Microbiome analysis data of MicrobeDB.jp ver. 3

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Abstract Microbes inhabit almost everywhere on earth and conduct a variety of metabolic process. Microbiome sequencing analyses (e.g., metagenomic analysis and 16S rRNA gene amplicon sequencing analysis) are powerful analysis methods to identify microbial community compositions (i.e., phylogenetic composition and gene function composition), and therefore widely applied to various microbial communities. We are developing MicrobeDB.jp (http://microbedb.jp/), which is an integrated database of publicly available microbial genome and metagenome data. We are conducting an automatic and manual annotations of microbial habitats of each genome and metagenome sample in MicrobeDB.jp using an onyology MEO. In addition, we are analyzing microbial community compositions of each microbiome sequencing data. These combination of data will support microbiome studies. MicrobeDB.jp web site (http://microbedb.jp).



