

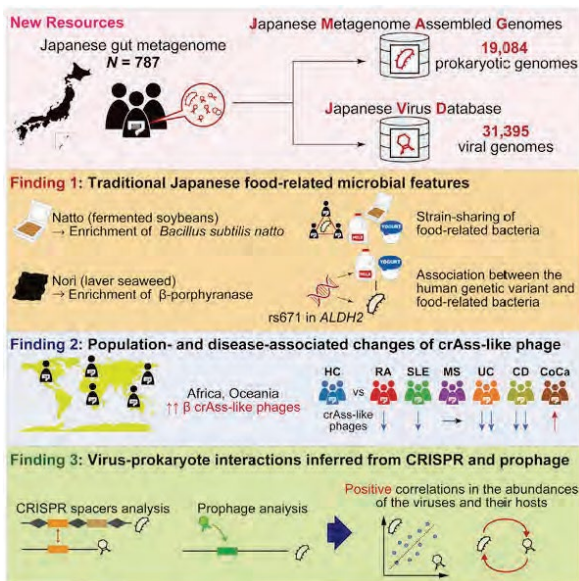
The intestinal microflora and viral flora of the Japanese population were characterized.

Keywords: Intestinal bacteria, intestinal viruses, intestinal microbiota sequencing information, bioinformatics

Points

- Assembly of 19,084 prokaryotic and 31,395 viral genomes from Japanese gut metagenome
- Traditional Japanese food-related features were observed in Japanese microbial genome
- crAss-like phages were associated with populations and diseases
- Abundances of bacteriophages and their hosts tended to be positively correlated

Abstract



The research group lead by Yukinori Okada (Graduate School of Medicine, Osaka University/IFReC/the University of Tokyo/RIKEN) reconstructed 19,084 prokaryotic and 31,395 viral genomes from Japanese gut metagenome shotgun sequencing data. They revealed the association between the gut microbiome and diet, populations, and diseases. Their genome catalog, JMAG and JVD, contributes to expanding the diversity of the microbial genome of a previously underrepresented population.

Journal: *Cell Genomics* (online) December 1, 2022

Title: "Prokaryotic and viral genomes recovered from 787 Japanese gut metagenomes revealed microbial features linked to diets, populations, and diseases"

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