fundamental research into consumer facing market innovations will unlock huge potential of skin microbiome research for the Beauty and Personal Care industry.
alteration in the production of microbial 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.

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.

microbiome’s obesity-associated 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.

at face value, standardization and innovation may seem like opposing forces. This feels especially true given the pace of change in the microbiome field and the expectations that accompany such a large influx of discovery capital. But upon closer examination, it’s actually difficult to achieve the necessary and sufficient conditions of a true innovation (i.e. utility and lasting impact) without standardization (i.e. rigor and reproducibility). In this talk we will discuss how standardization enables innovation in different scenarios. First, we will outline some of the technical challenges encountered while studying vulnerable populations (infants, the elderly, IBD patients) and how we overcame them. Second, we will cover some of the current standardisation initiatives in the field of microbiome and how building on best practices can accelerate our progress toward meaningful innovation.
**Combined effect of Scutellaria baicalensis with metformin on glucose tolerance via gut microbiota modulation in type 2 diabetes patients: A double-blind, randomized cross-over clinical trial**

Dongguk University, Korea

Department of Rehabilitation Medicine of Korean Medicine, NA RAE SHIN & HOJUN KIM

**Microbiome and Diet**

Chair: Uma Devi a/p Palanisamy, Associate Professor, Monash University, Malaysia

**Probiotics**

Chair: Lee Yeong Yeh, Professor of Medicine & Consultant of Gastroenterology, Hepatology & Internal Medicine, Universiti Sains Malaysia

**Psychological and Neurocognitive Outcomes**

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.

**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.
Changes in intestinal permeability modulates the gut microbiota population

Intestinal microbiota has been suggested to influence intestinal barrier strength, functional integrity, and permeability regulation. However, the relationship between changes in intestinal permeability and its effects on the gut microbiota is less clear. This study aimed to investigate the changes in intestinal permeability and its influence of the gut microbiota in rats. 68 male Sprague-Dawley rats were randomised to 4 groups (n=4/dose/timepoint) and injected intraperitoneally (i.p.) with LPS: 0, 0.5, 1, 2 mg/kg. Animals were euthanized at 2, 4, 7, 10 days post-LPS administration. Animals were gavaged 24 hrs prior to cull with a dual sugar solution, lactulose (100 mg)/rhamnose (50 mg) (L/R), after a 12 hr fast for intestinal permeability assessment. Faecal and intestinal samples were collected for microbiota and short chain fatty acid (SCFA) analyses, and histological assessment, respectively. LPS administration increased plasma LPS levels by 30-fold on average on Day 2, returning to baseline by Day 4. Bodyweight was significantly (p<0.05) decreased by 5.9% on average vs. controls. Histologically, the most damaged intestinal region was jejunum>duodenum>ileum. Intestinal permeability (L/R ratio) was increased (p<0.05) in the 1 and 2 mg/kg groups (by 2.7- and 2.9-fold) vs. controls. ZO-1 staining intensity was decreased (p<0.05) by 5.2% in the 2 mg/kg dose on Day 4 vs. controls. On Day 2, SCFAs were increased (p<0.05) by 3-fold in the 2 mg/kg dose vs. controls. Total gut microbiota population was significantly (p<0.05) reduced in all LPS-treated groups vs. controls. Our findings suggests that increased intestinal permeability modulates the gut microbiota population.

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.

Gut microbiota regulates social behaviour via stress response pathways in the brain

Social impairment is a major symptom of neuropsychiatric conditions, such as autism spectrum disorder (ASD), schizophrenia, anxiety and depression. While the microbiome has been linked to social interaction in animals, gut-brain connections that regulate this complex behaviour remain entirely undescribed. Herein, we demonstrate that depletion of microbiota in mice not only impairs social behaviour, but also activates specific brain regions related to canonical stress responses. Social deviation in germ-free and antibiotic-treated mice is associated with elevated levels of the stress hormone corticosterone, which is primarily produced via activation of hypothalamus-pituitary-adrenal (HPA) axis. Accordingly, removal of the adrenal gland, antagonism of the glucocorticoid receptor, and pharmacological inhibition of corticosterone synthesis effectively correct social deficits. Genetic ablation of the glucocorticoid receptor in specific brain regions and chemogenetic inactivation of hypothalamic neurons dramatically increase social behaviour. Further, we identify specific bacterial metabolites that suppress activation of the HPA axis and improve social impairment. These findings reveal that the gut microbiome regulates social behaviour by co-opting neuronal circuits that control stress responses in mice.
SATELLITE MEETING

TAIWAN MICROBIOME CONGRESS

IN CONJUNCTION WITH 5TH MICROBIOME R&D AND BUSINESS COLLABORATION CONGRESS: ASIA AND 4TH PROBIOTICS CONGRESS: ASIA

REGENT TAIPEI, TAIWAN

6-7 March 2019

Participating Organisations
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<td>Chair: Deron Raymond Herr, Associate Professor, National University of Singapore</td>
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<td>Co-Chair: Wilson Cheung, CEO, Bionefit Inc., USA</td>
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<td>09:00-09:35</td>
<td>JEN-HER LU</td>
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<td>Probiotics for Preterm Infants, Where is the Evidence</td>
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<td>09:35-10:05</td>
<td>SHAWN YH CHEN</td>
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<td>The cyanobacteria application on emerging viruses inhibition and future commericalization</td>
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<td>10:05-10:35</td>
<td>DERON RAYMOND HERR</td>
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<td>Lipidomic analysis of plasma sphingolipids in an East Asian population identifies novel associations with obesity- and diabetes-related characteristics</td>
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<td>Morning Refreshments / Poster Presentations / One-to-One Meetings</td>
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<td>Chair: Battogtokh Chimeddorj, Associate Professor, M.D, Ph.D. Mongolian National University of Medical Sciences</td>
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<td>Co-Chair: Roger Liu, Biotools Co, LTD., Taiwan</td>
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<td>12:15-12:40</td>
<td>YUH-SHYONG YANG</td>
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<td>Semiconductor based bacterial and cell sensors</td>
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<td>DR. CHIEN-LUNG CHEN, MD</td>
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<td>MD, Landseed Hospital</td>
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<td>SUNITA KESHARI</td>
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<td>National Central University, Taiwan</td>
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<td>Microbiome metabolites for treatment of pruritus in patients with kidney dialysis</td>
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# CONGRESS SCHEDULE

## DAY 1 WEDNESDAY 6TH MARCH 2019

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<td>14:35-15:00</td>
<td>ROGER LIU</td>
<td>The Taiwan Gut Project</td>
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<td>15:00-15:25</td>
<td>MANISH HARI, ROGER LIU</td>
<td>A Skin Probiotic Bank in Taiwan</td>
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<td>15:25-15:40</td>
<td>WEN-CHI CHENG</td>
<td>Oral bacterial detection for periodontal disease prevention and monitoring</td>
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<tr>
<td>16:40-17:05</td>
<td>WEN-CHI CHENG</td>
<td>Oral bacterial detection for periodontal disease prevention and monitoring</td>
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## DAY 2 THURSDAY 7TH MARCH 2019

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<tr>
<td>09:00-09:30</td>
<td>HENRY HORNG-SHING LU</td>
<td>A pilot study of the influence of probiotics on hair toxic element levels after long-term supplement with different lactic acid strains</td>
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<td>09:30-10:00</td>
<td>CHIN-CHU CHEN</td>
<td>Probiotics as Supplements</td>
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<td>10:30-11:30</td>
<td>SHIR-LY HUANG</td>
<td>Gut Microbiota and Autoimmune Diseases</td>
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**Chair:** Artem M. Guriev, Head of TIC SSMU, Russia  
**Co-Chair:** Chin-Chu Chen, Director, Grape King Bio, Taiwan
CONGRESS SCHEDULE

DAY 2 THURSDAY 7TH MARCH 2019

15 MINUTE COMPANY SHOWCASE:
ALBERT JACKSON
National Central University, Taiwan
A Prebiotic Screening Platform

13:15-14:15
3rd Floor
Lunch / Poster Presentations / One-to-One Meetings

Chair: Naranbat Nyamdavaa, CEO, Gyals LLC, Mongolia. Co-chair: Yong Jiang, CEO America Diagnosis, USA

ARTEM M. GURIEV
Head of TIC, Smolensk State Medical University, Russia
Clinical Microbiome Plan in Russia

BATTOGTOKH CHIMEDDORJ
Associate Professor, M.D, Ph.D, Mongolian National University of Medical Sciences, Mongolia
ANIR BATSUKH
National Central University, Taiwan
Blood sugar regulating probiotic bacteria isolated from Mongolia Aaruul

15:10 YONG JIANG
CEO, America Diagnosis, Inc., USA
A Quick and Reliable System for Quantitative Categorization of the Microbiota Species in Human Specimen

15:25 JOSHUA HSU
AI Architect, America Diagnosis, Inc., USA
Artificial Intelligence (AI) for Microbiome Application

CHI-CHANG HUANG
Professor, National Taiwan Sport University, Taiwan
R&D of Probiotics as Ergogenic Aids

TOBY HUANG
Business Development, AllBio Science Inc., Taiwan
Digital health and personalized genomics consumer products

16:45 Closing Remarks / Conference Close

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