

## CORE MICROBIOTA IN CARBONATE CHERNOZEM

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The purpose of this study is to evaluate, using next generation sequencing (NGS), the effect of long-term use of organic and mineral fertilizers on the core microbiota in Carbonate chernozem.

The research was carried out in the long-term field experiment (from 1950) on the Chetrosu (Ketrosy) Experimental Station situated in the Central Zone of Moldova. The following experimental plots were studied: 1 - control without fertilizers (CON), 2 – with organic fertilizers - manure (ORG), 3 – with mineral fertilizers (NPK). The soil layer of 0-20 cm was analyzed. The metagenomic analysis of soil was done using equipment of the Core Centrum ‘Genomic Technologies, Proteomics and Cell Biology’ in ARRIAM. Sequencing of 16S rRNA genes was carried out using the MiSeq genetic analyzer from Illumina (USA), taxonomic identification - using the RDP SILVA database (<https://www.arbsilva.de/>).

In total, 18 prokaryotic phyla (16 bacterial and 2 archaeal) were identified, unclassified and others were not included; 15 phyla of them constitute the core microbiota in the studied variants: Chloroflexi, Acidobacteriota, Proteobacteria, Planctomycetota, Nitrososphaerota (Thaumarchaeota), Halobacterota / Euryarchaeota, Fibrobacterota, Myxococcota, Verrucomicrobiota, Gemmatimonadota, Bacteroidota, Nitrospirota, Actinobacteriota. Only 65 out of 122 identified genera constitute the core microbiome of the studied variants, unclassified and uncultured genera were not included too. The phyla Nitrososphaerota (Thaumarchaeota), Firmicutes and Actinobacteriota were with the highest number of OTUs (Operational taxonomic units). The taxonomic composition at phylum level was dominated by bacterial phyla Actinobacteriota (11.8% in variant CON to 14.3% in variant NPK), Proteobacteria (9.3% in CON to 12.1% in ORG), Firmicutes (5.6% in ORG to 8.1% in CON) and archaeal phylum Nitrososphaerota (Thaumarchaeota) (9.3% in NPK to 12.2 % in ORG). At the genus level the most dominant genera were *Bacillus* (Firmicutes), *Microlunatus* (Actinobacteriota) and *Rubrobacter* (Actinobacteriota). The long-term use of fertilizer increased microbial diversity (Shannon's, Margalef's, Pielou's, Menhinick's and inverse Simpson's indexes).

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**Keywords:** soil metagenomic analysis, 16S ribosomal RNA gene, prokaryotes, mineral fertilizers, organic fertilizers, microbial diversity, long-term field experiment.