

Understanding the complex gut ecosystem via integrated omics approach

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The human gut is colonized with a wide variety of commensal microorganisms. These symbiotic gut microbes exert a strong influence on the metabolic phenotype of the mammalian host and participate in extensive microbial-mammalian co-metabolism. The symbiotic microbes form a highly complex microbial community in our gut, and they have a profound influence on human physiology, immunology, and nutrition. It has been postulated that imbalance in the composition of microbes could be a risk factor in human disorders including inflammatory bowel disease, metabolic syndrome, autoimmune disease, and colonic carcinogenesis. However, the molecular mechanisms of symbiotic gut microbes through host-microbial crosstalk remain obscure. To this end, we firstly established a highly integrated omics-based approach including genomic, transcriptomic, and metabolomic profilings to evaluate environmental changes in the gut and highlight the metabolic pathways of the symbiotic microbial community. Applying this novel method to a plant-fiber intake model in mice, we succeeded to predict the integrated metabolic networks regarding carbohydrate metabolism as a result of the changes in the gut microbial ecosystem. These results indicated that our integrated omics approach could provide a foundation for understanding the effect of diet on the complex gut ecosystem.

Biography

Since June 2012, Dr. Shinji Fukuda has been a project leader of gut environmental systems biology and an associate professor at the Institute for Advanced Biosciences, Keio University, Japan. Dr. Fukuda received his Ph.D. in 2006 at Meiji University, studying the generation of beneficial probiotics via genetic modification approach. Prior to joining Keio University, Dr. Fukuda worked as a research fellow at RIKEN Research Center for Allergy and Immunology, Japan, where he established a novel profiling techniques for understanding the molecular basis of host-microbial crosstalk in the gut.

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