

“Small Bugs, Big Data”: Developing an integrated Database for Microbes with Semantic Web Technologies.

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Microbes are essential for every part of life on Earth. Numerous microbes inhabit the biosphere, many of which are uncharacterized or uncultivable. They form a complex microbial community that deeply affects against surrounding environments. Metagenome analysis provides a radically new way of examining such complex microbial community without isolation or cultivation of individual bacterial community members. However, metagenome analysis is more complex than common genome analysis, because an analysis target is composed of enormous bacterial strains instead of a single strain. Moreover, the enormous amounts of sequencing data produced by next generation sequencers are difficult to effectively analyze using existing computational tools.

To untangle the complexity of metagenome analysis, we have been developing a global microbial database integrated by microbe genomics and metagenomics database with semantic web technologies named “MicrobeDB.jp”. In the symposium, I will present about an integrated database “MicrobeDB.jp”.