MRGM: Mouse reference gut microbiome enabling comprehensive comparison of gut microbiome between mouse and human

Nayeon Kim^{1,3}, Chan Yeong Kim^{1,3}, Dongjin Park², Sang-Jun Ha² and Insuk Lee^{1*}

Gut microbiome is associated with many diseases and can be modulated by diet and drugs. Mouse may provide effective in vivo model for the study of diet and drug effect on human gut microbiome. For the microbiome profiling with high resolution and coverage, a comprehensive reference gut microbial genomes needs to be available. We constructed mouse reference gut microbiome (MRGM) which include newly assembled genomes from >850 metagenomes. There are several improvements in our mouse reference gut microbiome compared with previous databases. First, we included metagenome-assembled genomes (MAGs) from many samples with ultra-deep sequencing (>20 Gb), which was found to improve quality of MAGs. Second, we filtered the assembled genomes not only by conventional criteria; completeness and contamination, but also by genome chimerism. Third, we chose genomes with completeness ≥70% for the database and found that this threshold achieves an optimal trade-off between accuracy of reference genomes and coverage of sequencing reads with taxonomic classification. The MRGM provides over 46,267 nonredundant genomes by 70% completeness and 5% contamination, comprising 1,689 representative prokaryotic species. MRGM also provides catalog of 15.2 million coding genes along with their functional annotations.

Department of Biotechnology, College of Life Science & Biotechnology, Yonsei University, Seoul 03722, Korea

² Department of Biochemistry, College of Life Science & Biotechnology, Yonsei University, Seoul 03722, Korea

³ These authors contribute equally.