

Biodiversity and Seasonal Changes of the Microbiome in Chernozem Agroecosystem

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Studies of the influence of different agricultural technologies on the soil microbiome are widespread; they are important for understanding the dependence of the microbiome on environmental and soil factors and solution of practical problems related to the control of biochemical processes in soils used in agriculture.

The seasonal variability (spring–summer–autumn) of the taxonomic structure of prokaryotic microbiomes in chernozems was studied using sequencing of the 16S rRNA gene.

The DNA preparation was used as the matrix for a polymerase chain reaction with the use of a pair of universal primers to the variable region V4 of the 16S rRNA gene – F515 (GTGCCAGCMGCCGCGGTAA) and R806 (GGACTACVSGGGTATCTAAT). The preparation of the samples and sequencing were made on a GS Junior.

The samples were collected from the topsoil (0–20 cm) horizons of a long-term fallow and croplands differing in the rates of application of mineral fertilizers (NPK).

The results of the weighted UniFrac analysis show that the microbiomes of the fallow and field were distinctly distinguished and that the type of land use significantly affected the structure of the microbial community. The most sensitive to the type of land use were the representatives of the Firmicutes, Gemmatimonades, and Verrucomicrobia phyla. The type of vegetation and aeration of the root-dwelling soil layer seem to be key factors of this influence.

The microbiomes analyzed also differed by seasons: in the autumn samples, they were closer to the spring ones than to the summer ones. This fact evidences that the seasonal differences in the microbiomes are not simple gradual temporal changes; they reflect the influence of some ecological factors transforming the phylogenetic structure of prokaryotic communities. As the seasonal shift was equally expressed in the microbiomes of the field and fallow, it is logical to assume that it was caused by the factors common for two systems of land use.

Statistically sensitive to seasonal environmental changes were representatives of the Taumarchaeota, Acidobacteria, Bacteroides, Firmicutes, and Verrucomicrobia groups.

The differences in the structure of the soil prokaryotic communities were more significant between seasons than those related to different systems of land use.

It is noteworthy that the UniFrac analysis did not practically reveal differences in the prokaryotic communities between the fertilized and unfertilized arable soils, since it was difficult to distinguish them from the differences related to the natural heterogeneity of the soil samples (replicates) analyzed. It is probably related to the high buffer capacity and the high adaptive potential of chernozems.

In this experiment, even taking into account the 30-year history, the application of fertilizers is a less significant factor affecting the structure of the microbiome than the type of land use or seasonal climate changes.

The phylogenetic diversity estimated by the Shannon index, the number of the operating taxonomic units found, and the Chao1 index little depends on the rate of the fertilizers applied and the type of land use; however, one can mention a rather higher diversity of the microbiomes in the summer and autumn periods compared to the spring one.