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BGI study gives insight into human gut microbiota

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Singapore: A novel metagenomic study on human gut microbiota and their potential impact on type 2 diabetes, the most common form of diabetes, has been published by a team of BGI researchers in the online publication of the international journal *Nature*.

The work lays an important foundation for comprehensively understanding the genetic characteristics of gut microbiota and their relationship to type 2 diabetes risk, as well as providing a new way of classifying microbes detected by DNA sequence. The work here also opens the way for transferring the potential value of a gut-microbiota-based approach into a means for clinical assessment and diagnosis of patients at risk of this disease.

Type 2 diabetes is a major chronic disease of modern societies and threatens the health of populations throughout the world. The continual and rapid increase in the prevalence of type 2 diabetes has created a race against time for researchers worldwide to find new approaches to diagnose and treat the disease. Type 2 diabetes is a heterogeneous and multifactorial disease, influenced by a number of different genetic and environmental factors. While there are treatments to modulate its impact available, there remains great need to improve these therapies, and the disease cannot be cured.

Considering the important impact of gut microbiota on human diseases, such as type 2 diabetes, BGI in collaboration with other institutes has focused on mining the gut microbiota information with the aim of fully understanding their molecular characteristics and using this to benefit human health. In this study, using deep next-generation shotgun sequencing, they developed a protocol for carrying out a metagenome-wide association study (MGWAS), and used it in a two-stage MGWAS analysis to better defining type 2 diabetes-associated metagenomic markers. They sequenced the gut microbial DNA from 345 Chinese patients with type 2 diabetes and identified approximately 60,000 type 2 diabetes-associated markers that might be useful for detecting and characterizing type 2 diabetes.

In addition to this new method and identification of type 2 diabetes associated, researchers developed the concept of metagenomic linkage group (MLG) that allows easy classification and description of the abundant metagenomic data in a taxonomic form that can be used to replace traditional taxonomic classification approaches. MLG can provide metagenomic species-level information even for unknown species, including bacterial species-specific regions on a chromosome, and mobile genetic elements, such as plasmids and bacteriophages.

In general, the researchers found that healthy individuals typically had a higher number of butyrate-producing bacteria, which the researchers theorize may play a protective role against several types of diseases. In the T2D patients, that saw an increase in the number of, opportunistic pathogens, with the type of pathogen being quite diverse from patient to patient. Such changes in the gut bacteria composition have recently been reported for colorectal cancer patients and ageing population.

Junjie Qin, primary investigator on this project at BGI, said, "Gut microbiota has been widely considered as an important contributor to many kinds of chronic disease, like type 2 diabetes. However, it is still unclear on what and how exactly these commensal microbes contribute to human health. BGI, with a great power for conducting such a large-scale and in-depth studies, will continue to develop more sophisticated tools, collect a larger amount of scientific evidence, and better exploit the industrial/clinical potential in this field than has been done before."

Jun Wang, executive director of BGI, said, "As the human's 'second genome', the gut microbiome has a tight relationship with human health. High-throughput sequencing technologies and Metagenomics serve as robust tools for researchers to comprehensively explore the gut microbiota related with diseases, and shed new light into disease prevention and treatment. I believe the epoch of personalized medicine based on gut microbiome is not far away."