

## **"Structure and function of gut microbiome of Asians associated with foods and host health"**

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Several hundred of microbial species form a complex ecological community residing in human digestive system, namely gut microbiota establishes a complex ecological community. The gut microbiota that influences on the host's physiology and susceptibility to disease via direct contact to human cells or their collective metabolic activities. Multiple intrinsic and extrinsic factors, e.g., diet, host genetics and physiology, drugs and disease, as well as living environments, are involved known to play an important role in structuring the gut microbiota and biosynthesis of their metabolites, such as diet, host genetics and physiology, drugs and disease, as well as living environments. Notably, diet is considered as one of the key drivers for gut microbial community as it contributes supplies nutrition and alters the environment for the microbes. Asian diet varies remarkably within the continent and significantly differs from the other continents, in which its main characteristic is high in carbohydrate, fiber, vitamins, antioxidants, but low in concentrated fat. Traditional Asian diet is basically considered as relatively beneficial food against, protecting against metabolic disease and being some are reported helpful to promote and inhibit the colonization of beneficial and non-beneficial gut bacteria, respectively. However, contemporary diet has recently influenced on dietary lifestyle habits of Asian people by rapid development of global food service chains that shape distort their local-eating lifestyles. For instance, a trend in increase of consumption of calorie-dense diet in Asian people, such as refined carbohydrate, fat, red meats, and low fiber has been largely confirmed by several studies. This occasionally distresses gut microbiota in Asian people, eventually leading to dysfunction of their gut microbial community.

Moreover, Asian people are known to have specific phenotypes, which are associated with metabolic disease. For example, Asian people have high prevalence of abdominal obesity although they are normally lean. They are also known to have high risk of insulin resistance caused by dysfunctional pancreatic insulin secretion. Altogether, these accelerate Asian people to easily take the risk of metabolic disease. The development of Next-Generation Sequencing (NGS) technology and progress of computer and database-assisted bioinformatics has revolutionized the genomic research fields in the past two decades. It includes studies on microbiome of human digestive system and we have gained insight into its variation among the people in the world including Asian people. Therein, we understand that gut microbiota plays an indispensable role as an interface between foods and host health. Asia is the world largest populous continent, accounting for proximately 60% of the world population and covering the great diversity in ethnicities with large variation in culture and lifestyle, notably in diets. Namely, each ethnic group owns each dietary culture. In this context, Asia is an attractive field to study on the interplay of gut microbial community and diets and its effect on the host health. Notably, Asian people have specific physiological aspect involved in vulnerability of metabolic diseases. Therefore, it warrants to capture the current status of Asian gut in association with host metabolic disorder and we have established Asian Microbiome Project (AMP) with 20 institutes of 10 countries to achieve this aim.

In the lecture, the current status of Asian gut microbiota, from child to adult, were introduced from our own AMP data, notably with the data showing that it is now under dynamic movement co-occurring with change in dietary life. Furthermore, how the changing microbiota is increasing the risk of metabolic diseases, e.g., obesity and type 2 diabetes (T2D) will be discussed.

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**Jiro NAKAYAMA** is Professor of Laboratory of Microbial Technology, Division of Systems Bio-engineering, Faculty of Agriculture, Graduate School, **Kyushu University**. After he graduated from master course of agricultural chemistry in Tokyo University in 1989, he became Assistant Professor of Bio-organic chemistry in Faculty of Agriculture in the University of Tokyo. Then, he received his PhD from the University of Tokyo in 1994 on studies on pheromone responsive conjugative plasmid in *Enterococcus faecalis*. In 2001, he moved to Faculty of Agriculture, Kyushu University as Associate Professor and in 2020, he promoted to Professor of the laboratory of Microbial Technology. His present

research focuses on structure and function of gut microbiota of Asian people which differs among countries in reflection to dietary culture in each country. Especially, he is interested in the impact of food urbanization and globalization rapidly occurring in Asia on their health through the alteration of gut microbiota.