181 Longwood Avenue
Boston, Massachusetts 02115-5804

Department of Medicine
Channing Division of Network Medicine

Channing Microbiome Seminar

November 19th (Friday), 2021, 9-10AM (ET)

Zoom link: https://us02web.zoom.us/j/81070959105?pwd=RFJNd3dSZmR6dXJZNjJiYVVzQ3NEQT09

Meeting ID: 810 7095 9105
Passcode: 984617

Chen Liao, PhD

Postdoc of Joao Xavier's lab
Computational & Systems Biology Program
Memorial Sloan-Kettering Cancer Center, USA

Oral bacteria in feces reflect the loss of intestinal bacteria

Abstract: The enrichment of oral bacteria in the fecal microbiota is often portrayed as a type of gut microbiome dysbiosis for its associated gastrointestinal diseases. Yet, the causes, mechanisms, and consequences of finding oral bacteria in feces remain unclear. We propose that the increased relative abundance of oral bacteria in feces indicates a decreased total bacterial density in the gut microbiome, and we develop a mathematical model to analyze the phenomenon quantitatively. We validate our hypothesis with a large-scale meta-analysis of human microbiome data from cancer patients receiving allogeneic hematopoietic cell transplantation (allo-HCT) and patients with multiple gastrointestinal diseases. We further show that the biomarker can broadly indicate disease status, severity, and treatment outcome. In particular for allo-HCT patients, the bimodally distributed fecal proportion of oral bacteria is caused by exposure to specific antibiotics (piperacillin/tazobactam and oral vancomycin) and associated with worse mortality. Recognizing the enrichment of oral bacteria in feces not as a bloom of these, but as a biomarker of depleted gut bacteria, changes our interpretation of microbiome compositional data.

Short bio: Dr. Liao is a postdoc from Joao Xavier's lab in the Department of Computational & Systems Biology at Memorial Sloan-Kettering Cancer Center. He received his Ph.D. from the Department of Bioengineering at the University of Illinois at Urbana-Champaign. Dr. Liao's current research uses mathematical modeling, bioinformatics, and machine learning approaches to elucidate the metabolic and ecological principles underlying the dynamics and function of the human intestinal microbiome, especially in cancer patients. Other than microbiomes, he has broader interests in the development of systems biology models to link gene functions, pathways, and phenotypes in bacteria and fungi.

Hosted by Tong Wang