ASIA SKIN MICROBIOME 2.0 CONGRESS

SINGAPORE

24-25 September 2019

Co-Hosts

Agency for Science, Technology and Research

Skin Research Institute of Singapore

SKIN RESEARCH SOCIETY (SINGAPORE)

#MicrobiomeSeries

www.global-engage.com
We are pleased to host our Asia Skin Microbiome 2.0 Congress, a spin-off from our Asia’s Microbiome series that has been around since 2014. This event is set to bring skin microbiome experts to Singapore on the 24th and 25th of September, 2019.

Co-hosted with the Agency of Science, Technology and Research (A*STAR), Skin Research Institute of Singapore (SRIS) and Skin Research Society of Singapore (SRSS), this event will promote understanding and reciprocal benefits of the latest scientific and business developments in skin microbiome research. Attracting more than 150 experts from Asia, Europe and US, this 2-day event will highlight cutting edge research, commercialization, and business case studies through presentations and panel discussions, an exhibition filled with solution providers showcasing their products, and ample networking opportunities promoting interactions and business reach. This congress includes both scientific and commercial interests with topics ranging from host-microbe interaction, skin disease, emerging technologies, interventional and cosmetic advancements, and regulatory considerations.

**HIGHLIGHTS OF THE CONGRESS**

- Over 100 regional and global skin microbiome researchers ranging from both scientific and industry backgrounds
- 20 expert presentations including a panel discussion
- 7+ hours of dedicated networking time
- Exhibition hall featuring cutting edge technology and solution providers
- Innovation Challenge*
- Complimentary networking drinks reception

**SPECIFIC FOCUS AREAS**

- Skin health, wellbeing, and microbiome-associated skin disease
- Skin immunology
- Microbe-based therapies
- Emerging technologies for skin microbiome research and innovation
- Cosmetic vs Therapeutic regulatory considerations
- Case studies
- Academic-Commercial partnerships

**EXPERT SPEAKERS Include:**

- **KIMBERLY KLINE**
  Associate Professor, Nanyang Technology University, Singapore

- **BERNARD PAETZOLD**
  Chief Scientific Officer, S-Biomedic, Belgium

- **SALOMÉ LEIBUNDBGUT-LANDMANN**
  Associate Professor for Immunology, University of Zürich, Switzerland
CONFIRMED SPEAKERS

NEELAM MUIZZUDIN  
President, Skin Clinical Research Consultants, USA

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

KIMBERLY KLINE  
Associate Professor, Nanyang Technology University, Singapore

YUGANDHAR REDDY  
Senior Research Scientist, Unilever, India

VERONIKA OUDOVA  
CEO, S-Biomedic, Belgium

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

THOMAS DAWSON, JR  
Senior Principal Investigator, Skin Research Institute of Singapore, A*Star

HUIYING LI  
Associate Professor, Department of Molecular & Medical Pharmacology, University of California Los Angeles (UCLA), USA

GREG HILLEBRAND  
Senior Principal Scientist, Amway, USA

BERNHARD PAETZOLD  
Chief Scientific Officer, S-Biomedic, Belgium

SHIGEFUMI OKAMOTO  
Professor, Department of Clinical Laboratory Science, Kanazawa University, Japan

ANINDYA DASGUPTA  
Work Stream Leader, Human Microbiome Unilever, India

XU YAO  
Professor and Chief, Division of Allergy and Rheumatology, Institute of Dermatology, Chinese Academy of Medical Sciences, China

SALOMÉ LEIBUNDGUT-LANDMANN  
Associate Professor for Immunology, University of Zürich, Switzerland

PATRICK LEE  
Associate Professor, School of Energy and Environment, City University of Hong Kong, Hong Kong

WONHEE JUNG  
Professor, Department of Systems Biology, Chung-Ang University, Korea

SAEKO NAKAJIMA  
Assistant professor, Department of Dermatology, Kyoto University Graduate School of Medicine, Japan

NIRANJAN NAGARAJAN  
(Chair) Senior Group Leader and Associate Director, Computational and Systems Biology, Genome Institute of Singapore (GIS)

ELIZABETH WU  
Manager, Consumer Scientific Innovation Manager, Johnson & Johnson, USA

JENNIFER YAU WING KI  
Department of Paediatrics, The Chinese University of Hong Kong, Hong Kong

ANNIKA KRUEGER  
Ian Frazer Laboratory, The University of Queensland Diamantina Institute, Australia

LI XI CECILIA  
Senior Manager and Department Head of APAC Clinical Science, Johnson and Johnson Consumer, China

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 USD 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.
Neutral processes drive the skin mycobiome assembly over seasons

Fungi are the key members of the human skin microbiota, but we know less about them compared to bacteria. In this work, the seasonal dynamics and assembly of skin mycobiomes of a healthy Chinese cohort were investigated. Significant differences in community composition between individuals were found and the community composition variation within an individual grew over time. We found that within a season, the occurrence frequency of a large number of taxa fitted the neutral model, indicating that passive dispersal and ecological drift are major forces influencing the community assembly. Across four seasons, conditionally rare taxa were detected, and these taxa were consistently selected against in the neutral model. Co-association network analysis indicated that taxa selected by the host skin environment were important to the community network. Overall, microbial ecological theory can aid our understanding of the assembly of skin microbiota.

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The Jekyll and Hyde Skin Microbiome: Good Bugs Behaving Badly

In 1886, two years after the Scottish surgeon Sir Alexander Ogston discovered Staphylococcus aureus in the pus of surgical absceses, fellow Scot, Robert Louis Stevenson published his famous gothic novel, The Strange Case of Dr. Jekyll and Mr. Hyde. The well-respected and community-minded Dr. Henry Jekyll fought with his alternate evil personality, Mr. Edward Hyde. Like Jekyll and Hyde, we know that our microbiome can also take on dual personalities. A so-called ‘good’ skin bug, like the universally commensal Staphylococcus epidermidis, can also be an opportunistic pathogen and cause serious life-threatening infections. Conversely, a ‘bad’ skin bug like Staphylococcus aureus, noted for its role in impetigo, boils and atopic dermatitis, colonizes 30% of the US population, most without issue. Exactly what causes ‘Jekyll bacteria’ to transform into ‘Hyde bacteria’ is multifactorial, with strain, host immunity, environment, and other factors at play. The transformation involves quorum sensing, biofilm formation, and polymicrobial nature. The goal of our research is to understand the molecular mechanisms by which Enterococcus faecalis interacts with other bacterial species and the host in the context of these polymicrobial, biofilm-associated infections. In this talk, I will present our latest research exploring how E. faecalis modulate the host immune response to create a hospitable environment for itself and co-infecting microbes and to promote chronic wound infections.

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.

**COMMERCIALISATION OF THE SKIN MICROBIOME RESEARCH**

**NEELAM MUIZZUDIN** (Chair)
President, Skin Clinical Research Consultants, USA

**VERONIKA OUDOVA**
Chief Executive Office, S-Biomedic, Belgium

**DISENTING THE HUMAN SKIN MICROBIOME IN HEALTH AND DISEASE**

**XU YAO**
Professor and Chief, Division of Allergy and Rheumatology, Institute of Dermatology Chinese Academy of Medical Sciences, Nanjing, China

A tryptophan metabolite of the skin microbiota attenuates inflammation in patients with atopic dermatitis through the aryl hydrocarbon receptor

Previous studies have revealed significant alterations in the skin microbiota of AD patients not only in diversity and composition but also in function, and the tryptophan (Trp) metabolic pathway is attenuated in the skin microbiota of AD patients. In the present work, by using a gel-patch method, we found that the level of indole-3-aldehyde (IAld), an indole derivative of Trp catabolism, was significantly lower in lesional and non-lesional skin of AD patients than that of healthy individuals. IAld significantly attenuated the skin inflammation in *C. albicans*-specific. In addition, adaptive response to *C. albicans* together with imiquimod significantly enhanced Neutrophil extracellular traps (NETs) formation and in vivo inhibition of NET formation was associated with significant reduction in disease severity. Together, our result showed that the skin microbiota play a significant functional role in the pathogenesis of AD.

**ADAPTIVE IMMUNITY TO COMMENSAL SKIN FUNGI PROMOTES INFLAMMATORY RESPONSES**

**SAEKO NAKAJIMA**
Assistant professor, Department of Dermatology, Kyoto University Graduate School of Medicine, Japan

Since the precise role of cutaneous microbiota in the control or promotion of skin inflammatory conditions remains unclear, we aimed to address how defined skin microbes could affect the development of psoriasis by using the imiquimod-induced psoriasis-like inflammation in mice associated with skin commensals. Candida albicans exacerbated epidermal thickness and neutrophil infiltration. Such enhanced inflammation was not associated with skin fungal invasion and was characterized by a dramatic influx of IL-17A producing CD8 effector T cells into the skin. Of note, the Th17 cells accumulating in the lesions were *C. albicans*-specific. In addition, adaptive response to *C. albicans* together with imiquimod significantly enhanced Neutrophil extracellular traps (NETs) formation and in vivo inhibition of NET formation was associated with significant reduction in disease severity. Together, our result showed that adaptive response to skin commensal fungi can have a dramatic impact on the severity of skin inflammatory disorder.

**SKIN MICROBIOME SIGNATURES IN HEALTH AND DISEASE CORRELATE WITH HOST IMMUNITY AND MICROBIAL VIRULANCE**

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

The skin is a challenging ecosystem to study meta-omics due to the low amount of biomass that can be recovered, which limits downstream techniques that are currently feasible on human subjects. We have recently been using metagenomics to investigate microbial communities present on the skin of atopic dermatitis patients to better understand shifts in community diversity and microbial functional characteristics. We can identify skin microbiome dermotypes that stratify groups of AD patients and observed that these groups correlate with host immunity and microbial virulence.
The skin mycobiome remains unexplored, elusive, and poorly understood. Only recently have investigations begun to focus on skin fungi, the majority to date primarily focused on bacteria via 16S sequencing or metagenomics without the read depth necessary to identify fungi beyond the class level. Every human being’s skin is occupied by fungi, and the vast majority of people will be affected by a fungal-associated disease at some point during their lifetime. Multiple studies indicate a likely causative role for fungi in common skin disorders such as pityriasis versicolor and seborrheic dermatitis, and a role in exacerbation of many others including chronic wounds, atopic dermatitis, atopic eczema, and psoriasis. In contrast, several recent studies have indicated a potential protective role for skin bacteria with higher abundance of pathogens. In summary, we showed that the skin microbiome and skin physiological functions of bedridden older individuals were changed compared to those of healthy participants, and the changes may be cause to the risk of skin injury in bed hidden elderly.

Role of skin-microenvironment in shaping the Microbiome

Thomas L. Dawson, Jr
Senior Principal Investigator, Skin Research Institute of Singapore, A*STAR and President, Skin Research Society, Singapore

The Cutaneous Mycobiome and its Role in Skin Disease: Malassezia, friend or foe?

While the human gut microbiome has realized virtual celebrity status amongst both the popular and scientific press, the skin microbiome remains unexplored, elusive, and poorly understood. Only recently have investigations begun to focus on skin fungi, the majority to date primarily focused on bacteria via 16S sequencing or metagenomics without the read depth necessary to identify fungi beyond the class level. Every human being’s skin is occupied by fungi, and the vast majority of people will be affected by a fungal-associated disease at some point during their lifetime. Multiple studies indicate a likely causative role for fungi in common skin disorders such as pityriasis versicolor and seborrheic dermatitis, and a role in exacerbation of many others including chronic wounds, atopic dermatitis, atopic eczema, and psoriasis. In contrast, several recent studies have indicated a potential protective role for skin fungi, the reduction in skin disease associated with puberty to atopic dermatitis. We have spent more than 20 years defining the role of fungi in seborrheic dermatitis, including definition of the causal species, identification of a pathogenic mechanism, and clinical proof of concept validating one pathway, lipase mediated inflammation.

Genomic analysis of antifungal resistance of the dandruff-associated skin fungus

Wonhee Jung
Professor, Department of Systems Biology, Chung-Ang University, Korea

The skin commensal yeast Malassezia at the interface of health and disease

Commensal fungi of the mammalian skin, such as those of the genus Malassezia, are associated with atopic dermatitis and other common inflammatory skin disorders. Understanding of the causative relationship between fungal commensalism and disease manifestation remains incomplete. By developing a murine epicutaneous infection model, we found Malassezia spp. selectively induce IL-17 and related cytokines. This response is key in preventing fungal overgrowth on the skin, as disruption of the IL-23/IL-17 axis compromises Malassezia-specific cutaneous immunity. Under conditions of impaired skin integrity, mimicking a hallmark of atopic dermatitis, the presence of Malassezia dramatically aggravates cutaneous inflammation, which again was IL-23- and IL-17-dependent. Consistently, we found a CCR6+ Th17 subset of memory T cells to be Malassezia-specific in both healthy individuals and atopic dermatitis patients, whereby the latter showed enhanced frequency of these cells. Thus, the Malassezia-induced type 17 response is pivotal in orchestrating antifungal immunity and in actively promoting skin inflammation.

Malassezia restricta is the predominant species on human skin and is particularly associated with dandruff, as suggested by recent large-scale mycobiome analyses. In this presentation, I will introduce our recent study on understanding the mechanism of ketoconazole resistance in clinically isolated M. restricta strains from dandruff patients. Comparative genome and transcriptome analyses were carried out, and the results were compared to that of a ketoconazole susceptible reference M. restricta strain. The results of our study suggest that genomic rearrangement, in particular, multiplications of locus encoding genes involved in drug resistance, is a common mechanism of ketoconazole resistance in M. restricta.

Wygandhar Reddy
Senior Research Scientist, Unilever, India

Role of skin-microenvironment in shaping the Microbiome

It is well recognized today that the skin microbiome and the host skin form a joint ecosystem, the health of which is governed by a balanced microbiome functioning in harmony with the host. The dynamics of this ecosystem is governed by a complex set of microbe-microbe and microbe-host interactions. Product usage and the resultant host micro-environment play an important role in further modulating...
these interactions. The nature of these interactions could be two-body or many-body in nature leading to emergent effects that cannot be predicted a priori. We have developed multipronged approach to combining microbiomics, in vitro models to study the role of substrate microenvironment, in silico approaches for microbial assemblies. We will discuss a few examples of this approach and its applications towards understanding the skin microbiome and relevant endpoints of skin health.

Johnson seeks to build collaborations with external partners to accelerate transformational healthcare solutions for our consumers. In addition to advancing the science of microbiome via internal research, we will share how Johnson & Johnson has gained a better understanding of the Chinese skin microbiome. The diversity profiling in dry skin and atopic dermatitis (lesional & non-lesional), and how it has guided our approach in finding technology that contributes to disease progression from AK to SCC. The current study aims to identify bioactive compounds with immunomodulatory and potentially pro-tumorigenic properties secreted by skin lesion-associated S. aureus. The proteomic content of sterile supernatants from 31 clinical S. aureus strains isolated from control and lesion swabs was determined via mass spectrometry (MS). Cultured human keratinocytes were stimulated with MS-defined S. aureus supernatants and subsequent cytokine responses measured. We found a specific S. aureus toxin secretory profile to correspond to increased keratinocyte pro-inflammatory responses in vitro. Further, S. aureus secretions were found to stimulate proliferation in cultured keratinocytes. Current experiments investigate whether pro-inflammatory and -proliferative toxins can influence skin carcinogenesis in an in vivo mouse model.

The microbiome is emerging as relevant along the entire consumer journey through health and disease, and we at Johnson & Johnson are excited to work in this space, in association with digestive health, oral health, and skincare. In this presentation, we will share some of our clinical research on advancing the understanding of the Chinese skin microbiome, including how cutaneous microbial distribution at different body sites interact with the topographic skin environment. We will also discuss on skin microbiome therapy, whether pro-inflammatory and -proliferative toxins can influence skin carcinogenesis in an in vivo mouse model.

The skin microbiome can be thought of as a living protective layer that partners with the skin to keep it healthy and in good condition; from preventing colonization of pathogens to supporting the immune system, to helping maintain skin’s normal pH, to the indirect benefits that come from metabolizing various compounds present in the skin. Following these reasons, the use of prebiotics as a source of food for the skin commensal bacteria is an attractive route to enhance and activate the skin commensals to do the above more efficiently. We have used glycerol, which is commonly used in skin care products, in our work to show that it has prebiotic effects. Glycerol is metabolized by skin resident bacteria releasing fermentation by-products, such as short chain fatty acids and other organic acids. While SCFAs are antimicrobial in nature and prevent colonization by invading pathogens, lactic acid is an alpha-hydroxy acid that has further benefits for skin health. This includes improving barrier function of epidermis and the firmness and elasticity/suppleness of skin, as well as stimulating the turnover of dead skin cells. Use of glycerol and other prebiotics is thus an effective way towards a healthier and more resilient skin.

Glycerol as a Prebiotic for Skin
ANINDYA DASGUPTA
Work Stream Leader, Human Microbiome Unilever, India

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In an in vivo mouse model.
CHUN-MING ERIC HUANG
Chair Professor, Department of Biomedical Sciences and Engineering, National Central University, Taiwan

Novel probiotics from electricity-producing skin microbes for microbiome editing

Our recent results have demonstrated that skin bacteria can yield electricity during the bacterial fermentation. By using electrogenic bacteria, we develop new technology derived from the concept of probiotic-prebiotic-postbiotic-“electrobiotic”. Next-generation sequencing (NGS), although it is a new approach to biomarker identification, may not be able to dynamically detect the dysbiotic microbiome. We here introduce the technology of “electrobiotic” for profiling and monitoring the skin dysbiosis in real time. Most importantly, these electrogenic skin bacteria will become novel probiotics for treatments of human diseases. For example, electrons produced by electrogenic bacteria can function as antioxidants for reduction of ultraviolet (UV)-induced skin damages. Furthermore, the electrogenic skin bacteria may affect the human mentality by regulation of brain waves. In this talk, the novel probiotics using electrogenic bacteria will be introduced. The application of these electrogenic probiotics for microbiome editing and banking as well as treatments of human diseases will be highlighted.
VENUE INFORMATION

ASIA SKIN MICROBIOME 2.0 CONGRESS 2019

Hotel Fort Canning,
11 Canning Walk, Singapore, 178881
www.hfcsingapore.com

Hotel Fort Canning is a magnificent and award-winning conservation hotel tucked within 18 hectares of lush greenery of Fort Canning Park. The award-winning boutique hotel is luxurious and trendy, and it combines the romance of a grand colonial edifice with lush green parklands in the heart of the city. Hotel Fort Canning was styled by the award-winning DP Architects to incorporate the finest hospitality amenities, while retaining and conserving its old-style, colonial glamour. Today, the hotel serves as one of the finest boutique hotels Singapore has to offer. It straddles the Orchard Road shopping belt, the Clarke Quay entertainment hub, the Central Business District and the Civic District.