



Channing Microbiome Seminar

April 19 (Friday), 2019, 11am @ 5th-floor (small) conference room



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Identifying Microbial Signatures of Gut Wellness through a Multi-study Integration of Human Stool Metagenomes

Abstract: Currently, many studies of the human gut microbiome focus on a specific disease context. Undoubtedly, disease-centric analyses are important for the development of better diagnostics and therapeutics. In comparison, the number of rigorous investigations into what characterizes a healthy gut are lacking; such studies are necessary not only for determining the characteristic features of a healthy gut, but also for rationally designing a systematic path to restoring gut wellness through targeted interventions. However, identifying health-associated microbial features through comparative studies between a particular disease and its control is limited in scope and specificity; rather, large scale, meta-analyses that include stool metagenomes from patients of multiple disease states, as well as from healthy individuals, may enable the framework to define robust features of gut microbiomes associated with health. In this talk, I will present my group's recent efforts to elucidate gut microbes that are associated with health. We performed a meta-analysis on a multi-study, integrated dataset of ~4,300 publicly available, metagenomic stool samples from ~2,600 healthy and ~1,700 unhealthy (i.e. diagnosed with a disease or having abnormal body weight) human individuals from ~35 published studies and 13 different health and disease states. We observed higher alpha-diversity (Shannon Index) and a higher number of prevalent species in the gut microbiomes of the healthy cohort in comparison to those of the unhealthy cohort. Interestingly, through a species-level analysis, we found 7 and 43 microbial species that were observed more and less frequently, respectively, in the healthy cohort in contrast to the heterogeneous, unhealthy population. By taking these 50 species, we developed a mathematical formula that compares the abundances of these 7 'health-positive' and 43 'health-negative' microbes in a stool metagenomic sample. This metric, which we call the 'Gut Microbiome Health Index (GMHI)', is a dimensionless value that describes the degree of the healthiness (or unhealthiness) of one's own gut microbiome. We demonstrate GMHI on the original healthy and unhealthy stool metagenomic datasets, and show that it is a much more accurate measure in determining health than the commonly used alpha-diversity. Furthermore, when GMHI was applied to independent datasets of fecal microbiota transfer (FMT) donors and recipients, we found that our metric provides the quantitative monitoring of recipient-specific, post-FMT outcomes; and could be used towards the more strategic selection of stool donors among a pool of potential candidates. Taken together, our study constitutes a step towards defining the design components of a healthy gut microbiome, and paves a path towards strategically restoring gut wellness through targeted interventions.

Bio: Jaeyun is an Assistant Professor and core member of the Microbiome Program at Mayo Clinic. He directs the Microbiome Systems Medicine Laboratory, whose overall goal is to better understand the connection between gut microbes and auto-immunity using multi-omics systems biology, machine-learning, and complex systems modeling approaches. Ultimately, his research group aims to develop the computational methods and analytical pipelines necessary to design probiotic consortia for promoting gut wellness. Jaeyun obtained his PhD in Chemical Engineering from the University of Illinois at Urbana-Champaign, and completed postdoctoral research fellowships at the Asia-Pacific Center for Theoretical Physics (Pohang, South Korea) and at Harvard Medical School/Broad Institute.

Hosted by Yang-Yu Liu