



## **Changes in the structure and functioning of soil microbial communities in response to multidirectional influence of the nutrient and toxic substances**

Aliya Gilmullina, Polina Galitskaya, and Svetlana Selivanovskaya  
Kazan, Russian Federation (svetlana.selivanovskaya@kpfu.ru)

Importation of organic matter to the soil is often accompanied with metals. This is observed when using as non-traditional fertilizers such as sewage sludge, compost from organic fraction of municipal solid wastes or mineral fertilizers on the background of organic. One of the most toxic heavy metals introduced into the soil together with fertilizers is cadmium. Microorganisms play an essential role in the cycles of nutrients, energy flow and decomposition of organic matter, thus they are recognized as an integral component in ensuring soil fertility. Therefore, the main aim of the study was analysis of changes in the structure and functional activity of soil microbial community in response to the multidirectional influence of the nutrient and toxic substances.

The analysis of the structure of microbial communities and their functional activity were carried out in samples of gray forest soil sampled at different depths of soil cut (0-20, 20-40 and 40-60 cm), located in Republic of Tatarstan (Russia). The soil samples were contaminated by cadmium in form of CdCl<sub>2</sub> salt in the amount of 300 mg Cd/kg, amended with glucose in the amount of 10,000 mg/kg, and simultaneously with cadmium and glucose. The change of the community structure (Protocol Illumina MiSeq) and the abundance of certain groups of microorganisms (real-time PCR) were determined in the dynamics of the 14 day experiment. It was revealed that the number of copies of bacterial 16S rRNA genes, reflecting the number of bacteria decreases from the upper to the lower horizon. The introduction of glucose and the mixture was led to an increase in the number of copies of bacterial genes, while the introduction of cadmium is not affected. Changes in the structure of the microbial community were assessed using 352678 sequences that were combined into 23 Phil, 53 class, 72 order and 85 families. Bacteria dominated on the domains level, the proportion of archaea was considerably lower. The position of the dominant groups of bacteria were taken by representatives of Phylum Proteobacteria (mainly Alphaproteobacteria and Gammaproteobacteria), Acidobacteria and Bacteroidetes in control samples (without Cd or glucose). Subdominant were Actinobacteria, Gemmatimonadetes and Verrucomicrobia. The introduction of glucose in a sample, selected in the upper layer, led to a sharp increase in the dominance of phylum roteobacteria (Gammaproteobacteria), with up to 70% of the community consisted of bacteria of the genus *Pseudomonas*. In samples of the lower strata bacteria of the Betaproteobacteria and Actinobacteria groups (the main representatives of bacteria of the family Micrococcaceae and the genus *Burkholderia*) dominated. The structure of bacterial community of the samples with the introduced cadmium was comparable with the control options. To assess the differences between communities the analysis of the diversity by means of metric multidimensional scaling (MDS) was carried out.