



6TH MICROBIOME R&D & BUSINESS COLLABORATION CONGRESS **5TH PROBIOTICS & PREBIOTICS CONGRESS: ASIA**

An Interactive Forum on Research, Development and Application of Microbiome, Probiotics and Prebiotics

REGENT TAIPEI, TAIWAN

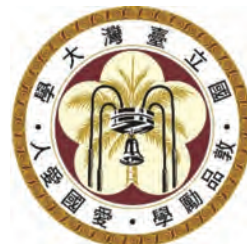
4 - 5 June 2020



Co-Hosts



National Central University



National Taiwan University



Global Engage is pleased to announce, as part of their worldwide microbiome series, the **6th Microbiome R&D and Business Collaboration Congress** and co-located **5th Probiotics and Prebiotics Congress** which will be held on June 4-5, 2020 in Taipei, Taiwan. This year's meeting is co-costed with the National Central University and National Taiwan University.

The congress which hosted close to 280 attendees in 2019, will bring together an even split of industry and academic delegates to discuss the latest microbiome and probiotic science, the development of partnerships and commercial collaborations in this area and the growth of product pipelines.

The 2020 co-located meetings will stage more than 50 top scientists presenting on their latest scientific and business developments in microbiome and probiotics through individual presentations and panel discussions. Topics to be addressed include microbiome communities, how the microbiome affects health, disease, and the therapeutic industry, skin microbiome, probiotics and prebiotics, brain health as well as the regulatory and business considerations, to name a few.

Be part of the event to network with over 300 delegates during ample breaks and luncheons onsite and expand your business reach offsite while exploring what Taipei has to offer. Take advantage of the exhibition hall which will host over 30 solution providers showcasing the latest products and solutions in the market. There will be many opportunities to broaden your connections and maximise your time at the meeting!

MICROBIOME DISCOVERIES

- Latest updates on the microbiome movement in Asia and across the globe
- Bacteriophage
- Early Life and development

TOOLS AND TECHNIQUES FOR STUDYING MICROBIOME

- Sequencing method development
- Multi-omics approaches; genomics, metagenomics, metabolomics
- Bioinformatic tools; data analysis and integration
- Systems biology and modelling microbial communities

MICROBIOME IN HEALTH AND DISEASE

- Inflammation
- Gut-brain axis
- Microbiome pathogen interactions
- Antibiotics resistance
- Microbiome and cancer
- Microbe-host interactions
- Faecal microbiome transplant

OUTSIDE THE GUT

- Skin microbiome
 - Strategies and tools for studying skin microbiome
 - Barrier integrity / wound healing / inflammation / gut-skin axis
- Women's health
 - Host-interactions, vaginal microbiome, preterm birth and pregnancy progression
- Oral and respiratory microbiome

A COMMERCIAL PERSPECTIVE OF MICROBIOME

- Promoting partnerships to support research and collaborations
- Practical and regulatory considerations in microbial products
- Pharma and biotech case studies and strategies

PROBIOTICS DISCOVERY AND R&D

- Strain discovery
- Role of probiotics in IBS management
- Efficacy and effectiveness of different strains
- Probiotics and the gut-brain axis
- Food and fermentation

PREBIOTICS AND DIET

- The potential for prebiotics
- Short chain fatty acids (SCFAs)
- Diet and disease
- The role of diet in shaping the microbiome
- Microbiome and food allergy
- Breastfeeding and the milk microbiome (HMOs)
- Mechanisms of action

BUSINESS CONSIDERATION AND REGULATION

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CONFIRMED SPEAKERS



KAREN NELSON

President and Professor, Genomic Medicine Group, J. Craig Venter Institute, USA



SAMUEL FORSTER

Group Leader, Microbiota and Systems Biology, Hudson Institute of Medical Research, Australia



MORTEN ISAKSEN

Founder and CEO, Bio-Me



LUTZ KRAUSE

Head of Data-Mining and Artificial Intelligence, Microba, Australia



SUNNY WONG KEI

Assistant Professor (Clinical), Medicine and Therapeutics, Institute of Digestive Disease, The Chinese University of Hong Kong, Hong Kong



TSAI-KUN LI

Professor, College of Medicine, National Taiwan University, Taiwan



YUG VARMA

CEO, Phi Therapeutics, USA



DRAGANA GAGIC

Senior Research Fellow, Microbiology, Massey University, New Zealand



JEROEN RAES

Professor, Faculty of Medicine, KU Leuven Microbiome and Group Leader, VIB, Belgium



SARAH LEBEER

Research Professor, Microbiology and Biotechnology (ZAPBOF), Department of Bioscience Engineering University of Antwerp, Belgium



NAGENDRA SHAH

Professor of Food Science, School of Biological Sciences, Hong Kong University, Hong Kong



WEI-LIAN WILLIAM HUNG

Director of Scientific Research Head of Probiotics Research Center, Yili Group, Mongolia



GREGORY LAMBERT

CEO and VP R&D, TargEdys, France



YASUHIRO KOGA

Visiting Professor, Department of Gastroenterology, Tokai University School of Medicine, Japan, President, Japanese Society for Probiotic Science, Japan



YEN-HSUAN NI

Distinguished Professor of Pediatrics and Dean of College of Medicine, National Taiwan University, Taiwan



THOMAS DAWSON JR.

Senior Principal Investigator, Skin Research Institute, A*STAR, Singapore



OLIVER CHAO

Head, Emerging Biomedical Sciences, Sanofi, France



MARGARET MORRIS

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



DAMIEN KEOGH

CEO and Co-Founder Maiden Therapeutics, Singapore



CHERI CHU

Senior Research Manager, Unilever Discover Shanghai, China



JENNIFER WING-KI YAU

Department of Pediatrics, The Chinese University of Hong Kong



ELSA JUNGMAN

Founder and CEO, ELSI, USA



MUHAMMAD BILAL ABID

Assistant Professor, Division of Infectious Diseases, Medical College of Wisconsin, USA



LUIS VITETTA

Adjunct Professor, Pharmacology, University of Sydney, Australia



MICHAEL CONLON

Senior Research Scientist, CSIRO, Australia



YU WEIZHU

Vice President of R&D and Innovation, Mengniu Dairy Group, China



CHUN-MING ERIC HUANG

Chair Professor, Department of Biomedical Sciences and Engineering, National Central University, Taiwan



LIONG MIN TZE

Professor, Bioprocessing Technology, Universiti Sains Malaysia, Malaysia



EVGUENI DOUKHANINE

Scientist Microbiome, R&D, DNA Genotek, Canada



JANE MULLANEY

Scientist, AgResearch, New Zealand



PAUL RYAN

Chief Business Development Officer, Labskin UK



ALEX CHAPMAN

Head of Operations, Labskin UK



JQ LIU

Principal Scientist, Procter & Gamble, Singapore



TZEHAU LAM

Senior Scientist, Procter & Gamble, Singapore



NICOLE ROY

Professor, High-Value Nutrition National Science Challenge, New Zealand



WEI-LI WU

Assistant Professor, National Cheng Kung University, Taiwan



MING-JU CHEN

Professor, Department of Animal Science and Technology, National Taiwan University



DEOG-HWAN OH

Professor, Food Microbiology, Seoul National University, Korea



HANNA SIDJABAT

Honorary Fellow and Chief Investigator, University of Queensland Centre For Clinical Research, Australia



YING-CHIEH TSAI

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



TZU-MING PAN

Professor Emeritus of Department of Biochemical Science and Technology, National Taiwan University, Taiwan



KRIBEN GOVENDER

Food Scientist and Registered Nutritionist, Allele Microbiome and Nourishme Organics, Australia

08:00-08:50

Registration & Refreshments

MICROBIOME

08:50-09:00

Global Engage Welcome Address and Morning Chair's Opening Remarks: Thomas Dawson Senior Principal Investigator, Institute of Medical Biology, A*STAR, Singapore



KEYNOTE PRESENTATION: KAREN NELSON

President and Professor, Genomic Medicine Group, J. Craig Venter Institute, USA

Progress update on Human Microbiome Studies

Global research over the past 13 years has begun to show us the breadth of microbial species that live in and on the human body and which we term the human microbiome. Essentially, the human microbiome refers to the collective of bacteria, archaea, viruses, phages and small eukaryotes that are found to inhabit the human body. It is also considered by some to be our second genome. Although there is limited evidence of disease causation, the microbiome has been shown to be correlated with several diseases ranging from oral cavities, to irritable bowel diseases, to various skin disorders. Many attempts are being made by both academic and commercial entities to further understand how this collective can be manipulated to benefit human health using naturally occurring microbial species and consortia, metabolites produced by these species, or synthetic constructs of some of our normal flora. The continuous expansion of knowledge in the human microbiome field with respect to number of microbial species in humans, changes in microbial diversity with age, geographical location of individuals, environmental exposure, use of medications etc., has allowed us to expand our view of human microbiomes. This diversity appears to have impeded the progress of potential commercial applications. These issues will be discussed.

09:00-09:35



KEYNOTE PRESENTATION: JEROEN RAES

Professor, Faculty of Medicine, KU Leuven and Microbiome Group Leader, VIB, Belgium

Quantitative microbiome profiling in health and disease

Alterations in the gut microbiota have been linked to various pathologies, ranging from inflammatory bowel disease and diabetes to cancer. Although large numbers of clinical studies aiming at microbiome-based disease markers are currently being performed, our basic knowledge about the normal variability of the human intestinal microbiota and its determining factors remains limited. Here, I will discuss our findings studying a large-scale study (Flemish Gut Flora Project; n=3400) of the gut microbiome variation in a geographically confined region (Flanders, Belgium), in which analysis of microbiome variability in health identified the primary parameters associated to microbiome composition. In this presentation, I will discuss our experiences in large-scale microbiome monitoring, show how the development of dedicated computational approaches can assist in microbiome analysis and interpretation, and which confounders are essential for inclusion in microbiome disease research. In addition I will show how Quantitative Microbiome Profiling (QMP; Vandeputte et al. Nature 2017), which combines microbiomics with flow cytometry-based cell counts, is profoundly changing our view on gut microbiota variation and allowed the identification of an inflammation-associated, cross-disease enterotype.

09:35-10:10

10:10-10:40

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PROBIOTICS & PREBIOTICS

08:50-09:00

Global Engage Welcome Address and Morning Chair's Opening Remarks: Nagendra Shah Professor of Food Science, School of Biological Sciences, Hong Kong University, Hong Kong



KEYNOTE PRESENTATION: SARAH LEBEER

Research Professor, Microbiology and Biotechnology (ZAPBOF), Department of Bioscience Engineering University of Antwerp, Belgium

Lactobacilli for topical probiotic applications

Lactobacilli have a long history of beneficial safe use in fermented foods and as probiotics for gut health. However, considering their ecology and evolutionary history, they have even more potential to improve human health in more topical applications, such as in the female reproductive tract, on the skin and in the nose. We have recently found some interesting novel strains, taxa and functions of lactobacilli in the vagina, on the skin and in the nose. We are currently exploring whether selected strains can be potential probiotics for vaginal, skin and nasal applications. Hereby, we translate concepts and known mechanisms from the gut to the other mucosal surfaces. We have managed to isolate and characterize lactobacilli that are specifically adapted to the vaginal, nasal and skin environment and that are able to exert the required antimicrobial and anti-inflammatory activities. Subsequently, we were able to formulate them in specifically designed vaginal gels, nasal sprays and skin creams, respectively. After testing their potential efficacy and safety in various lab models, safety and tolerance studies were done in healthy volunteers. Now we are ready for clinical efficacy tests, but the regulatory pathway for these live biotherapeutic products (LBP) is and will not be straightforward.

09:00-09:35



KEYNOTE PRESENTATION: CHUN-MING ERIC HUANG

Chair Professor, Department of Biomedical Sciences and Engineering, National Central University, Taiwan

A Skin Probiotic Bank for Electronic Microbiome Banking and Personalized Skincare

A Skin Probiotic Bank with hundred skin bacterial strains allows us screen and identify bacterial specific Prebiotic. The bank contains two major skin probiotic bacteria: Fermenting and Electrogenic bacteria. Analogs of short chain fatty acids (SCFAs) as post-biotics have been designed as anti-inflammatory or antimicrobial agents. Prebiotics are utilized to trigger the electron production of specific skin bacteria. Our in vitro and in vivo experiments have demonstrated that electron functions as an antioxidant which can quench the free radicals induced by UV radiation, skin aging, inflammation and itchy. Various skin prebiotics with/without INCI names are available in our lab. The electron produced by electrogenic skin bacteria have been successfully applied for skin microbiome banking via an electronic skin patch in conjunction with an App in a smart phone. The electronic skin patch monitors your skin microbiome profile and provides you the best personalized skincare. In this talk, I will introduce you the commercial potentials of skin probiotic, prebiotic, post-biotic and electro-biotic at personalized skincare via skin microbiome banking.

09:35-10:10

10:10-10:40

Solution Provider Presentation

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10:40-11:40

Morning Refreshments / Poster Presentations / One-to-One Meetings

MICROBIOME IN HEALTH AND DISEASE

Chair: Muhammad Bilal Abid Assistant Professor, Division of Infectious Diseases, Medical College of Wisconsin, USA



NICOLE ROY

Professor, High-Value Nutrition National Science Challenge, New Zealand
Immune and microbial

signatures underlying functional gastrointestinal disorders

Irritable Bowel Syndrome (IBS) is a functional gastrointestinal (GI) disorder featuring chronic or recurrent abdominal discomfort, usually with changes in GI habit. To improve our understanding of links between the microbiome and the host, we aimed to identify perturbations in these interactions between healthy control (HC) and IBS individuals (Ethics Reference H16/094). LC-MS metabolite profiling was performed on plasma and faecal samples and shotgun sequencing on faecal samples. Metabolomic analysis of plasma samples showed significant differences in propanoate, pyrimidine and some amino acid and lipid metabolic pathways observed between IBS-C and HC individuals. A wide range of microbial genes involved in carbohydrate, energy, and sulphur metabolism differed significantly in relative abundance between groups. RNA-Seq profiling of peripheral blood mononuclear cells were performed. The metabolome and metagenome datasets will be discussed in relation to the systemic immune gene expression profiles to provide new insights into the alterations in host-microbial metabolism in functional GI disorders.

11:45-12:10



SAMUEL FORSTER

Group Leader, Microbiota and Systems Biology, Hudson Institute of Medical Research, Australia

Combining metagenomic and culturing for the next generation of microbiome-based medicines

This presentation will cover on the following points:

- Whole genome metagenomic sequencing is essential for the development of novel microbiome-based therapeutics
- Combining culturing with genomics provides the capacity to measure microbiome samples with strain level resolution
- Applying functional validation with extensive libraries of bacterial isolates enables advancement to causative validation
- These approaches have delivered significant insights and therapeutic candidates in IBD, Infections and therapies.

12:10-12:35

SKIN MICROBIOME

Chair: Elsa Jungman Founder and CEO, ELSI, USA



THOMAS DAWSON JR.

Senior Principal Investigator, Institute of Medical Biology, A*STAR, Singapore

Microbe/Host interactions with

Malassezia: Implication for Human Skin Health

Malassezia yeast are occupants of all human (and animal) skin. Modern next generation sequencing, coupled with lipidomics, metabolomics, and data integration, have led to a resurgence of Malassezia in the literature and their investigation as a target for skin health intervention. Malassezia have been implicated as commensal, pathogenic, and protective in various inflammatory skin conditions including seborrheic dermatitis, atopic dermatitis, pityriasis versicolor, psoriasis, and others. However, it remains unclear how Malassezia communicate with the human host, and vice versa. We have investigated specific signalling molecules secreted by Malassezia and how they interact with the human immune system and other skin micro-organisms. We are currently probing a large, well characterized Singaporean cohort in an effort to determine how the skin microbiome, and specifically Malassezia, are involved in skin health. Future work will entail isolation of specific molecules which can interrupt Malassezia to host signalling to improve skin health.

11:45-12:10



CHERI CHU

Senior Research Manager, Unilever Discover Shanghai, China
Title TBC

12:10-12:35

FUNCTIONAL FOODS

Chair: Deog-Hwan Oh Professor, Food Microbiology, Seoul National University, Korea



Professor of Food Science, School of Biological Sciences, Hong Kong University, Hong Kong

Challenges of synthesizing GABA) in milk by a novel strain of Lactobacillus brevis

In the present study, we have developed a novel screening and identification method for gamma-aminobutyric acid (GABA)-producing LAB from Korean kimchi. The amount of GABA produced in MRS by the LAB at various monosodium glutamate (MSG) concentrations and incubation time was quantified by HPLC. Genetic identification of high GABA-producing LAB was carried out by both 16S rRNA gene and glutamate decarboxylase gene (GDG). Nine potential GABA-producing LAB isolates were selected by observing gas release during fermentation. The conversion ability of MSG into GABA by the isolates varied with MSG concentration. The isolates were genetically identified as Lactobacillus brevis by 16S rRNA gene and confirmed by GDG. The genome of L. brevis NPS-QW-145 has been completely sequenced in our lab. Due to absence of extracellular proteinases and being of plant origin, in L. brevis was not able to produce GABA in milk. However, dairy starters were able to support the growth of L. brevis and GABA biosynthesis. Two GAD genes, gadA and gadB, were identified in L. brevis 145. S. thermophiles improved the viability of L. brevis 145 in milk. Dairy S. thermophilus metabolized more glutamate supplemented to milk than L. bulgaricus.

11:45-12:10



WEI-LIAN WILLIAM HUNG

Director of Scientific Research Head of Probiotics Research Center, Yili Group, Mongolia

Characterisation of a Bifidobacterium strain BL-99 and its application in fermented milk

In this present study, Bifidobacterium lactis strain BL-99 which was isolated from a healthy Chinese infant, was evaluated for its ability to regulate the gut microbiota and improving digestion function in animal models. The mice/rats were given live B. lactis BL-99 for gut microbiome test (3.88×10⁹, 3.88×10¹⁰, 3.88×10¹¹cfu/d) and digestion function test (1×10⁶, 1×10⁷, 1×10⁸, 1×10⁹, 1×10¹⁰cfu/d). The diversity of the mouse intestine microbiota was evaluated using 16S sequencing, whereas ink propulsion test, and measurements of body weight, food intake, and pepsin digestibility were used for digestion function test. After 14- or 30-days intervention, the relative abundance of Bifidobacterium and Lactobacillus was increased, while the relative abundance of Clostridium, Enterobacter, and Enterococcus was

12:10-12:35

12:10-12:35

Continued



MORTEN ISAKSEN
 Founder and CEO, Bio-Me
**GutCheck™ - A novel
 microbiome analysis
 platform**

Current DNA sequencing technologies are useful for exploratory purposes and has given rise to much of our understanding of how the microbiome contributes to disease and health. In order to translate this knowledge into practical applications, GutCheck™ has been developed. GutCheck™ is the first and only rapid, detailed and accurate gut microbiome analysis platform. In this presentation, some of the features of GutCheck™ will be presented, along with examples of the power of the technology in preventive health, as a research tool and in clinical settings.



12:35-13:05

12:10-12:35

Continued



**SPEAKER TO
 BE ADVISED**
 MGI Tech
Title TBC

12:35-13:05

12:10-12:35

reduced when compared to the control group, whereas rats in the middle dose group (1x10⁸cfu/d) and high dose group (1x10⁹ cfu/d) had significantly higher gastric juice secretion than the control model group. The middle dose group (1x10⁸cfu/d) had a significantly higher pepsin excretion than the control group. The results indicate that B. lactis strain BL-99 have potential to positively regulate the intestinal flora composition and improving digestion function of mice that was later added to a yogurt product "Yixiao" in China.

12:35-13:05

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13:05-14:05

Lunch / Poster Presentations / One-to-One Meetings

Chair: Muhammad Bilal Abid Assistant Professor, Division of Infectious Diseases, Medical College of Wisconsin, USA



LUTZ KRAUSE
 Head of Data-Mining and Artificial Intelligence, Microba, Australia
Title TBC

14:05-14:30

Chair: Elsa Jungman Founder and CEO, ELSI, USA



JQ LIU
 Principal Scientist, Procter & Gamble, Singapore
TZEHOU LAM
 Senior Scientist, Procter & Gamble, Singapore
Case studies of using microbiome-based indices for personal and home care product efficacy evaluation

Having a balanced microbial community is critical to personal health. It is of a great interest to develop microbiome-based indices for health status diagnosis and product efficacy evaluation. This presentation will highlight the development and application of microbial index of skin health (MiSH), microbial index of gingivitis (MiG), and microbial index of built environment (MiBE). Three case study results demonstrated that the microbiome-based indices have the potential to be used not only for diagnosing skin/oral health and built environment desirability, but also for the associated personal and home care product efficacy evaluation.

14:05-14:30

Chair: Hanna Sidjabat Honorary Fellow and Chief Investigator, University of Queensland Centre For Clinical Research, Australia



TZU-MING PAN
 Professor Emeritus of Department of Biochemical Science and Technology, National Taiwan University, Taiwan

Chemotherapy with Lactobacillus paracasei subsp. paracasei NTU 101 fermented product inhibits colorectal cancer and ameliorates the side effects

Oral administration of chemotherapy drugs could induce chemotherapeutic side effects. However, oral administration of Lactobacillus paracasei subsp. paracasei NTU 101 fermented skim milk (NTU 101FM) for 4 weeks could significantly improve the appetite and weight loss which induced by chemotherapeutic. Compared to the chemotherapy-only group, NTU 101FM combine chemotherapy treatment significantly reduced the tumor volume and tumor weight to 1/3 and 1/4, respectively (p<0.05). When NTU 101FM extracts combination with the chemotherapeutic drug 5-fluorouracil (5-FU) in the colorectal cancer cell (CRC) model, the extracts of NTU 101FM could effectively reduce CRC cell viability to 76% (p<0.05), but it did not induce cytotoxicity to colon epithelial cells and significantly increased RAW 264.7 cell viability up to 150% (p<0.05). The anti-CRC

14:05-14:30

14:05-14:30

Continued



SUNNY WONG KEI

Assistant Professor (Clinical), Medicine and Therapeutics, Institute of Digestive Disease, The Chinese University of Hong Kong, Hong Kong

Gut microbiota as for clinical application in colorectal cancer

Colorectal cancer (CRC) is an important cancer globally. Metagenomic studies have revealed microbial changes in CRC patients, and functional studies have pinpointed the role of several bacteria in colorectal carcinogenesis, including *Fusobacterium nucleatum*, certain strains of *Escherichia coli* and *Bacteroides fragilis*. Recent studies have also pointed to the importance of gut microbiota in the cancer treatment, particularly on immunotherapy. These findings give new opportunities to harness these microbes for clinical applications. One of the emerging translational applications of the gut microbiota is on biomarker discovery. A biomarker is an indicator of the presence or severity of a disease. Given its significant global health burden, slow progression from detectable pre-cancerous lesions, treatability of early cancers, and proven efficacy to reduce mortality, an accurate, affordable and non-invasive test for CRC is highly needed. The gut microbiota serves as a rich source for identifying potential biomarkers for CRC screening as well as disease prognostication. Furthermore, the gut microbiota may be potentially manipulated to help prevent or treat the cancer. In this talk, I will review latest literature on the colorectal cancer microbiota and discuss clinical applications of gut microbiota for diagnosis and treatment of colorectal cancer.

14:30-14:55



EVGUENI DOUKHANINE

Scientist Microbiome, R&D, DNA Genotek, Canada

At-home collection device to effectively collect & stabilize faecal samples for metabolomic analysis

Metabolomics analyses provide additional layer of data in the form of a phenotypic readout, complimentary to traditional metagenomics approaches. To date,

14:55-15:10



14:05-14:30

Continued



JENNIFER WING-KI YAU

Department of Pediatrics, The Chinese University of Hong Kong

The role of skin microbiome in paediatric atopic dermatitis

Atopic dermatitis (AD) is a prevalent childhood allergy around the globe. Although dysbiosis of skin microbiota was shown to take part in the disease pathogenesis, our understanding on microbiome was mainly sourced from the amplicon sequencing data on bacteria. Our goal is to also identify multi-kingdom species resided on skin in the paediatric population using whole-genome shotgun sequencing and delineate their roles on childhood AD. We conducted a cross-sectional study, recruiting a hundred subjects, and collected control, non-lesional and lesional skin swabs for their microbial signatures. Several unreported non-*Staphylococcus* bacterial species, fungal and viral members were identified to be associated with childhood AD. They were key contributors of lipid metabolism, antimicrobial biosynthesis and amino acid metabolisms at healthy state. A shift of contributors responsible for these core pathways during AD, implies possible mechanisms of how the commensals influence the epidermal barrier, modulate host immunity and interact with one another on the skin.

14:30-14:55

14:55-15:10

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14:05-14:30

effect of bioactive compounds in NTU 101FM ethanol extract were identified as a mixture of palmitic acid, stearic acid and glyceryl 1,3-dipalmitate (PSG). PSG significantly decreased CRC cell viability at dosages that were not cytotoxic to normal colon epithelial cells or macrophages. Moreover, the inhibitory effect of the combination of PSG and 5-fluorouracil (5-FU) was significantly greater than that of 5-FU alone ($p < 0.05$). In conclusion, NTU 101FM would possibly be a favorable candidate in food supplement for auxiliary anti-colorectal cancer or moderation chemotherapeutic side effects.



DEOG-HWAN OH

Professor, Food Microbiology, Seoul National University, Korea

Application of Bioconversion technology using Synbiotics for Gut Microbiota Modulation

Human-milk-and fermented soybean-based probiotics play a major role against gastrointestinal infection and High blood pressure. Among 41 Lactic acid bacteria (LAB) strains, four strains showed high antimicrobial activity and one strain showed antihypertensive activity. Four LAB strains showed high resistance to digestive enzyme (80%–94%). All four selected isolates were resistant to antibiotic. The results show that *Pediococcus acidilactici* is likely an efficient probiotic strain to produce <3 Kda pediocin-based antimicrobial peptides, confirmed by GCMS and HPLC with the corresponding sequences from class 2 bacteriocin. Likewise, fermented soy protein product (P-SPI) based on *Lactobacillus rhamnosus* to reduce high blood pressure in hypertensive mice and spontaneous hypertensive rats (SHR) and how they modulate the gut microbiota after oral administration. Both BPH/2J mice and spontaneous hypertensive rats were fed with P-SPI, Captopril or physiological saline and their blood pressures were monitored. Consumption of P-SPI significantly reduced systolic and diastolic blood pressure by inhibiting serum angiotensin converting enzyme activity. Analysis of fecal microbial 16S rRNA of SHR after six weeks of feeding revealed a significant reduction in microbial richness and diversity in the gut. Our results show that, long-term consumption of P-SPI modulates the gut microbiota and reduces high blood pressure.

14:30-14:55

14:55-15:10

Solution Provider Presentation

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14:55-15:10

challenges surrounding the collection of samples for metabolomics, flash freezing with dry-ice transport, has limited the scope of most studies in terms of scale of sample size, accessible population and geographic range available for sampling. DNA Genotek offers a unique and comprehensive solution for the collection and stabilisation of microbial DNA from feces in the form of its OMNIgene.GUT collection device. Using the unique physical design of the OMNIgene.GUT kit, which ensures sample ease-of-use, reproducibility and homogeneity, we have developed a novel complement of physical form and buffer for collection and ambient stabilization of fecal metabolites, while preserving compatibility with common metabolomics processing platforms. In this presentation, we will review some of the validation data generated for this new device with the support of Metabolon Inc.

14:55-15:10

Continued

14:55-15:10

Continued

15:10-15:35



TSAI-KUN LI

Professor, College of Medicine, National Taiwan University, Taiwan

Potential of Urogenital

Core Microbiota Signatures as Biomarkers and Interventions for Female Reproductive Health

Female urogenital microbiota is mainly composed of urinary, cervix and vaginal commensal bacteria. Though metagenomic approaches and innovative culture-based strategies (culturomic) being rapidly advanced, identification of core components/ signatures of microbiota playing key roles in women health remains a challenging endeavor. With the urgent needs to characterize the female urogenital microbiota signatures in Taiwan, our study design has then collected the cervical and vaginal swab and urine samples at three different time spots from 57 Taiwanese female clients receiving assisted reproductive treatment. The profiling of microbiota from those samples was determined by both the NGS on 16S rDNA and the culturomics with MALDI-TOF for rapid identification. We found that the urinary microbiota vary with different time spots, and potential microbial core compositions differ among urine, cervix, and vagina. Importantly, similarities and differences of identified microorganisms between the sequencing and culturomics methods were compared. Furthermore, several types of Taiwanese local vaginal microbiota were grouped and compared to the Asian population in the United States. Armed together, we identified the potential of utilizing urogenital core microbiota for early-stage detection/biomarkers of female reproductive health states. Their usages for early preventive and/or therapeutic intervention as well as reproductive health supplements will also be discussed.

15:10-15:35

15:10-15:35

TAIWAN REPRESENTATIVE

(Reserved)
Title TBC

15:35-16:35

Afternoon / Poster Presentations / One-to-One Meetings

MICROBIOME

**YUG VARMA**

CEO, Phi Therapeutics, USA

Precise Microbiome Editing: A Pathway to Mechanistic and Clinical Insights into the Microbiome

The study of the microbiome brings us to the cusp of a new age of cellular therapies. Phi's novel approach to 'kill and replace' pathogens with high specificity offers a different paradigm to treat chronic bacterial diseases.

16:35-17:00

**DRAGANA GAGIC**

Senior Research Fellow, Microbiology, Massey University, New Zealand

Finding a "needle in a haystack" using phage display and DNA normalisation methods

Genomic technologies have revolutionised microbial ecology, particularly in the area of the "rare biosphere". Now, one of the major challenges is characterising this discovered rarity in microbiological ecosystems by identifying those rare species and associated molecular targets that have agricultural, medical and industrial importance. Here, I will discuss how our group has applied phage display technology and metagenomics to mine the "rare" species in microbiomes, with a specific focus on microbial symbioses in the animal and human gastrointestinal tract.

17:00-17:25

17:25

Summary / End of Day 1

PREBIOTICS

**MICHAEL CONLON**

Senior Research Scientist, CSIRO, Australia

Prebiotic Fibres and the Production of Beneficial Short Chain Fatty Acids

There is a growing recognition that the production of short chain fatty acids (SCFA) by microbes within the large bowel plays a vital role in the health of the gut and possibly other tissues. One of the SCFA, butyrate, is a fuel for cells lining the colon and has multiple physiological and biochemical effects, including impacts on the immune system. Another key SCFA, acetate, can have a significant influence on modulating the growth of potentially pathogenic microbes. Diet has a significant influence on the composition and activities of gut microbes, including the ability to produce SCFA. Dietary complex carbohydrates which are not digested in the small intestine and which reach the large bowel (dietary fibre), and which are also fermentable by gut microbes, are the primary dietary substrates to promote SCFA production. Prebiotic fibres which can be shown to stimulate SCFA production and hence promote health via this mechanism are likely to become more prevalent in the coming decade. This presentation will discuss the health benefits of SCFA, some of the key SCFA producing microbes which could be prebiotic targets to stimulate SCFA production, and some of the prebiotic fibres and other dietary components which can influence SCFA production and gut health. There will be a focus on dietary resistant starches, which have been shown to be especially good at stimulating butyrate production and benefiting aspects of gut health.

16:35-17:00

**LUIS VITETTA**

Adjunct Professor, Pharmacology, University of Sydney, Australia

Title TBC

17:00-17:25

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

1. Submit your entry prior to the closing deadline 26th February 2020 (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

08:00-08:45

Refreshments

MICROBIOME

08:45-08:50

Morning Chair's Opening Remarks: Sunny Wong
Assistant Professor (Clinical), Medicine and Therapeutics, Institute of Digestive Disease, The Chinese University of Hong Kong, Hong Kong

08:50-09:25

Invitation Out

09:25-10:00



KEYNOTE PRESENTATION: YEN-HSUAN NI

Distinguished Professor of Pediatrics and Dean of College of Medicine, National Taiwan University, Taiwan
Gut Microbiota Signatures in Infancy Herald the Onset of Allergic Diseases

The origin of the bacteria colonizing the neonatal gastrointestinal tract is supposed to be affected by mode of delivery, feeding and maternal conditions. Proteobacteria, Actinobacteria, Bacteroidetes, and Firmicutes were the major bacterial phyla patterns in infancy. The infants' gut microbiota pattern gradually trans it into the adult pattern around the age of three, when the food intake of the children is similar to that of the adults. More interestingly, the gut microbiota signature acquired in infancy may predict or incline to the future development of diseases, for example, allergic diseases or metabolic diseases. We hypothesized an early dysbiosis can herald the development of later allergic disease. We then utilized a twin cohort to control the various environmental and genetic factors and aimed to tease out the possible allergy-causing bacteria. Once we found the twins who were discordant in terms of diseased or healthy status, we would compare their stool microbiota compositions and detect the bacterial species which discriminated the discordant twins. Increased Ruminococcus gnavus levels in the stool of these babies were associated with respiratory allergies. We verified this finding by feeding the mice and proved the experimental animal model could be triggered an allergic airway inflammation. We conclude an early colonization with R. gnavus in the gut may promote allergic disease in infants. In the future, our study will be more focusing on the functions of these gut microbiota.

PROBIOTICS & PREBIOTICS

08:45-08:50

Morning Chair's Opening Remarks: Liong Min Tze
Professor, Bioprocessing Technology, Universiti Sains Malaysia, Malaysia

08:50-09:25



KEYNOTE PRESENTATION: YU WEIZHU

Vice President of R&D and Innovation, Mengniu Dairy Group, China

Breakthrough innovation of traditional probiotics - development and application of postbiotics

Driven by the national "healthy China" strategy, the market scale of probiotics has expanded rapidly. In 2018, China has formed an industry and a huge market of nearly 100 billion yuan. According to the latest scientific consensus on probiotics in China in 2019, the function of probiotics should be based on live bacteria, but the health effects of material derived from dead bacteria and metabolites (Postbiotics) are not excluded, and need further scientific research and confirmation. In recent years, in the academic community in Japan, Europe and the United States, a large number of studies have demonstrated that some specific postbiotics have different functions and mechanisms from the characterization and mechanism, and have been clinically proved. Postbiotics is even more effective than probiotics in the prevention and treatment of certain diseases because of bacterial metabolites are the most direct agents regulating intestinal health. At the same time, as it is different from the limited application conditions of probiotics, the use of postbiotics is broader and more convenient. At present, in Japan, Europe and the United States and other places, the research and application of postbiotics research technology has developed rapidly, has been used as functional ingredients in a large number of health food and general food, and formed a large industrial scale. Mengniu has made a series of active exploration and research with the resources of its own probiotics. One strain of Streptococcus thermophilus, MN002, not only has good milk fermentation characteristics, cell and animal experiments have shown that it can inhibit fat cell differentiation and immune regulation in the inactivated state. This will lay a good research foundation for the independent postbiotics research and development of Mengniu, and provide consumers with more choices of functional and convenient dairy products, such as functional ambient yogurt, and will also provide new ways for the development of new functional food.

09:25-10:00



KEYNOTE PRESENTATION: GREGORY LAMBERT

CEO and VP R&D, TargEDys, France

Gut-Brain axis mechanism of action and Clinical results on Hafnia alvei HA4597, a new probiotic strain for the regulation of appetite and weight management

TargEDys is a French clinical stage biotech company aiming to control metabolic disease by modulating the appetite through an intervention on the microbiome. TargEDys' innovative, satiety inducing technology (ProbioSatys), is based on a unique understanding of appetite regulation by the microbiome at the molecular level. Bacteria can send signals of satiety to the brain from the gut by molecularly mimicking satiety hormones, thus activating natural satiety pathways. The basis of the technology is a commensal, enterobacteria probiotic strain, Hafnia alvei HA4597[™], that produces the ClpB protein, a mimetic of the satiety hormone MSH. The pre-clinical data have demonstrated the beneficial anti-obesity effects of Hafnia alvei 4597[™] in mice. Treatment with Hafnia alvei4597[™] was associated with decreased body weight and fat mass gain along with reduced food intake as well as positive effects on glycemia and OGTT. A randomised, multicentric, double-blind, placebo controlled clinical trial in 240 subjects has been completed. The trial met the primary endpoint: statistical difference in the proportion of subjects who lost at least 3% of body weight at 12 weeks. Amongst other findings, the mechanism of action is confirmed by achieving secondary endpoints such as an increase in

09:25-10:00

Although people in different geographic area may display different gut microbiota signatures, their gut microbiota may have the similar function. With the advent of next generation sequencing technology and the combination with proteomics and metatranscriptomics, a long-term prospective monitoring on the development of diseases and the evolution of gut microbiota will be very helpful to unravel their critical role in the pathogenesis of many diseases and the gut microbiota may be utilized as the therapeutic targets.

10:00-10:30

Solution Provider Presentation

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09:25-10:00

the feeling of fullness in the verum group. This talk covers ProbioSatys journey from its preclinical and clinical stage to commercialised product, EnteroSatys, including formulation, manufacturing and control. First results of clinical trial will be presented and discussed.

10:00-10:30

Solution Provider Presentation

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

11:30-12:15

PANEL DISCUSSION:

From Microbiome to Market: Challenges in Advancing Microbiome Discovery

This session aims to explore the current global scope of microbiome and unveil possible challenges faced by scientists and industry players in bringing microbial products to the market. Some of the key takeaways include:

- Regulatory hurdles in the microbiome movement in Asia and international
- Bridging the lab-field microbiome research through "omics"
- Elucidating the roles of microbiome in human health through viable products / therapeutic strategies
- Prospect of the microbiome research for the future



THOMAS DAWSON JR. (Moderator)
SRIS, Singapore



OLIVER CHAO
Sanofi, France

11:30-12:15

PANEL DISCUSSION:

Towards Prevention and Cure: The Current Landscape and Future Perspectives of Probiotics and Prebiotics Use in Asia

This panel discussion highlights on the progress of prebiotics and probiotics in providing health benefits. This session will also include a crosstalk between the probiotic production, regulatory and scientific community on the development and use of prebiotics and probiotics in health as well as the new directions of these exciting areas for an emerging market.



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



KRIBEN GOVENDER
Food Scientist and Registered Nutritionist
Allele Microbiome and Nourishme Organics, Australia

EARLY LIFE AND DEVELOPMENT



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

obesity on growth and gut microbiome in the next generation - opportunity for intervention

Maternal obesity is associated with a range of metabolic disturbances in offspring and there is an urgent need to address the intergenerational increased disease risk. Our lab is exploring the beneficial effect of exercise in both mothers and offspring, examining metabolic regulation, markers of inflammation and the gut microbiome. Female Sprague Dawley rats were fed chow (C) or high fat diet (HFD); half were exercised from 10 days prior to mating until the end of gestation, and half remained sedentary. Exercise was modest, with no significant effect on dam's body weight. At PND1, male pups from obese dams were significantly smaller (FS vs CS; P<0.01) with no significant difference in females. In lean dams, maternal exercise was associated with smaller pups (CE vs CS, P<0.01). At weaning, body weights of pups were significantly higher in pups from obese dams (P <0.01) regardless of pup sex and maternal activity. In lean dams, exercise significantly reduced pup adiposity, and reduced insulin was observed in offspring

12:15-12:40

SKIN MICROBIOME



ELSA JUNGMAN
Founder and CEO, ELSI, USA

How to approach the growing sensitive skin issue & the impact of cosmetics on the skin microbiome

Skin health is affected by weather changes, toxic environment and the products we apply on our skin every day. As a result, 50% of the U.S. population has a sensitive skin and severe dermatological conditions. ELSI is an early stage start-up that is based on ten years of dermatological research with renowned French and US institutions, and we aim to look at the damage on our skin that is caused by beauty products and the environment. We are currently studying the impact of cosmetic products on in vitro and in vivo of the skin microbiome, and at the same time working with our strategic partners to develop an in vitro and in vivo evaluation platform. Our goal is to launch uniquely designed clean cosmetics to minimally impact our skin's ecosystem and improve overall skin health & wellbeing, and develop a direct-to-consumer distribution strategy to co-create products with our community.

12:15-12:40

PROBIOTICS AND BRAIN HEALTH



LIONG MIN TZE
Professor, Bioprocessing Technology, Universiti Sains Malaysia, Malaysia
Probiotic and the Brain: Evidence and Mechanisms

Probiotic microorganisms have a long history of safe use and have been documented for their various health benefits. Many strains of lactic acid bacteria (LAB) from the genera of Lactobacillus have been identified to possess probiotic properties. They have been much emphasized on their roles to regulate gut well-being, including the alleviation of lactose intolerance, improvement of diarrhoea and inhibition towards pathogenic bacteria in the gut. Recent evidences have illustrated the potential of LAB for brain health, ranging from neurodegenerative diseases to stress, memory and cognition. Lactobacillus plantarum DR7, a cow's milk isolate from Penang, Malaysia has shown a reversal of symptoms associated with Alzheimer's Disease in a fruit fly model, accompanied by distinct changes of gut microbiota profiles. In aging and hyperlipidemia rats, DR7 has shown improved stress and anxiety symptoms, accompanied by improved memory. The administration of DR7 for 12-weeks in stressed adults has contributed to improve stress and anxiety scores, in

12:15-12:40

12:15-12:40

in both CE and FE. Significant decreases in gut bacterial diversity were observed in obese versus lean dams, with little impact of maternal exercise. Maternal obesity significantly impacted offspring microbiome composition. Maternal exercise altered the abundance of 88 microbial taxa in offspring of lean dams, with modest effects in those from obese dams. Behaviour was tested in brothers of these rats at 6 weeks of age, and increased anxiety-like behaviour was observed in offspring of lean dams who exercised.

12:15-12:40



DAMIEN KEOGH

CEO and Co-Founder
Maiden Therapeutics,
Singapore

Discovering Molecular Therapeutics from Natures 'Transfer Microbiome' - Human Milk

Exclusive breastfeeding over the first six months of life is the gold standard for an infant's nutrition, health, and disease risk reduction, having a lasting impact into adulthood. The microbiome of an infant gut is distinct from an adult gut, taking years to develop. Human milk microbiota are among the first colonisers of the infant and represent a natural 'transfer microbiome'. Maiden Therapeutics is a young biotechnology company that develops a drug discovery platform technology and generates new therapeutics from the human milk microbiome. While microbiome studies have largely focused on Western microbiomes with other ethnicities underrepresented, Maiden highlights the functional attributes of the Asian microbiome. Most small molecule drugs approved by the FDA's derive from microbial sources, therefore new human microbiomes represent an ideal biocompatible source. Maiden's Human Microbiome Medicines™ discovery platform focuses on the molecular blueprint of the microbiome and selects microbiome-derived molecular therapeutics for human diseases.

12:40-13:05

12:40-13:05

Invitation Out

12:15-12:40

addition to memory and cognitive abilities, primarily via enhancement along the serotonin pathway and maintenance of the dopamine pathway. My talk will highlight the evidence of a probiotic strain, primarily targeting brain health, via models ranging from insects to human.



YING-CHIEH TSAI

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

Psychobiotics as Biotherapeutic Agents for Neurodegenerative Diseases

Psychobiotics, a class of probiotics with psychotropic activities, integrate neural, hormonal, and immunological signalling via the gut-brain axis to combat a broad spectrum of psychiatric diseases. We evaluate the effects of Lactobacillus plantarum PS128 in animal models of Parkinson's disease (PD) and Alzheimer's disease (AD). In the MPTP-induced PD-like mouse model, pre-treatment of PS128 alleviated the motor deficits, protected the dopaminergic neurons both in substantia nigra and striatum, ameliorated the monoamines reduction, α-synuclein accumulation and glial cell activation in striatum, and suppressed MPTP-induced elevation of TNF-α, IL-1β, IL-6 in striatum and midbrain regions. In the 6-OHDA rat hemi-PD model, pre-treatment of PS128 suppressed the M1 beta-oscillation and improved the locomotor activity in stepping test. Intracerebroventricular streptozotocin (icv-STZ) injection was conducted in C57BL/6J, as a model of late-onset sporadic AD. From behavioural results, we found that pre-treatment of PS128 ameliorated the icv-STZ caused mouse deficit in spatial learning and cognitive function. Our study demonstrates psychobiotic PS128 could be a potent alternative for the treatment of neurodegenerative diseases, including PD and AD.

12:40-13:05

13:05-13:35

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13:05-13:35



PAUL RYAN LABSKIN

Chief Business Development Officer, Labskin UK



ALEX CHAPMAN

Head of Operations, Labskin UK
Labskin and the future of skin health
• Labskin HSE Platform

- Cloning the Human Microbiome
- AI Data Analysis
- Towards a new pigmented skin model

13:05-13:35

Solution Provider Presentation

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13:35-14:35

Lunch / Poster Presentations / One-to-One Meetings

MICROBIOME IN HEALTH AND DISEASE

POSTER COMPETITION WINNERS TALK

14:35-14:50

**JANE MULLANEY**

Scientist, AgResearch, New Zealand

Diversification of the infant gut microbiome during transition to weaning foods

During the transition to solid foods the introduction of complementary feeding alters the infant gut microbiome. A cohort of infants from the Auckland metro area consumed either 5g of powdered New Zealand kumara or a commercially available probiotic every day for the first six months of consuming solid foods. Samples collected when the infants were approximately 6, 9, and 12 months of age were analysed using shotgun metagenomic sequencing from 35 mother-infant pairs, who also provided 3-day food records prior to sample collection. We hypothesized that the composition and functional profile of the faecal microbiome will show increasing species and functional diversity over time, correlating with the introduction of specific food groups, for example, starch. Through integration of microbiome data with clinical data measures, we hope to better understand these food/microbe interactions and what impact overall diversification of the diet has on an infant faecal metagenome over time.

14:50-15:15

**MUHAMMAD BILAL ABID**

Assistant Professor, Division of Infectious Diseases, Medical College of Wisconsin, USA

It Takes Guts to Rev Up CARs: Harnessing the Power of Gut Microbiome to Modulate Responses of**Novel Cancer Therapies—The New Frontier in Precision Medicine**

Considerable progress has been made in cancer therapeutics recently with targeted strategies that are efficacious and less toxic. Immunotherapy and chimeric antigen receptor (CAR) T-cells are increasingly being evaluated in a variety of tumors in the relapsed/refractory disease settings. Despite impressive outcomes in select patients, there remains significant heterogeneity in clinical response with some achieving long-term remissions while others failing to respond. One strategy to improve current outcomes would be to better understand and modulate hosts' factors. One such host factor, generating tremendous interest recently, is the gut microbiome. Loss of microbiome diversity or "dysbiosis," and compositional differences have been implicated in the differential response to therapy. A greater understanding of the human microbiome carries the potential for improving treatment response rates. Several recent human studies receiving immune checkpoint inhibitors (ICI) showed a significantly superior response in patients with a more diverse gut microbiome. These findings illustrate how controlled manipulation of the gut microbiome can be a rather inexpensive way to substantially enhance responses to engineered therapeutic modalities such as immunotherapy and CAR T-cells.

15:15-15:40

**WEI-LI WU**

Assistant Professor, National Cheng Kung University, Taiwan

Title TBC

15:40-16:05

16:05

Summary / End of Day 2

PROBIOTICS R&D

POSTER COMPETITION WINNERS TALK

14:35-14:50

**YASUHIRO KOGA**

Visiting Professor, Department of Gastroenterology, Tokai University School of Medicine, Japan, President, Japanese Society for Probiotic Science, Japan

Gastric microbiota: its role in the pathophysiology of upper GI diseases

The number of gastric commensal bacteria is very small (~10³ CFU/mL in the gastric fluid [GF]) by traditional culturing methods because the strong gastric acid kills most of the bacteria in the stomach. However in the stomach with low acidity such as persons with atrophic gastric mucosa (most of them with long history of H. pylori infection) and acid-inhibitor users, the count of live bacteria in the GF dramatically increase thus is considered they may exert a significant role in the pathophysiology of upper GI diseases such as development of gastric cancer, NERD, and functional dyspepsia. Based on the studies performed in our group, the following topics will be presented; Difference in the microbial community structure among saliva, GF and feces, Influence of gastric acid on the gastric microbiota, Involvement of gastric microbiota in the development of gastric cancers, and A probiotic strain LG21 for the upper GI.

14:50-15:15

**MING-JU CHEN**

Professor, Department of Animal Science and Technology, National Taiwan University

Potential probiotics on alleviating chronic kidney disease progression and anti-aging effect through regulating intestinal microbiota

Chronic kidney disease (CKD) is a global health issue that has a substantial impact on affected individuals. The regulation of intestinal bacterial growth and metabolism might provide the potential solution for CKD. The efficacy of probiotics to decrease uremic toxin production and to improve renal function has been investigated in in-vitro models and in various animal and human CKD studies. Minipigs are an appropriate biomedical model for humans not only due to many genetic and physiological similarities to human, but also due to the anatomically similar in kidneys and their microbiological characteristics. In the present study, the effects of probiotics on preventing CKD using a cisplatin induced CKD mini-pig model, previously developed in our lab was investigated. The possible mechanism including regulating microbiota and identifying biomarkers was also studied. Additionally, since cisplatin is a strong oxidant agent, one of the mechanisms involving in uremic toxin-reducing effect of probiotics might be due to its antioxidant activity. Thus, the protection effect of probiotics on the D-galactose-induced aging mice model was evaluated. Its related mechanisms were also investigated.

15:15-15:40

**HANNA SIDJABAT**

Honorary Fellow and Chief Investigator, University of Queensland Centre For Clinical Research, Australia

Proteomic analysis of Lactobacillus spp. with and without pathogen interference

15:40-16:05