

THE EFFECT OF FARMING SYSTEM ON SOIL PROKARYOTIC COMMUNITIES IN MOLDOVA

Indoitu D.

Institute of Microbiology and Biotechnology, Moldova

e-mail: diana.indoitu@imb.md

CZU:579.64+631.461

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The soil microbiome plays an important role in the functioning of ecosystems. The influence of farming systems on the soil prokaryotic communities has not been sufficiently studied. Using metagenomic analyzes (high-throughput sequencing of the 16S rRNA gene on the Illumina platform), we studied the abundance, structure, and diversity of the prokaryotic community of the typical low-humus chernozem in two forage crops rotations (with and without inclusion of alfalfa) on the following variants: control without fertilizers (CON), mineral fertilizers (NPK) and organic fertilizers - manure (ORG). The research was carried out in the long-term field experiment on the “Biotron” Experimental Station of the Academy of Sciences of Moldova (Chisinau). The doses of fertilizers were calculated according to the crop in order to compensate for the quantitative content of NPK used, 100 tons of manure instead of $N_{450}P_{109}K_{470}$. Soil samples were taken from the top soil layer (0-30 cm) in 2021. The metagenomic analysis of soil was done using equipment of the Core Centrum ‘Genomic Technologies, Proteomics and Cell Biology’ in ARRIAM. This research was conducted as part of state projects of the Republic of Moldova 20.80009.5107 “Efficient use of soil resources and microbial diversity through the use of elements of biological (organic) farming”.

Analysis of the soil prokaryotic communities in typical chernozem of the Central Zone of Moldova revealed the dominant presence of 5 phyla of bacteria in 2020 and 4 phyla of bacteria in 2021: *Proteobacteria*, *Actinobacteriota*, *Bacteroidota*, *Firmicutes* and *Acidobacteriota* (in 2020) (table 1). Only one of identified phyla belongs to the archaea – *Nitrososphaerota* (*Thaumarchaeota*).

Table 1. The dominant phyla, 2021

	Crop rotation with alfalfa					
	CON		NPK		ORG	
1	<i>Proteobacteria</i>	14,67%	<i>Thaumarchaeota</i>	15,32%	<i>Proteobacteria</i>	11,64%
2	<i>Actinobacteriota</i>	14,04%	<i>Actinobacteriota</i>	14,04%	<i>Thaumarchaeota</i>	11,33%
3	<i>Thaumarchaeota</i>	10,39%	<i>Proteobacteria</i>	10,81%	<i>Actinobacteriota</i>	8,90%
5	<i>Bacteroidota</i>	6,84%	<i>Firmicutes</i>	4,56%	<i>Bacteroidota</i>	4,33%
6	<i>Firmicutes</i>	4,00%	<i>Bacteroidota</i>	2,46%	<i>Firmicutes</i>	3,05%
	Crop rotation without alfalfa					
1	<i>Proteobacteria</i>	13,00%	<i>Actinobacteriota</i>	14,62%	<i>Thaumarchaeota</i>	16,23%
2	<i>Thaumarchaeota</i>	12,99%	<i>Thaumarchaeota</i>	13,36%	<i>Actinobacteriota</i>	10,14%
3	<i>Actinobacteriota</i>	11,92%	<i>Proteobacteria</i>	12,02%	<i>Proteobacteria</i>	7,08%
5	<i>Bacteroidota</i>	4,18%	<i>Firmicutes</i>	4,10%	<i>Firmicutes</i>	3,94%
6	<i>Firmicutes</i>	3,46%	<i>Bacteroidota</i>	3,24%	<i>Neclasificat Bacteria</i>	1,94%

Proteobacteria and *Actinobacteriota* dominated in all studied variants and in all studied years. The content of *Actinobacteriota* was slightly lower in the rotation with alfalfa in all studied variants. The content of *Bacteroidota* was higher in the crop rotation without alfalfa in all variants. The most numerous family in 2020 was *Micrococcaceae* family from the phylum *Acidobacteriota*, then *Chitinophagaceae* from the phylum *Bacteroidota* and *Sphingomonadaceae* from the phylum *Proteobacteria*.

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