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Department of Medicine
Channing Division of Network Medicine

Channing Microbiome Seminar

April 19 (Friday), 2024, 9AM (ET)

MCP 5th-floor large conference room & Zoom:

<https://us02web.zoom.us/j/81070959105?pwd=RFJNd3dSZmR6dXJZNjJiYVVzQ3NEQT09>

Meeting ID: 810 7095 9105; Passcode: 984617



Xiaofang Jiang, PhD

National Library of Medicine
National Institutes of Health

BilR is a gut microbial enzyme that reduces bilirubin to urobilinogen

Metabolism of haem by-products such as bilirubin by humans and their gut microbiota is essential to human health, as excess serum bilirubin can cause jaundice and even neurological damage. The bacterial enzymes that reduce bilirubin to urobilinogen, a key step in this pathway, have remained unidentified. Here we used biochemical analyses and comparative genomics to identify BilR as a gut-microbiota-derived bilirubin reductase that reduces bilirubin to urobilinogen. We delineated the BilR sequences from similar reductases through the identification of key residues critical for bilirubin reduction and found that BilR is predominantly encoded by Firmicutes species. Analysis of human gut metagenomes revealed that BilR is nearly ubiquitous in healthy adults, but prevalence is decreased in neonates and individuals with inflammatory bowel disease. This discovery sheds light on the role of the gut microbiome in bilirubin metabolism and highlights the significance of the gut–liver axis in maintaining bilirubin homeostasis.

Bio: Xiaofang Jiang earned her Ph.D. in Genetics, Bioinformatics, and Computational Biology from Virginia Tech in 2016. She completed her postdoctoral research at MIT and the Broad Institute in 2019. Xiaofang Jiang is now a principal investigator at National Library of Medicine, National Institutes of Health at Bethesda. She is interested in advancing our understanding of the microbial world, focusing on the intricate host-microbe interactions, viral genomics, and the pivotal role of the gut microbiome in human health through integrated genomics, bioinformatics, and computational modeling. She is particularly drawn to the study of microbial enzymes within the gut microbiome, including those involved in glycan synthesis and degradation.

Hosted by Yang-Yu Liu