BRIGHAM AND WOMEN'S HOSPITAL

HARVARD MEDICAL SCHOOL

181 Longwood Avenue
Boston, Massachusetts 02115-5804

Department of Medicine
Channing Division of Network Medicine

Channing Microbiome Seminar
November 18 (Friday), 2022, 9AM-10AM (EST)

Zoom: https://us02web.zoom.us/j/81070959105?pwd=RFJNd3dSZmR6dXJZNjJiYVVzQ3NEQT09
Meeting ID: 810 7095 9105
Passcode: 984617

Jingyuan Fu, PhD
Department of Genetics
Department of Pediatrics
University of Groningen
University Medical Center Groningen
the Netherlands

The gut microbiome as a window into individual vulnerability and resilience

Abstract: The gut microbiome plays an important role in human health and disease, and its individual specificity highlights its potential in personalized medicine. Large-scale, prospective cohort design combined with metagenomics sequencing, deep omics profiling, and comprehensive phenotyping allow us to leverage the gut microbiome and other omics in explaining phenotypic differences, thereby aiding disease diagnosis and stratifying individuals for their susceptibility of developing complex disease. Specifically, our study focuses on the gut-liver axis in metabolic regulation and engages innovative organ-on-a-chip technologies to study host-microbe interactions.

Bio: *Dr. Jingyuan Fu is currently a full professor of Systems Medicine in the University Medical Centre Groningen, the Netherlands. She studied Biochemistry (BSc) in China and then developed her scientific career in the fields of systems genetics and integrative genomics. In the Netherlands she gained an MSc in bioinformatics (with distinction) from Wageningen University in 2003 and a PhD cum laude from University of Groningen in 2007. In 2008, Dr. Fu joined the University Medical Centre Groningen. Dr. Fu's research involves multi-dimensional "omics" integrative analysis towards a better understanding of the development of complex diseases, including their genetics, genomics, transcriptomics, and metabolomics. In recent years, her research has expanded to performing population-based gut microbiome analyses. These aim to identify genetic, dietary and environmental factors underlying inter-individual variation in gut microbial composition and function profiles in the general population and to unravel the host-microbe interactions in the human immune and metabolism systems.*

Hosted by Yang-Yu Liu