International Symposium 1-2

NGS-based analysis of human gut microbiomes

○ Masahira Hattori, Suguru Nishijima
Center for Omics and Bioinformatics, Graduate School of Frontier Sciences, the University of Tokyo

Our human bodies are colonized with over 100 trillion cells of microbes. The majority reside in the intestinal tract and form complex bacterial communities (gut microbiota) which have profound influences on various human physiologies including disease. The gut microbiome (collective genomes of the gut microbiota) is estimated to encode more than 10-fold genes than that of human genome.

Analysis of human gut microbiome has recently become more practical due to remarkable advances in next-generation sequencing technologies (NGS). Several studies using NGS-based metagenomic approaches have been conducted to comprehensively analyze genes/functions and species composition in human gut microbiomes. These NGS-based approaches have demonstrated that their ecological and biological features that have been rather difficult to pursue can now be characterized with relative ease.

Given unique diet and genetic background of the Japanese population, metagenomic analysis of Japanese gut microbiome is attractive to elucidate variations in the gut microbiome among human populations with different genetic background, geography or diet, and physiological state. However, little is known about the overall structure of genes and species in Japanese gut microbiome as compared with those of other populations like Western countries. To explore differences in gut microbiome between different populations, we performed metagenomic analysis of Japanese gut microbiomes using NGS and compared them with the European and other datasets publically available.

We obtained about 4.6 million non-redundant genes from metagenomic sequencing data generated from 167 fecal samples of 100 individuals. The analysis revealed that *Bifidobacterium* was the major species in the Japanese dataset, while *Bacteroides* was the most abundant in the European and American dataset. We also found several enriched functions such as carbohydrate metabolism, while functions such as glucan metabolism were depleted in the Japanese dataset. These data suggest that there are some ecological and functional variances in gut microbiomes between human populations, providing new insights into the evolution of the human gut microbiome.