

METAGENOMIC CHARACTERIZATION OF THE BIODIVERSITY A ANTHROPICALLY CHERNOZEM

Frunze Nina*, Bolocan Nistor, Tonu Nicolai

*Institute of Microbiology and Biotechnology of the Technical University
Chisinau, Republic of Moldova*

E-mail: ninafrunze@mail.ru

The purpose of our research was to evaluate the efficiency of soil resources and microbial biodiversity through the use of elements of organic farming. Methods unrelated to the cultivation of microorganisms were used to assess biodiversity. This allowed assessment of the entire diversity of microbial communities, including non-cultivable microorganisms.

The object of the study was the microbial communities of a typical chernozem of two land use systems: in the forest belt and on the arable land of the Biotron long-term hospital. Soil samples were studied in a layer of 0-20 cm in the spring of 2022. Agrochemical analyzes were carried out according to classical methods. The metagenomic analysis of soil microbiomes was carried out using the technology of high throughput sequencing of the 16S rRNA gene. The work was carried out using the equipment of the Central Collective Use Center "Genomic Technologies, Proteomics and Cell Biology" FGBNU VNIISM, St. Petersburg, Russia.

It was established that the studied land use systems determined the formation of the following structure of the prokaryotic community: about 268-270 genera, 172-177 families, 27-30 classes and about 16-19 types. Pearson's correlation analysis revealed the priority of soil structure in the formation of microbial diversity in comparison with other studied factors (16), assigning a secondary or statistically insignificant role to the content of soil biophilic elements through low values of the Pearson coefficient or through their statistical insignificance. In accordance with this, the nutritional requirements of the studied prokaryotes do not fit into the known algorithm for cultured prokaryotes; therefore, no statistically significant correlations were found between the diversity of microorganisms and the content of certain nutrients in the soil.

Therefore, agricultural practices must be carried out not only in accordance with the needs of plants, but also in accordance with the needs of the soil. This could be an alternative with the potential to improve soil resources and microbial diversity.

Acknowledgments: this study was supported by the PS research project "Efficiency of soil resource use and microbial diversity using elements of biological (organic) agriculture" Nr. 20.80009.5107, funded by the National Research and Development Agency.

Keywords: *typical chernozem, succession, land use system, metagenome, 16S rRNA gene, pyrosequencing, abundance, biodiversity microbiome.*