



## Bacterial diversity of soil aggregates of different sizes in various land use conditions

Ekaterina Ivanova, Thakahova Azida, and Kutowaya Olga

V.V. Dokuchaev Soil Science Institute, Soil Science, Moscow, Russian Federation (ektrnivanova@gmail.com)

The patterns of soil microbiome structure may be a universal and very sensitive indicator of soil quality (soil “health”) used for optimization and biologization of agricultural systems. The understanding of how microbial diversity influenses, and is influenced by, the environment can only be attained by analyses at scales relevant to those at which processes influencing microbial diversity actually operate. The basic structural and functional unit of the soil is a soil aggregate, which is actually a microcosm of the associative co-existing groups of microorganisms that form characteristic ecological food chains. It is known that many important microbial processes occur in spatially segregated microenvironments in soil leading to a microscale biogeography.

The Metagenomic library of typical chernozem in conditions of different land use systems was created. Total genomic DNA was extracted from 0.5 g of the frozen soil after mechanical destruction. Sample preparation and sequencing was performed on a GS Junior (“Roche”, Switzerland) according to manufacturer’s recommendations, using the universal primers to the variable regions V4 gene 16S - rRNA - F515 (GTGCCAGCMGCCGCGGTAA) and R806 (GGACT-ACVSGGGTATCTAAT).

It is shown that the system of land use is a stronger determinant of the taxonomic composition of the soil microbial community, rather than the size of the structural units. In soil samples from different land use systems the presence of accessory components was revealed. They may be used as indicators of processes of soil recovery, soil degradation or soil exhaustion processes occurring in the agroecosystems. The comparative analysis of microbial communities of chernozem aggregates investigated demonstrates the statistically valuable differences in the amount of bacterial phyla and Archean domain content as well as the species richness in aggregates of various size fractions. The occurrence of specific components in the taxonomic structure of micro-and macro-aggregates may indicate the presence of a certain size fraction in the structure of the investigated soil. The study of soils’ metagenome is promising for the development of both soil microbiology, and for the soil processes trends in soils of anthropogenic origin.