

PROTEOBACTERIA WITH BIOTECHNOLOGICAL POTENTIAL IN TYPICAL CHERNOSIUM

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The aim of the research was to study by metagenomic methods the structure of the bacterial community of the phylum Proteobacteria and to identify some taxa with biotechnological potential.

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).

The phylum Proteobacteria includes an enormous morphological, physiological and metabolic diversity; its representatives are of great importance for the global carbon, nitrogen and sulfur cycle. The microbial community of the chernozem of the „Biotron” Experimental Station was dominated by the phylum *Proteobacteria*, which had an abundance that varied between 14-34%. The lowest relative abundance was recorded in the soil of the forest strip, and the highest in the soil with mineral and organic fertilization. The dominant genera of *Proteobacteria* were *Sphingomonas*, *Microvirga*, *Skermanella*. The highest relative abundance (1.2-6.8%) was determined for the genus *Sphingomonas*. Species belonging to the genus *Sphingomonas* possess various functions. Many members of the *Sphingomonas* genera possess unique abilities in degrading refractory organic pollutants. Some of the species of the genus *Sphingomonas* improve plant growth under drought, salinity and heavy metal stress conditions in agricultural soils. This role has been attributed to their potential to produce plant growth hormones, for example, gibberellins and indole-3-acetic acid. The genera *Microvirga*, *Skermanella* are also of particular interest for agricultural biotechnologies as microorganisms capable of stimulating plant growth under abiotic stress conditions and degrading various soil pollutants.

Most *Sphingomonas* species possess the ability to degrade a variety of aromatic compounds and industrial pollutants, thus contributing significantly to environmental remediation and industrial production. Deep knowledge about the ecological distribution and diversity of bacteria of the genera *Sphingomonas*, *Microvirga*, *Skermanella* associated with plants can provide new insights to explore its agricultural potential for promoting plant growth.

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