Singapore
Immunology Network
SIgN

SIgN SEMINAR

Hosted by Dr LAM Kong Peng

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Expanding the Multi-Omics Toolbox to Unravel Microbiome Function

The microbiome plays a crucial role in immune homeostasis and health, yet scalable approaches to study its function remain limited. Here, we demonstrate the utility of two multi-omics approaches to uncover host-microbe and microbe-microbe interactions. First, we developed a robust, clinically applicable skin metatranscriptomics workflow that overcomes low microbial biomass, yielding reproducible profiles and strong microbial mRNA enrichment. This revealed that *Staphylococcus* and *Malassezia* species dominate the skin metatranscriptome despite modest genomic abundances. Species- and gene-level analyses showed niche-specific adaptations (e.g. propionate metabolism) and expression of diverse antimicrobial genes, including uncharacterized bacteriocins. Second, we adapted spatial-omic technologies to map microbes and immune signals within colorectal tumors, offering a powerful tool for studying host-microbe interactions *in situ*.

Dr. Chia Minghao is a GIS/BII fellow in the Laboratory of Metagenomic Systems and Microbial Technologies at the Genome Institute of Singapore. He received his PhD training at the Francis Crick Institute (UK) where he profiled RNA isoforms and alternative promoter usage during yeast gametogenesis. His current research interests are themed around uncovering native host-microbial interactions and advancing microbiome research towards clinical and functional relevance. He currently leads a team focused on developing RNA technologies to study the spatial distribution or role of expressed genes of the human microbiome.

12 August 2025 (Tuesday)
10 – 11 AM (Singapore Time)
SIgN Seminar Room
8A Biomedical Grove, Immunos, #04-06
Singapore 138648

Seminar is open for all to attend.

Registration is not required.