

International Conference on

Environmental Microbiology & Microbial Ecology

International Conference on

Ecology, Ecosystems & Conservation Biology

Clustering analysis of global soil microbe metagenome for characterizing community diversity

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Microbial communities in soil depend on environmental features such as land use and geographic isolation. In this study, we have analyzed soil metagenomes sampled from a wide range in the globe and variety of land use in the context of the environment or ecosystem, from Earth Microbiome Project, containing 4998 samples and 48674 operational taxonomic units (OTUs). The main goal of this work is to discover characteristic microbiota that corresponds to land use and environment. It is worth noting that microbiome OTU data is high dimensional but sparse and many OTUs are phylogenetically related. By taking those factors into consideration, we tried to develop bioinformatics, computational methods as follows:

- (1) Data were labeled into 8 land use categories and applied to Random Forest to reduce variables, and we selected OTUs which relates to land use categories.
- (2) By using these OTUs, the differences between microbial communities were defined and clustered by UniFrac Distance which computes the distance difference based on the phylogenetic information.

The results lead to the interpretation that some clusters are composed of the samples from specific areas and environments, such as cropland in Japan, montane grassland in Mongolia, tundra, and forest, and some of those clusters are characterized by different dominant OTUs, e. g. DA 101, which is known as the one of the most abundant microbial phlotypes. We have concluded that the clusters of individual lands are quite clearly reflecting the ecosystems and can be characterized by the OTUs in the microbial community.

Biography

Tetsushi Tanaka belongs to Computational Systems Biology Laboratory in Nara Institute of Science and Technology and has studied bioinformatics, especially microbiome analysis. He is also familiar with molecular biology and was graduated from Saitama University with a bachelor's degree in Science.

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