



## **Pyrosequencing of microbial community of typical chernozem in contrast land use conditions**

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Chernozems are the principal soil resource of Russia, so the sustainable use of these fertile soils in the intensive agricultural production is of great importance, especially in terms of agro-ecological security of the country. The increase in agricultural inputs - intensive cropping, soil fallowing application accompanied with high frequency of mechanical treatment, result in decrease in soil organic matter content as well as soil structure degradation and, finally, lead to the loss of soil fertility. Soil microorganisms can serve as bioindicators of anthropogenic stress experienced by the soil during its agricultural use, so they may be universal indicators of soil quality (soil health) used for optimization and biologization of agricultural systems. The way to study the relationship between the structural status of the soil, its microbial communities and the organic matter content is the comparative analysis of soil aggregates in conditions of different land use practices.

The objects of our research were soil samples of soil with permanent wheat cropping (50 years), continuous dead fallow (50 years) soil, and recovering soil (for 18 years under native steppe vegetation, fallowed in previous).

The analysis of 16 S rRNA gene amplicon libraries of typical chernozem in conditions of different land use systems revealed that the way of agricultural use is a strong determinant of soil microbiome taxonomic composition. It was shown that the continuous «dead fallowing» application (for 50 years) lead to the establishment of oligotrophic components of microbial community, including spore-forming members of phylum Firmicutes. The increase of Acidobacteria lineages in this variant may be an indicator of some acidification of soil during long-time fallowing application. The variant of continuous wheat cropping lead to increasing in Proteobacteria lineages. The variant of soil under native steppe vegetation was characterized by the highest values of biodiversity indices - species richness and evenness, which can indicate the occurrence of soil recovering. This variant was also characterized by the maximum content of agricultural valuable aggregate fraction of 2-5 mm size.

In soil samples from different aggregate fractions the presence of accessory components was revealed. It was determined that Actinobacteria lineages preferred microaggregates (less than 0.25 mm) rather than coarse aggregate fractions (more than 7 mm). The opposite trend was determined for Proteobacteria: the amount was maximum in aggregates more than 7 mm in diameter. 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.

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