UDC 633.15:631.461

PLANT RYIZOSPYERE: SOIL MICROORGANISMS, FUNCTIONS, FERTILITY, SMART-AGROENGINEERING OF BIOLOGICAL SYSTEMS

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The formation of soil as a habitat for various organisms can be globally compared to a living and dynamic organism, the stable development of which determines the diversity of functional and ecological features, and understanding the depth and degree of study of all factors makes it possible to reveal the mechanisms underlying them and innovatively ensure the sustainable development of agroecosystems. Soil microbiota plays a key role in maintaining soil fertility and stability. The growth of food production, necessary to meet the needs of an ever-increasing population, largely depends on the integrated management of trophic flows of nutrients. However, the potential of microbial bioagents often remains underestimated. The importance of rhizosphere microorganisms is enormous, as they contribute to the transformation of nutrients, their absorption and use, thereby optimizing the ontogenesis of plants, which in turn contributes to obtaining high sustainable yields. The stability of soil trophic regimes as a basis for soil health and, accordingly, the efficiency of nutrient use can be significantly improved by modifying and managing the rhizosphere using optimal methods of influence, such as the implementation of the biological potential of the soil metagenome, methods for regulating trophic flows through biological regulation of plant rhizosphere colonization, the use of organic and biological fertilizers, as well as optimization of processes occurring in the root zone.

Microorganisms are one of the most common living things on the planet, making up about 17% of the world's biomass. Soil, being one of the most complex ecosystems, contains a huge amount of microbial life, including about $4\text{-}5\times10^{30}$ microbial cells. The soil microbiome is mainly made up of bacteria, archaea, fungi, and viruses. According to known data, one gram of soil can contain 10^8-10^9 bacteria, 10^7-10^8 viruses and 10^5-10^6 micromycetes. Soil microbial communities perform important ecosystem functions such as transforming nutrients, sequestering carbon, sequestering water, promoting plant growth, and protecting against pathogens. Interest in the study of soil microbiota has increased due to its role in the global Carboniferous cycle, climate change and sustainable agricultural production. The diversity and abundance of microorganisms depend on land use methods and soil characteristics. Agrarian ecosystems are more homogeneous than natural environments due to less plant diversity and regular anthropogenic influence. On the basis of the strength of the connection with the root systems of plants, two types of soil niches can be distinguished: soil that is not connected or is weakly connected to the roots of plants, and rhizosphere soil, which is directly adjacent to the root system. The composition of bacterial groups is also significantly differentiated between unbound and rhizosphere soil, with a decrease in diversity as one approaches the root system of plants. The rhizosphere is an important biological inducer where key interactions between plants and microorganisms occur, as well as between the microorganisms themselves that form the composition of the microbial community. Plant roots secrete organic compounds that support microbial activity. Rhizosphere soil contains 10^8-10^{11} cells per gram, which is equivalent to about 10^4 species of microbes. In addition to rhizobacteria, which promote plant growth, soil is also a habitat for phytopathogenic microorganisms and opportunistic bacteria for humans.

Major environmental factors such as pH, salinity, humidity, temperature, and nutrient content (including the ratio of carbon to nitrogen) play a critical role in shaping the structure of the rhizosphere microbiome. However, the peculiarities of the plant culture also have a significant influence. These environmental factors create unique ecological niches that contribute to the formation of certain microbial groups. Studies show that environmental stress can alter microbial diversity and ecosystem functional characteristics. Niche studies demonstrate that important processes of microbial communities depend on both the adaptive properties of microorganisms and their habitat conditions.

The spatial heterogeneity of the soil microbiome was studied on the example of millet, where the structure of bacterial communities turned out to be heterogeneous, and the amount of the dominant *Verrucomicrobia phylum* changed by 2.5 times over an area of 10 cm^3. Differences between the microbiomes of different plant types (legumes, cereals, and forbs) showed that 4% of the variation in bacteria and 11% in micromycetes was associated with plant groups, and 30% with plant species.

A study of different wheat varieties revealed significant differences in the microbial groups of *Planctomycetes*, *Acidobacteria,* and *Actinobacteria*, and smaller differences in *Chloroflexi*, *Fibrobacteria,* and *Verrucomicrobia*. Structures of bacterial groups at lower taxonomic levels (families, genera, species) changed depending on the stage of corn ontogeny. bacterial species of the genera *Massilia*, *Flavobacterium*, *Arenimonas* and *Ohtaekwangia* predominated, while in the later stages species of the genera *Burkholderia*, *Ralstonia*, *Dyella*, *Chitinophaga*, *Sphingobium*, *Bradyrhizobium* and *Variovorax dominated*.

Anthropogenic impacts causing biotic and abiotic stresses, as well as changes in climatic conditions, affect the diversity of microbial and plant communities of the soil. Drought-tolerant bacteria have been identified in drought-prone cotton plants and thermophilic bacteria belonging to the phylums *Chloroflexi* and *Gemmatimonadetes,* prevail in environments where there was a drought impact. In agroecosystems, the use of fertilizers, farming and tillage practices leads to changes in soil microbiomes. In the case of the millet rhizosphere microbiome, fertilizer application reduced the relative abundance of *Verrucomicrobia*. Various soil additives also reduced the diversity of the soil microbiome and affected the rhizosphere communities of maize. Changes in the community structure were caused by a decrease in the abundance of *Actinobacteria* and *Firmicutes* and an increase in the abundance of *Proteobacteria*, *Bacteroidetes*, *Verrucomicrobia* and *Acidobacteria*. The type and dose of fertilizer also contributed to changes in the structure of the rhizobia community under maize, with differences in the abundance of microbial groups correlated with changes in nutrient content. Tillage practices altered the bacterial communities associated with rapeseed roots and shoots, while agricultural production practices influenced the structure of the rice microbial community.

In microbial communities, it is important to study the species composition and existing ecological functional groups. Different microbes play different roles in the structure of the community, which can support soil health and plant productivity. Microbial communities are complex dynamic networks with various interactions between microorganisms, such as competition for resources, metabolic interactions, spatial organization, in particular, biofilm production, signalling, horizontal gene transfer, coevolution and viral infection. Usually, a higher diversity of microorganisms increases the number of metabolites, secondary metabolites, phytohormones, biocontrol substances and other beneficial substances, thereby contributing to soil structure and fertility, root system architecture and nutrient retrieval, plant nutrition and hormonal balance, plant stress tolerance, agricultural productivity and resistance to climate, land use and agronomic practices. Thus, the role of the original microbiome in the emergence of phytopathognos *Rhizoctonia solanum* was studied. A large number of *Alphaproteobacteria*, *Firmicutes* and *Cyanobacteria* were found in soils associated with healthy tomato plants, while diseased plants were found in soils rich in *Acidobacteria, Actinobacteria* and *Verrucomicrobia*.

Thus, stratification and diversity of microhabitats in the soil contribute to the formation of complex microbial communities. One of the main tasks of modern science is the analysis of data from microbial communities. In addition to taxonomic classification, understanding the functional groups of bacterial taxa and the dynamics of the structure of the bacterial community, which is necessary for a thorough understanding of ecosystem processes in soil, are key aspects.

The rhizosphere is recognized as an important zone for the horizontal transfer of microbial genes, and the soil microbiome acts as a rich reservoir of genetic diversity. In this regard, genetic engineering of beneficial soil bacteria (PGPR) is a promising tool for the development of sustainable agriculture. There is a need to understand how the ecological functions of the soil are altered by the environment and how these functions can be maintained by applying sustainable agricultural practices. The specifics of interactions between plants and microorganisms also require further research.

Another tool for sustainable agriculture is plant genome engineering, based on an understanding of the specific mechanisms of communication between plants and microbes. The key to sustainable agriculture, therefore, lies in an in-depth understanding of the complex relationships between soil, microbes and plants, and their impact on sustainability in both the short and long term.In view of the above, future research should focus on the following areas: the use of genetically modified microbes and plants for sustainable agricultural production, the long-term impact of immobilized bioformulations on the soil and microbiome, the development of reliable and sustainable methods for processing products for soil improvement.

Theses material is written based on the authors' generalizations.