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Small player, large role: Microbial metabolic pathways associated with metabolic risk of cardiovascular disease

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Abnormal metabolism is a precursor of cardiovascular disease (CVD). Emerging evidence supports a link between the gut microbiome and the development of metabolic syndrome and CVD. However, we know little about the functional connection between host-microbe metabolisms and need interdisciplinary integrative analyses to understand their complex metabolic interaction. Over the past few years, we have built up LifeLines-DEEP, a multi-omics biobank that is a part of LifeLines, the large population cohort study in the northern Netherlands. LifeLines-DEEP consists of 1,500 individuals (42% males, age range 18-81 years), from which dietary, genetic, gut flora and metabolic profiles have been generated. To determine an individual's metabolic risk of developing CVD, we measured 33 serum metabolic biomarkers using a nuclear magnetic resonance (NMR) platform; the biomarkers included various lipoprotein particles, fatty acids, amino acids and glycolysis-related metabolites. We reported association to 48 bacterial metabolic pathways which were derived from metagenomics shotgun sequencing data. In particular, our data showed that microbial energy metabolism and various biosynthesis pathways leading to the production of pyruvate, amino acids, vitamins, short-chain fatty acids and polyunsaturated fatty acids might impact CVD risk. Our current study also presents an integrative analysis and provides a deeper insight into the complex diet-microbe-host dialogue in metabolism and inflammation that are relevant to CVD development. This knowledge can help pave the way towards the development of therapies to modulate the microbial metabolism and help prevent CVD.

Biography

Jingyuan Fu has completed her PhD in 2007 at University of Groningen and she is currently an Associate Professor at University Medical Center Groningen, Netherlands. Her 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.

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