

THE INFLUENCE OF THE AGRICULTURAL MANAGEMENT SYSTEM ON THE SOIL MICROBIOME

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Soil is the fundamental resource of an agricultural ecosystem. Agricultural practices influence the composition of soil bacterial communities. The aim of our work was to study the structure of the soil microbiota in the case of different crop rotation and types of fertilization. The research was carried out in the long-term field experiment on the “*Biotron*” Experimental Station of the Academy of Sciences of Moldova in two crop rotations (with and without alfalfa). Characterization of the compositional diversity of the soil microbiome was achieved by sequencing amplicons targeting the 16s rDNA gene of prokaryotes (Scientific Center “Genomic Technologies, Proteomics and Cell Biology” of FSBSI ARRIAM, St. Petersburg, Russia).

Anthropogenic soil loading, agricultural management system influenced the formation of soil prokaryote communities. This influence is evident from the analysis of the abundance of *Actinobacteriota* phylum, which in our experiment was second in abundance after Proteobacteria. In the variant *Mineral background* (N45-90P30-60K60-90) was determined the highest abundance of *Actinobacteriota* phylum, being 19.0% in the alfalfa crop rotation and 20.1% in the rotation without alfalfa, respectively. The soil in the forest strip was characterized by the lowest abundance of *Actinobacteriota* filum - 16.0 %. Actinobacteria of the family *Sterptomycetaceae* had the highest relative abundance in the alfalfa rotation, variant *mineral background* (N45-90P30-60K60-90). The forest floor is exposed to less anthropogenic pressure and some oligotrophic-nutrient phyla are more abundant than in agricultural soils. The *Acidobacteriota* phylum had the highest abundance in the forest floor soil - 5.7%. These results can be explained by the fact that *Acidobacteriota* have mostly oligotrophic nutrition strategy with low growth rates and seem to be favoured in resource-limited conditions due to high substrate affinities. The group of microorganisms (clade) *Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium*, which fixes atmospheric nitrogen and promotes plant growth, has the highest share - 1.1 % in the crop rotation without alfalfa, *Organic Fund* variant. The genus *Ensifer*, which includes bacteria capable of inducing root-knot formation in legumes, was detected only in the alfalfa soil with the mineral background variant (N45-90P30-60K60-90). The genus *Streptomyces* (biocontrol agents) had the highest relative abundance (1.3%) in the alfalfa soil with the organic backgroundvariant.

Agricultural practices alter the diversity and composition of soil microbial communities, and these altered communities impact the functioning of agricultural ecosystems. Organic fertilization leads to a significant increase in the abundance of some nutrition-related bacteria.

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