GLOBAL ENGAGE’S 3RD
MICROBIOME R&D AND BUSINESS COLLABORATION CONGRESS
COLLABORATIONS IN MICROBIOTA RESEARCH, LIVE BACTERIAL THERAPEUTICS, HUMAN HEALTH & DISEASE

GLOBAL ENGAGE’S 2ND
PROBIOTICS CONGRESS
RESEARCH, DEVELOPMENT & APPLICATION OF PROBIOTICS AND PREBIOTICS IN HUMAN AND ANIMAL HEALTH

—HONG KONG—
1-2 March 2017
Thank you for your interest in the 3rd Global Engage Microbiome R&D and Business Collaboration Forum and Probiotics Congress. As part of its international microbiome series, Global Engage is pleased to announce the co-located event which will be held on 1-2 March, 2017 in Hong Kong.

Developments in the field of metagenomics have allowed researchers to explore the diverse microbiota in the human body. Research has shown that the microbiome is linked to natural immunity, metabolism, behavioural traits, and broadly speaking, plays an instrumental role in health and disease. With large-scale collaborative projects underway and sequencing data placed in the public domain, there is a rich source of information for researchers and companies looking for opportunities in this exciting field. Increasingly, there are indications that the human microbiome is key to curative and preventative medicine, so efforts are being focused on expanding investment opportunities, performing more clinical trials and spurring innovative research in this area. Coupled with an increasing focus on healthy living, and a therapeutics market that is expected to grow to $1.2 trillion by 2016, microbiome research is set to make waves in the science and medical world through its applications in preventative treatments, cures, therapies and supplements.

Attracting over 250 attendees, the 10th meeting in the global series will build upon the success of last year’s meeting which attracted over 200 attendees as well as on our highly popular European and American forums. Bringing together experts in all areas of microbiome and probiotics research, the congress will explore the interface between the microbiome and our evolving cultures and technologies as well as the development of next generation probiotics, prebiotics and functional foods. During the two-day conference, there will be networking breaks to promote interaction with your peers, expert led case study presentations, a dynamic exhibition room filled with technology providers showcasing their technologies and solutions, and panel discussions exploring key issues in the field. Together, we can further develop microbiome and probiotics research across the Asia-Pacific region, and begin to look towards forging collaborations and commercializing the research.

EXPERT SPEAKERS Include:

YUAN KUN LEE
Associate Professor, Department of Microbiology, National University of Singapore

PHILIP HUGENHOLTZ
Director, Australian Centre for Ecogenomics; Professor, School of Chemistry & Molecular Biosciences, The University of Queensland, Australia

LARRY WEISS
Chief Medical Officer, AOBiome, LLC, USA

NEERJA HAJELA
General Manager – Science and Regulatory Affairs, Yakult Danone India Pvt. Ltd.
GUT MICROBIOTA IN HEALTH AND DISEASE
- Updates on the Asian gut microbiome project
- Novel models for studying gut-microbe interactions
- Connections to IBD, IBS and diarrheal diseases
- Fecal transplantation
- Innate immune system and host-pathogen interaction
- Associations with obesity and metabolic disease
- The virome and its role in health and disease
- Role of synthetic biology
- Gnotobiotic mice studies
- Gut-brain interactions – depression, anxiety and autism?
- Development of bacteriophage therapeutics
- Metagenomics – microbiome sequencing and bioinformatics

SKIN, ORAL AND VAGINAL MICROBIOTA
- Diversity of skin communities
- Interactions between host genotype and microbial abundances
- Skin and scalp microbiomes
- Case studies and therapeutic potential in acne, eczema, atopic dermatitis, and microbiomes of chronic and acute wounds
- Oral cancer associated microbiome
- Microbiome of the female urogenital tract and pregnancy
- Research into the microbiome and HIV

PREBIOTICS AND DIET
- Dietary modulation of the human gut microbiome
- Gut microbiota in varying nutritional states
- Role of short-chain fatty acids
- Milk-oriented microbiota
- Developing nutritional products utilising microbiome research

COMMERCIALIZATION OF THE MICROBIOME & PROBIOTICS
- Collaborations/partnerships – the global scope of microbiome research/structuring successful collaborations
- Bringing live microbial products to market – IP, regulation
- Bugs as drugs – microbiome therapeutic development
- Contemplating novel antibiotic therapies that do not destroy the healthy microbiome
- Probiotic strain identification, designation and safety

PROBIOTICS AND DISEASE
- Probiotics and digestive health
- Probiotics in pediatrics
- Probiotics and dietary interactions

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

PROBIOTICS FOR ANIMAL HEALTH
- Feed additives to target disease
- Antibacterial resistance
- Aquaculture, companion and production animals

PANEL DISCUSSIONS
- What is a healthy, balanced microbiome? How important is gut microbial diversity?
- Current research and future developments in animal probiotics

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CONFIRMED MICROBIOME SPEAKERS

HIROSHI OHNO
Group Director, Laboratory for Intestinal Ecosystem, RIKEN Center for Integrative Medical Sciences (IMS), Japan

YUAN KUN LEE
Associate Professor, Department of Microbiology, National University of Singapore

G. BALAKRISH NAIR
Ag Regional Advisor, Research Policy Cooperation Unit, Communicable Diseases Department, World Health Organization, India

MARGARET MORRIS
Professor, Chair and Head of Pharmacology, School of Medical Sciences, University of New South Wales, Australia

HEENAM STANLEY KIM
Professor, College of Medicine, Korea University

LARRY WEISS
Chief Medical Officer, AOBiome, LLC, USA

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Senior Scientist Gut Microbiology, Life Science Innovation – Early Life Nutrition, Danone Nutricia Research, Singapore

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Senior Project Leader Microbiomics, Department of Health, NIZO Food Research, The Netherlands

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Professor, Director, Division of Laboratory Medicine, Zhujiang Hospital, Southern Medical University, China

AARON DEL DUCA
VP Technology & Lead, Microbiome Program, DNA Genotek, Inc.

LYNETTE FERGUSON
Director of Mutagen Testing, Auckland Cancer Society Research Centre (ACSR) & Professor of Nutrition, The University of Auckland, New Zealand

COLLEEN CUTCLIFFE
Co-Founder & CEO, Whole Biome, USA

PETER CHI KEUNG CHEUNG
Professor, School of Life Sciences, Director, Food and Nutritional Science Program, Chinese University of Hong Kong

YOSHIHISA YAMASHITA
Professor & Chairperson, Section of Preventive and Public Health Dentistry, Kyushu University, Japan

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Associate Professor & Principal for Sexual and Reproductive Health, Head Retroviral Biology and Antivirals Laboratory, Burnet Institute, Australia

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

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Head, Immunology and Diabetes Laboratory, Monash University, Melbourne, Australia

NICOLE ROY
Principal Scientist and Science Team Leader, Food Nutrition & Health, AgrResearch Grasslands, Adjunct Associate Professor, Riddet Institute, Massey University, New Zealand

KIYOSHI TAKEDA
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Postdoctoral Research Officer, School of Chemistry and Molecular Biosciences, Australian Centre for Ecogenomics, The University of Queensland, Australia

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Founder & CEO, QuantHealth, China

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Senior Scientist, Procter & Gamble, Singapore

ERIC HUANG
Professor, Department of Dermatology, University of California, San Diego, USA

NICHOLAS WEST
Research Fellow, Mucosal Immunology Research Group, Griffith University, Australia

LOUISE VIGSNAES
Preclinical Development Manager, Glycom A/S, Denmark

DAVID J. KYLE
CEO, Evolve BioSystems

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Associate Professor in Paediatrics, School of Medicine, Deakin University, Australia

DIETER BULACH
Senior Research Scientist, Victorian Life Science Computation Initiative, The University of Melbourne, Victoria, Australia

JIAN-YONG WU (TRACK CHAIR)
Associate Professor, Department of Applied Biology & Chemical Technology, The Hong Kong Polytechnic University

KENNETH GAO
Manager, Corporate Development and Strategy, Assembly Biosciences, Inc., USA

JONATHAN KRIVE
CEO, Civet Biosciences, Hong Kong
CONFIRMED PROBIOTICS SPEAKERS

GORDON HOWARTH
Professor of Gastrointestinal Physiology, School of Animal and Veterinary Sciences, University of Adelaide, Australia

PATRICIA CONWAY
Professor, School of Biological, Earth and Environmental Sciences, UNSW Australia

HAU YANG TSEN
Professor of Food Science and Technology, Hungkuang University, Taiwan

ROBERT MOORE
Research Professor of Biotechnology, RMIT University, Melbourne, Australia

KANWALDEEP CHADHA
Vice President, Next Gen Pharma India Pvt. Ltd.

YING-CHIEH TSAI
Professor, National Yang Ming University, Taiwan

ŞEBNEM HARSA
Professor, Faculty of Engineering, Food Engineering Department, Izmir Institute of Technology, Turkey

HARJINDER SINGH
Distinguished Professor and Director, Massey Institute of Food Science and Technology, Massey University, New Zealand

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ROSHADA HASHIM
Professor, Fish Nutrition and Feeding Management, Faculty of Science and Technology, Universiti Sains Islam Malaysia

INGRID SURONO
Head of Food Technology Department, Binus University, Indonesia

STEPHEN OHARA
Founder and CEO, OptiBiotix Health plc

YASUHIRO KOGA
Professor, Tokai University School of Medicine; President, Japanese Society for Probiotic Science, Japan

MOHD REDZWAN SABRAN
Senior Lecturer, Department of Nutrition and Dietetics, Faculty of Medicine and Health Sciences, Universiti Putra Malaysia

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Science Group Leader, Food, Nutrition & Health, The NZ Institute for Plant & Food Research Ltd.

SHIVANANDA MURTHY
Professor & Head, Karnataka Veterinary & Fisheries Sciences University, College of Fisheries, Mangalore, India

RINA AGUSTINA
Scientist, Southeast Asian Ministers of Education Organization Regional Center for Food and Nutrition (SEAMEO RECFON) / Pusat Kajian Gizi Regional (PKGR), Universitas Indonesia, Head of Human Nutrition Research Cluster and Research Coordinator Department of Nutrition, Faculty of Medicine, Universitas Indonesia – Dr. Cipto Mangunkusumo General Hospital, Indonesia
The structure and function of the human gut microbiome is rapidly being revealed through culture-independent molecular techniques. Despite a great deal of interpersonal variability due to factors such as diet, age and ethnicity, there are a small number of relatively abundant microbial species that are widespread in the human population. Some of these are well known, such as Faecalibacterium prausnitzii, but others are as yet uncultured and uncharacterised. In this talk, I will introduce the audience to some of the lesser-known but potentially important members of the healthy human gut microbiome.
The human gastrointestinal tract, the major site of nutrient assimilation and mucronutrient production, is populated with trillions of microbial species from all three domains of life (Archaea, Bacteria and Eukarya). Several species of commensal bacteria play important role in synthesis of essential mucronutrients and other metabolites, which are the key components for the maintenance of human health. Pathobionts, in turn, have developed maneuvers to escape the protective influence of commensal bacteria. The interplay between pathobionts and commensals can also impact host physiology. Our studies attempt to understand the prevalence, diversity, and abundance of low-abundant pathobionts in the gut microbiota of children and adults. We believe that these findings may lead to new insights into examining their involvement in human physiology and the significance of their low-abundance presence in the gut microbiota.

**The role of the skin microbiome in eczema**

- Pathogenesis of experimental autoimmune encephalomyelitis (EAE) is affected by the gut microbiota composition.
- Small intestinal bacteria affect the EAE pathogenesis by inducing Th1 and Th17 cells in the small intestinal lamina propria.
- A combination of bacteria, rather than a specific strain of bacterium, seems to play a role in the strong induction of EAE.

**The interplay of enteric pathogens in the gut microbiota of children and adults**

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**The impact of gut microbiota on the pathogenesis of experimental autoimmune encephalomyelitis in mice, a model of multiple sclerosis**

- Pathogenesis of experimental autoimmune encephalomyelitis (EAE) is affected by the gut microbiota composition.
- Small intestinal bacteria affect the EAE pathogenesis by inducing Th1 and Th17 cells in the small intestinal lamina propria.
- A combination of bacteria, rather than a specific strain of bacterium, seems to play a role in the strong induction of EAE.
PANEL DISCUSSION:
What is a healthy, balanced microbiome?
How important is gut microbial diversity?

PANEL CHAIR:
YUAN KUN LEE
Associate Professor, Department of Microbiology,
National University of Singapore

CONFIRMED PANELLISTS:
PHILIP HUGENHOLTZ
Director, Australian Centre for Ecogenomics;
Professor, School of Chemistry & Molecular Biosciences, The University of Queensland,
Australia

CHRISTOPHE LAY
Senior Scientist Gut Microbiology, Life Science Innovation – Early Life Nutrition, Danone Nutricia Research, Singapore

KENNETH GAO
Manager, Corporate Development and Strategy, Assembly Biosciences, Inc., USA

ERIC HUANG
Professor, Department of Dermatology,
University of California, San Diego, USA
Zymologic editing of skin dysbiotic microbiome
A Skin Probiotic Bacteria Bank with more than fifty fermenting skin bacteria for treatment of twenty skin disorders has been established in our laboratory. Carbohydrates, polyethylene glycol (PEG) macromers and their conjugates were synthesized as selective fermentation initiators (SFIs) for specifically enhancing the fermentation (zymological) activities of skin probiotic bacteria. Acne dysbiosis occurs when there is a microbial imbalance of the over-growth of Propionibacterium acnes (P. acnes) in the acne microbiome. We have identified several SFIs which can selectively promote the zymological activities of skin probiotic bacteria against P. acnes. Unlike live microorganisms (eg bacteriophages), SFIs are used as non-microorganism agents for editing dysbiotic skin microbiome.

MOHD REDZWAN SABRAN
Senior Lecturer, Department of Nutrition and Dietetics, Faculty of Medicine and Health Sciences, Universiti Putra Malaysia
Dietary approach using probiotics to prevent human exposure to aflatoxin
• Human dietary aflatoxin exposure is ubiquitous and probiotics are used to prevent the absorption of aflatoxin in the gastrointestinal tract
• Probiotics act as biological barrier by binding aflatoxin into the bacterial cell walls
• Findings from animal and human intervention studies showed the potential use of probiotics as a detoxification agent of aflatoxin.

SOLUTION PROVIDER PRESENTATION:
NICHOLAS WEST
Research Fellow, Mucosal Immunology Research Group, Griffith University, Australia
Probiotics for allergy care: growing evidence of benefit
The benefit of probiotics is based on growing knowledge that the gut microbiota plays an important role in health and disease. Reduced microbial diversity is considered a key factor in the increase in allergies observed in developed countries. The World Allergy Organisation recommends the use of probiotics for the primary prevention of eczema while clinical trial evidence indicates a moderate benefit for allergy in a number of population groups. This talk will review the latest research on the use of probiotics for allergy, limitations to the research and whether sufficient evidence is available for clinical recommendations on the use of probiotic supplements in allergy.
**GUT MICROBIOTA IN HEALTH & DISEASE**

**TRACK CHAIR:**

**YUNN-HWEN GAN**
Associate Professor, Department of Biochemistry, National University of Singapore

**LYNETTE FERGUSON**
Director of Mutagen Testing, Auckland Cancer Society Research Centre (ACSRC) & Professor of Nutrition, The University of Auckland, New Zealand

*Can we modify the microbiome of an inflammatory bowel disease population using a dietary supplement without prebiotics or recognised probiotics?*

**PETER VUILLERMIN**
Associate Professor in Paediatrics, School of Medicine, Deakin University, Australia

*The maternal microbiome during pregnancy and offspring allergic disease and asthma*

Evidence from animal models suggest that a maternal diet high in microbiota accessible carbohydrates (MACs) may be associated with decreased offspring allergic disease and asthma. However the relevance of these findings to humans remains uncertain. The Barwon Infant Study (BIS) is the only extant birth cohort to combine the assembly of maternal dietary data and faecal samples during pregnancy with detailed phenotyping of offspring immune function, allergy status (including challenge proven food allergy), lung function and respiratory health. In this session Prof Vuillermin will present exciting findings from BIS regarding the relationship between the maternal diet and microbiome during pregnancy and offspring allergic disease.

**DIETER BULACH**
Senior Research Scientist, Victorian Life Science Computation Initiative, The University of Melbourne, Victoria, Australia

*Using whole metagenome sequencing (WMS) to investigate the onset of Bacterial Vaginosis*

- An outline of the WOW study led by Dr Catriona Bradshaw healthy BV specimens
- Overview of microbial communities present in specimens from WOW study using 16s gene sequencing
- Use of these data to select specimens for WMS
- Outline of analysis strategy used to investigate WMS data sets with emphasis on evaluation of Gardnerella genetic types present in specimens

**DIARY WOOD**
Postdoctoral Research Officer, School of Chemistry and Molecular Biosciences, Australian Centre for Ecogenomics, The University of Queensland, Australia

*A natural history of the actinic keratosis microbiome in immunocompetent men*

Actinic keratosis is a condition where pre-malignant lesions develop on sun-damaged skin, and if untreated, a small percentage progress to cutaneous squamous cell carcinoma (cSCC). Human skin hosts resident bacterial and fungal populations that may be associated with AK and cSCC. We applied culture-independent community profiling and shotgun metagenomics to longitudinally investigate the AK and cSCC microbiome in a cohort of ten immunocompetent men with a history of cSCC. Our results indicate highly patient-specific communities and taxa significantly associated with AK and cSCC lesions and also different taxa associated with non-lesional skin. These findings indicate the personalised nature of AK lesion pathology, and may aid in the treatment of AK and subsequent cSCC lesions.

**HARJINDER SINGH**
Distinguished Professor and Director, Massey Institute of Food Science and Technology, Massey University, New Zealand

*Technological challenges for enhancing the stability of probiotic bacteria in functional foods*

Probiotic bacteria have been increasingly added to various foods. To achieve a significant benefit of probiotics, we need to consume relatively high number of live bacteria (108 – 109 CFU/day), which need to reach the intestine safely in a viable state. However, probiotics when administered as a part of food product experience many unfavourable conditions, such as adverse processing parameters (heating, low pH, oxygen etc.), and exposure to gastric acid in the stomach and bile salts in the intestine. Therefore the incorporation of probiotics into functional foods presents a formidable challenge, primarily in terms of shelf-life and viability through to time of consumption. Traditionally, chilled dairy products have been the main formats for delivery of probiotics in foods. Incorporation of probiotic bacteria into food products that are stored at room temperature creates an overwhelming challenge for probiotic stability. The presentation will mainly focus on recent approaches for stabilization of probiotic cells to deliver probiotics through shelf stable foods.

**PATRICIA CONWAY**
Professor, School of Biological, Earth and Environmental Sciences, UNSW Australia

*The role of probiotics in infant health and well-being*

The composition and function of the developing gut microbiome of the infant has huge ramifications for the health and well-being of the infant and through-out life. It is therefore important to understand the factors which impact on the gut microbiome, and how the microbiota impacts on the health of the infant, in order to appreciate how and when intervention with probiotics can be most beneficial. Many different probiotic strains have been trialled for infants, both single and multiple strains. The various studies will be reviewed for infants from birth onwards. It can be concluded that some strains have been shown to be efficacious for specific indications, and routine use for infants can be recommended for specific probiotics, but caution in the strain selection is imperative.
The microbial colonization of the infant gut plays a key role in immunological and metabolic pathways, and alterations of this process have been associated with an increased susceptibility to diseases later in life. It is therefore critical to gain in-depth insights on how the early colonization process occurs and the key factors in early life that can be of long term importance. It has been previously thought that the in utero environment was largely sterile and that the fetus was not colonized with microorganisms until birth. Increasing evidence such as the presence of bacteria in the placenta, meconium or cord blood suggests that the origin and establishment of the neonatal gut microbiota begins well before delivery. This initial exposure to an antenatal source of bacteria is followed by a postnatal exposure occurring during and shortly after birth, where a larger inoculum is transferred during vaginal delivery (fecal and vaginal microbiota) and breastfeeding (human milk microbiota). Besides mode of delivery (vaginal birth vs cesarean section) and type of feeding (human milk vs formula feeding), other factors such as gestational age, introduction of solid foods, environmental factors (urban vs rural; presence of pets or siblings) and antibiotic treatment are known to influence this process. Clues from epidemiological studies have shown associations between these factors and long-term health implications.

The relevance of the gut microbiota in the first 1,000 days

Gut microbiota alteration has been associated with inflammatory bowel disease (IBD) and colorectal cancer. Sequencing technologies have recently boosted metagenomics of microbiota in human health. Since the dietary habits of Indian are different from that of Western world therefore, results of studies on Western population cannot be extrapolated to their Indian counterparts. A study has been carried out in Indian population with IBD and colon carcinoma patients. 16S ribosomal RNA amplicon sequencing has been carried out. Operational Taxonomic Units (OTUs) and relative abundance of bacteria were assessed. Control group included healthy vegetarian group and non vegetarian group. Eubacterium, Ruminococcus, Faecalibacterium, Prevotella, Bacteroides and Lactobacillus were core genera in all groups. There was significant difference in the OTUs and presence of genera and species unique to different subjects and groups.

The origin and establishment of the neonatal gut microbiota begins well before delivery. This initial exposure to an antenatal source of bacteria is followed by a postnatal exposure occurring during and shortly after birth, where a larger inoculum is transferred during vaginal delivery (fecal and vaginal microbiota) and breastfeeding (human milk microbiota). Besides mode of delivery (vaginal birth vs cesarean section) and type of feeding (human milk vs formula feeding), other factors such as gestational age, introduction of solid foods, environmental factors (urban vs rural; presence of pets or siblings) and antibiotic treatment are known to influence this process. Clues from epidemiological studies have shown associations between these factors and long-term health implications.


gut microbiota alterations in inflammatory bowel disease and colon carcinoma

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was a threefold improvement in cholesterol reduction than that achieved by LP-LDL\(^*\) alone. The biological effect correlated with Lactobacillus concentrations indicating a synergistic effect that was not observed when LP-LDL\(^*\) was used in combination with a control GOS, which had no an impact on cholesterol reduction.

These studies suggest potential for:

- The development of species or genera specific prebiotics which can selectively enhance the growth and health benefits of existing probiotic products. This new product concept, called an OptiBiotic\(^*\), has the potential to enhance probiotic health benefits and provide product differentiation in the probiotic market, a market forecast to be worth more than $46.5bn by 2020 (Markets and Markets).
- Designer ingredients which can modify an individual's current microbiome to improve health. As LPGOS is heat resistant and stable during processing this creates the opportunity to incorporate low cost, safe, cholesterol lowering ingredients, in a wide range of food products.

CONTINUED
HONGWEI ZHOU
Professor, Director, Division of Laboratory Medicine, Zhujiang Hospital, Southern Medical University, China

Population survey reveals regional distribution of gut microbiota with universal microbiome signatures for metabolic syndrome

- We performed a cross-sectional survey of gut microbiome for 8600 individuals using stratified randomized sampling in Guangdong Province, China.
- Gut microbiome from different sampling sites obviously aggregated, and social-economic factors showed great impact on the distribution.
- Even though the baseline of gut microbiome were different from various regions, there were similar patterns of microbiome signatures for people with metabolic syndrome from different regions.

RINA AGUSTINA
Scientist, Southeast Asian Ministers of Education Organization Regional Center for Food and Nutrition (SEAMEO RECFON) / Pusat Kajian Gizi Regional (PKGR), Universitas Indonesia Head of Human Nutrition Research Cluster and Research Coordinator Department of Nutrition, Faculty of Medicine, Universitas Indonesia – Dr. Cipto Mangunkusumo General Hospital, Indonesia

Advancing probiotic research in the Southeast Asia Region: updates from the probiotic working group

Probiotic research is relatively new and fast growing in the Southeast Asia (SEA). The 2nd SEA Probiotic Working Group (PWG) workshop attended by 7 countries experts from multi-disciplines and sectors was organized by SEAMEO RECFON in collaboration with Faculty of Medicine, Universitas Indonesia in Jakarta (2016). The workshop indicated that approximately 250 studies were conducted in this region with around 34 probiotic randomized controlled-trials mainly in Indonesia, Thailand, Malaysia, Singapore, Vietnam and Myanmar. The above studies focused on acute diarrhea, child growth, antibiotic-associated diarrhea, lactose intolerance, Helicobacter pylori infection, and allergic diseases. Lactobacillus sp. appears to be the most studied strain and its application are considered safe. Although probiotic products are widely marketed especially in vulnerable groups, probiotic regulations on the development of new strains, products and claims in promoting human health is limited and non-harmonized. A huge diversities of microbiota among Asian populations was reported but information on country-specific microbial genes was lacking due to complex interaction between various local diets and gut microbiota in various ethnicities, lack of laboratory facilities, and low financial research investment. The PWG recommended to initiate a multicenter studies focusing on certain outcome (acute diarrhea and respiratory diseases treatment and prevention) or strain (a combined strain(s) with/without micronutrients) with appropriate design and duration. Probiotic studies on other outcomes (immunity, inflammation or metabolic markers) and traditional fermented foods must also be conducted. The SEA microbiota mapping using metagenomics should be used as one of the most powerful approach. Advanced techniques and high quality methodology in probiotic researches are necessary. Thus, the development or harmonization of clinical trial guidelines on safety, efficacy and effectiveness of probiotics are needed for consumer protection and advancement in probiotic science in the region. Therefore, concrete networking activities and collaboration between scientists, medical associations, industries, and regulators should be further enhanced.
KEYNOTE ADDRESS:
YUAN KUN LEE
Associate Professor, Department of Microbiology, National University of Singapore

Human microbiota: A bioresource for gene mining and microbial prospecting
- Human microbiota highly concentrated and diverse, adapting to extreme ecological environment.
- Produce wide range of enzymes that react with food constituent, for food application and processing.
- Produce signal molecules, which control host gene expression in local and remote organs, for medical application and modulation of gut microbiota.

SIEW NG
Professor, Department of Medicine & Therapeutics, Institute of Digestive Disease, The Chinese University of Hong Kong

Gut microbiota and fecal microbiota transplantation
Alterations in the intestinal microbiota is associated with several digestive diseases and systemic diseases, including clostridium difficile infections, inflammatory bowel disease, irritable bowel syndrome, colorectal cancer, obesity, atherosclerosis, diabetes and metabolic syndrome. Faecal microbiota transplantation (FMT) represents a clinically feasible way to restore the gut microbial ecology, via infusion of intestinal microbiota from a healthy donor into a diseased recipient. FMT has proven to be a breakthrough for the treatment of recurrent Clostridium difficile infection. There are many unanswered questions regarding FMT, including donor selection and screening, routes of administration including the development of a fecal capsule, long-term safety, and regulatory issues. We will share the Chinese University of Hong Kong's experience in FMT for digestive diseases and address the current status and future perspective of FMT for treating human diseases.

NICOLE ROY
Principal Scientist and Science Team Leader, Food Nutrition & Health, AgResearch Grasslands, Adjunct Associate Professor, Riddet Institute, Massey University, New Zealand

The first 2000 days of life, a milk story
Human milk is rich in a family of structurally diverse unconjugated glycans that are prebiotics and improve the maturation of the gastrointestinal tract among other functions. The number of oligosaccharides reported thus far in mature bovine ruminant milks is far less than the 200 different structures reported in human milk. The paucity of studies exploring the biological functions of these oligosaccharides is attributable to the limited number of efficient methods of producing oligosaccharide enriched products. This presentation will present new findings on the molecular and physiological analyses of the host and microbiota responses to diets enriched in oligosaccharides or other milk components. It will provide new insights into this complex relationship and its relevance to growth and development in the first 2000 days of life.
YOSHIHISA YAMASHITA
Professor & Chairperson, Section of Preventive and Public Health Dentistry, Kyushu University
Diagnostic value of salivary microbiome to grasp periodontal health condition and susceptibility to periodontal disease

We previously showed the association between salivary microbiome composition and oral health related factors in the study with 2,343 community-dwelling subjects. In the study, we proposed core oral OTUs composed of 72 OTUs commonly observed. On the other hand, we recently found that most of bacteria species corresponding to minor OTUs in saliva of subjects exhibiting higher phylogenetic diversity are periodontal pathogens mainly harboring in subgingival pocket. Furthermore we defined two community types (Type I and Type II) of salivary microbiome based on relative abundances of major 22 core OTUs occupying ≥1% of mean relative abundance. Type II showed close relationship with better periodontal health condition. I will discuss diagnostic value of salivary microbiome to grasp periodontal health condition and susceptibility to periodontal disease.

HANI EL-NEZAMI
Associate Professor; School of Biological Sciences, The University of Hong Kong
Liver cancer a potential target for probiotic intervention

Hepatocellular carcinoma (HCC) is the sixth most common cancer and the second leading cause of all-cancer related deaths in the world. It is a disease with poor prognosis with unsatisfactory long-term survival of patients, and thus new strategies to control this disease are warranted. This presentation describes a series of studies showing the path from laboratory-based findings in vitro and animal experiments to confirm the in vitro findings in vivo, to field studies in human subjects. The relevance of the data collected in various stages is discussed, and a proof of concept study on the interaction of well-defined probiotic bacteria with a liver cancer associated dietary contaminant will be presented.
## ROUNDTABLE DISCUSSIONS:

### TABLE 1: MARGARET IP  
Professor, Department of Microbiology, The Chinese University of Hong Kong  
**Antimicrobial resistance**  
In September 2016, the United Nations (UN) General Assembly highlighted the problem of antimicrobial resistance (AMR) and the action plans underpin the need to understand the scale of the problem and stop misuse of antimicrobials in human, animal health and agriculture.  
- **What is antimicrobial resistance?**  
- **How do antimicrobials impact on our human microbiota?**  
- **Can we harness innovative approaches to tackling infections via modulation of our microbiota?**

### TABLE 2: YING-CHIEH TSAI  
Professor, National Yang Ming University, Taiwan  
**Gut-brain axis**  
- How does the microbiota influence brain, behavior, and the development of neurological disorders?  
- What are the mechanisms behind psychobiotics and their effect on the MGBA?  
- How can we bridge the gap between research and clinical application for treatment in humans?

### TABLE 3: LARRY WEISS  
Chief Medical Officer, AOBiome, LLC, USA  
**Skin microbiome**

### TABLE 4: NIRANJAN NAGARAJAN  
Associate Director and Group Leader, Genome Institute of Singapore, A*STAR, Singapore  
**Microbiome data analysis – establishing correlation & causation**  
- 16S versus Metagenomic sequencing  
- > Poll on what is more widely used  
- > Provocative questions: Should we stop using 16S sequencing? Is metagenomic sequencing data overload?  
- Is there any utility for long-read platforms?  
- > Correlation versus causation in Microbiome Research  
- > Is this a valid criticism? If so, how do we go about addressing this (longitudinal studies, multi-omics)?  
- > What are the missing bioinformatics solutions?  
- What do you believe is the single biggest bioinformatics challenge in Microbiome research?  
- > Can we ever build true “systems biology” models?  
- Can we predict microbial community dynamics?  
- > Nature versus nurture: what shapes the microbiome more, genetics or environment?

### TABLE 5: PRAMOD GOPAL  
Science Group Leader, Food, Nutrition & Health, The NZ Institute for Plant & Food Research Ltd.  
**Prebiotics, diet and microbiota**  
- Prebiotics in early childhood nutrition  
- Prebiotics effects in the context of background habitual diets  
- What will be the next generation of prebiotics?

### TABLE 6: SEAN HALL  
MD, MBA, CFEO/MD – Medlab Clinical Ltd, Australia  
**Business development and regulation**  
- What is the attraction to research in this area?  
- What are some of the major stumbling blocks in conducting research in this area?

### TABLE 7: HARJINDER SINGH  
Distinguished Professor and Director, Massey Institute of Food Science and Technology, Massey University, New Zealand  
**Probiotics delivery – encapsulation, survival, quality control**  
- Challenges for the delivery of viable functional probiotic bacteria in food formulations  
- Encapsulation and other technological approaches for protection of probiotics  
- Protection during food processing and subsequent storage of food products  
- Protection in the gastro-intestinal tract and physiological processing
COMPANY SHOWCASE:
AARON DEL DUCA
VP Technology & Lead, Microbiome Program, DNA Genotek, Inc.

Applying quality engineering principles to enhance reproducibility of longitudinal metagenomics studies
Study designs for longitudinal clinical trials and for validating biospecimen collection/stabilization devices share a surprisingly common architecture.
In this talk we’ll discuss the QC practises and metrics we find most helpful to identifying sources of bias in a metagenomics workflow. In particular:

- Practical considerations for establishing ‘ground truth’, and strategies for measuring small changes over time
- Disentangling cause and effect when comparing longitudinal relative abundance measurements (with 16S or shotgun NGS)
- In silico methods for standardized phenotyping and managing confounding variables

PREBIOTICS & DIET

SOLUTION PROVIDER PRESENTATION:
DAVID J. KYLE
CEO, Evolve BioSystems

The Infant Gut Microbiome: From Dysbiosis to Recovery
Human milk has been the sole source of nutrition for infants for millions of years, and is rich in species specific oligosaccharides (HMO). Not surprisingly, the infant gut microbiome is dominated by a species of Bifidobacteria exceptionally well suited to consume HMOs. Through the unintended consequences of formula feeding, antibiotic use, and C-section deliveries, this natural infant microbiome has been radically changed in much of the world today. This gut dysbiosis leads to significant changes in the colonic microenvironment and may result in the increased prevalence of autoimmune and metabolic dysfunction seen over the past 60 years. We have developed a solution to rescue the natural microbiome from this dysbiosis through early intervention in healthy infants, returning the colonic microenvironment to its natural state.

PROBIOTICS IN ANIMAL HEALTH & AQUACULTURE

PANEL DISCUSSION:
Probiotics in animal health & aquaculture

TRACK CHAIR:
INGRID SURONO
Head of Food Technology Department, Binus University, Indonesia

PANEL CHAIR:
ROBERT MOORE
Director, Australian Centre for Ecogenomics; Professor, School of Chemistry & Molecular Biosciences, The University of Queensland, Australia

PANELLIST:
SUHIT NITISINPRASERT
Associate Professor, Department of Biotechnology, Faculty of Agro-Industry, Kasetsart University, Thailand

PANELLIST:
HAU-YANG TSEN
Professor of Food Science and Technology, Hungkuang University, Taiwan

PANELLIST:
SHIVANANDA MURTHY
Professor & Head, Karnataka Veterinary & Fisheries Sciences University, College of Fisheries, Mangalore, India

Lunch

12:40-12:55
COMPANY SHOWCASE:
AARON DEL DUCA
VP Technology & Lead, Microbiome Program, DNA Genotek, Inc.

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12:55-13:25
SOLUTION PROVIDER PRESENTATION:
DAVID J. KYLE
CEO, Evolve BioSystems

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13:25-13:55
PANEL DISCUSSION:
Probiotics in animal health & aquaculture

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PANELLIST:
SHIVANANDA MURTHY
Professor & Head, Karnataka Veterinary & Fisheries Sciences University, College of Fisheries, Mangalore, India
**MARGARET MORRIS**
Professor, Chair and Head of Pharmacology, School of Medical Sciences, University of New South Wales, Australia

**Effects of diet on cognition – role of the microbiota**
Rats exposed to diets rich in either fat and sugar, or sugar, showed cognitive impairment – specifically on hippocampal-dependent place recognition memory. Changes in gut microbiota are observed in response to such diets, with reduced diversity. Even short-term exposure to diets rich in sugar or saturated fat, in the absence of weight gain, impaired cognition. The sugar- and fat-enriched diets had specific effects on the fecal microbiome. Changes in microbiota profile were associated with altered hippocampal mRNA expression of inflammatory markers.

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**ELIANA MARIÑO**
Head, Immunology and Diabetes Laboratory, Monash University, Melbourne, Australia

**Gut microbial metabolites regulate autoimmune T cell responses and protect against type 1 diabetes**
Diet and gut microbial ecology may underlie the increasing incidence of certain inflammatory diseases. Here, we found that key features of autoimmune diabetes in NOD mice correlated closely with fecal concentrations of the short chain fatty acids (SCFAs) acetate and butyrate. High acetate- or butyrate-yielding diets significantly reduced progression to diabetes, towards changes in the microbial community, improved gut epithelial integrity and reduced concentrations of pro-inflammatory cytokines. Both acetate and butyrate diets led to dramatically decreased numbers of autoreactive T cells. A high butyrate-yielding diet promoted conversion of naïve Foxp3+ T cells into Foxp3+ Tregs in vivo. In contrast, an acetate-yielding diet directly targeted B cells, which led to a markedly control of autoimmune T cell frequencies, and protection from diabetes.

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**YUNN-HWEN GAN**
Associate Professor, Department of Biochemistry, National University of Singapore

**Differential host and bacterial virulence factors driving Klebsiella liver abscess in ethnically diverse Singapore**
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. The bacteria are believed to translocate from the intestines to the liver. However, factors which predispose and facilitate the colonisation in the gut are not clearly understood. We examined prospectively the profiles of 70 patients together with their isolates’ genotypic and phenotypic characteristics in ethnically diverse Singapore. The majority of isolates belonged to capsule type K1, which carried higher frequencies of virulence-associated genes. The Chinese, mostly non-diabetic, had higher prevalence of K1 infection than the predominantly diabetic non-Chinese. We also study the nutritional and colonization requirements of various isolates in the gut to understand the link to disease.

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**ROSHADA HASHIM**
Professor, Fish Nutrition and Feeding Management, Faculty of Science and Technology, Universiti Sains Islam, Malaysia

**Opportunities in probiotic intervention for warm freshwater fish aquaculture**
Probiotic supplementation in fish feeds is now widely accepted as a possible solution to address the emergence of a large variety of pathogens and bacterial resistance caused by the indiscriminate use of chemotherapeutic agents in fish health management. However, little attention is given to understand how probiotics improve growth and nutrient utilization in diets specifically in feeds containing plant based proteins. This presentation will highlight how probiotic intake enhances growth by influencing digestive enzyme activities, gut morphology and microbiota in Channa straita and Pangasianodon hypophthalmus fingerlings compared to prebiotics. It also discusses how long the advantages attained from probiotic intake is retained and if growth can be further enhanced when a combination of probiotics and prebiotics is used. These will provide a basis for the feeding management of these two species in the future. Finally, the sustainability of probiotics to overcome the drawbacks of intensive aquaculture will be discussed.

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**ROBERT MOORE**
Research Professor of Biotechnology, RMIT University, Melbourne, Australia

**Are in vitro assays of value in assessing potentially probiotic strains of bacteria?**
In vitro assays have been widely used to screen collections of bacterial strains for properties that are believed to indicate the potential in vivo merits of probiotics. Assays that are routinely used include resistance to acid and bile, adhesion to cultured eukaryotic cells, and production of antimicrobial compounds. Surprising, there is little formal proof that performance in such assays is linked to probiotic performance in vivo. The presentation will explore this issue and ask if there are more effective ways to identify probiotic bacteria by directly screening strain collections in vivo.

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**HAU-YANG TSEN**
Professor of Food Science and Technology, Hungkang University, Taiwan

**The Development of Live and Heat Killed Probiotic with Multiple Functions for Animal Feed Use**
Probiotics are live organisms that may beneficially affect the host upon ingestion. The major strains with probiotic functions are those of lactic acid bacteria (LAB). These strains may enhance the immunomodulatory activity of the host and are able to protect the host against the infection of pathogenic bacteria. Selection of the strains for animal feed use and preserving its beneficial functions after feed processing is important. Previously, we have selected four LAB strains with basic probiotic properties and high immunomodulatory activities from 140 strains of different origins. Examples for feed supplement use of these strains include: (1). The multistrain combination of these four LAB strains, i.e., MLAB, when fed mice or chicks, was able to enhance the immunomodulatory activity of their host animals. Furthermore, this MLAB was able to reduce the invasion of pathogenic bacteria, such as the invasion of Salmonella to the liver and spleen of mice and broiler chicks, and also reduce the induced inflammation of the host animals. (2). In addition, it was able to ameliorate the growth rate and the inflammation of broiler chicks caused by Eimeria tenella infection. (3). Moreover, it was also able to enhance the growth rate and the antibody production in chicks vaccinated with New Castle Disease Virus (NCDV). (4). Heat killed cells of this MLAB or the individual strains of this MLAB also has similar functions, which is important for feed processing use. One of the individual strains of this MLAB also has been proved to be useful for pig feed supplement use. Thus this MLAB has multiple beneficial functions when used as the feed supplement.
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