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## Soil prokaryotes: The inexhaustible metagenomic source for plant fertility promotion

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At the end of the 20<sup>th</sup> century microbiological science faced the fact that most of the prokaryotic communities on our planet are formed by so-called uncultivable bacteria and archaea. The presence of these organisms has changed the estimates of prokaryotic diversity to several billions of species. Soil microbial communities are especially diverse one gram of fertile soil can be inhabited by 10 billions of microbial cells belonging to hundreds of species; more than 90% of them avoid laboratory cultivation. These organisms can be studied only by the use of modern methods of metagenomic analysis, including high-throughput sequencing and subsequent bioinformatics analysis of environmental DNA. These approaches give the unique opportunity to study structural and functional properties of intact microbial communities, treating them as the integrative and continuously evolving genetic systems. In this respect, new perspectives can be seen in studying the rhizosphere effect; the selective concentration of certain microorganisms in the root zone of plants. Apparently, it is the high genetic diversity of plant associated microorganisms that allows it to improve their adaptive capacity. As in the case of the human intestinal metagenome, rhizosphere metagenome can be named the second plant genome. This talk will highlight the first results of the study of the formation of rhizosphere microbiome in two types of soils (sod-podzolic soil and chernozem) by two plant species *Secale cereale* (rye) and *Triticum aestivum* (wheat). The taxonomic structure of prokaryotic communities was analyzed for bulk and rhizosphere soil by use of V4 16S rRNA gene pyrosequencing after 42 days of greenhouse growth. Soil type seemed to be the major factor influencing the formation of rhizosphere microbiome, while the plant species affiliation had lesser (but still significant) effect on the microbial composition. Rhizosphere effect was largely associated with the increase of beta *proteobacteria* group. Rye rhizospheres were more similar to each other compared to wheat rhizospheres. The most significant differences between the bulk and rhizosphere soils were detected for wheat cultures and were likely associated with the increased amount of the genus *Flavobacterium* (phylum Bacteroidetes) in the rhizosphere of this plant. Our research demonstrates that the rhizosphere effect is the interplay of plenty factors including soil type and its agrochemical properties, plant and its multifaceted features and many other, leaving a large room for further analysis and investigation.

### Biography

Elizabeth V Pershina has completed her PhD from All-Russia Research Institute for Agricultural Microbiology in 2013. She has published 11 papers and 2 chapters in books. In 2015 she was awarded by the Russian Federation Government for the development of metagenomic approach for microbiological monitoring of health and resource potential of the Russian soils.

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