



Biotechnological aspects of the formation of the metagenome of potato rhizosphere microorganisms under the influence of microbial preparations

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Abstract. The study aimed to assess the impact of microbial preparations on the structural and functional characteristics of the potato rhizosphere metagenome and the associated changes in plant growth and productivity. Within the framework of the vegetation experiment, whole-genome metagenomic profiles of the potato rhizosphere were obtained for five variants: untreated, three separate microbial preparations, and their combination. A total of 11.8 million sequencing reads were obtained, which underwent basic quality filtering; 2,950 taxonomic units were identified, taxonomic and functional annotation was performed, diversity indices were calculated, and a correlation analysis with morphological and yield indices was conducted. The study determined that representatives of the Proteobacteria, Actinobacteriota, Bacteroidota and Firmicutes types dominated in all variants, with a total share exceeding 80% of the metagenome structure, while the use of microbial preparations was accompanied by an increase in species richness and diversity: the Shannon index increased from 4.82 in the control to 5.12-5.18 in the experimental variants, and the Chao1 richness estimate increased from 830 to 960-975 taxa. An increase in the proportion of genera associated with plant growth was observed, as well as in the relative number of genes associated with nitrogen fixation, phosphorus mobilisation, potassium transport, sulphur assimilation and stress resistance, with maximum values in the variants with the third preparation and its combination with the first. These options ensured an increase in tuber weight per plant to 495-510 g and an increase in the proportion of medium and large fractions of the harvest, with correlation coefficients between the total proportion of beneficial microorganisms, functional genes and productivity reaching 0.6-0.7. The results obtained showed that targeted microbial treatment can form a rhizosphere metagenome with increased biotechnological potential and can be used by practising agronomists, developers of microbial preparations, potato breeders, and specialists in integrated soil fertility management to optimise microbial consortia in potato cultivation technologies.

Keywords: variant; quantity; type; genus; nitrogen fixation; phosphorus

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INTRODUCTION

The research relevance is determined by the need to improve methods of managing the rhizosphere microbiome of cultivated plants, in particular potatoes, to increase their productivity and resistance to stress factors. Modern agricultural technologies, such as biological preparations, genetically modified organisms (GMOs), robotisation and automation of agricultural processes, are aimed at integrating biological preparations containing beneficial microorganisms to optimise plant nutrition processes, stimulate their growth and improve soil fertility. Biological products can be used to improve the structure of the rhizosphere microbiome, which in turn affects the morphological and productive indicators of plants. Genetically modified plants improve resistance to pests and diseases, reducing the need for chemical agents. Robotisation and automation of agronomic processes reduce labour costs and improve the accuracy of operations, which contributes to more efficient crop cultivation. The use of biological products, in particular to improve the rhizosphere microbiome, has the potential to change the composition of microbial communities, which can lead to improved plant health and higher yields. Research into the metagenomic profile of rhizosphere microorganisms further contributes to the analysis of their functional potential, creating new opportunities for the introduction of innovative biotechnologies in agriculture and contributing to the sustainable development of agricultural production.

The effect of microbial preparations on the response of potato varieties to treatment with nitrogen-fixing bacteria and mycorrhiza was studied in a paper by V. Kovalenko *et al.* (2024). The study determined that the use of microbial preparations improves potato growth and productivity by promoting more efficient nitrogen use. A. Melnyk & M. Kyryk (2020) analysed the effectiveness of biological preparations in reducing potato alternaria in the forest-steppe zone of Ukraine. The study found that the use of biological preparations reduces disease incidence and improves crop quality, confirming the potential of biological agents in crop production. M.O. Kirovants (2024) studied the formation of the barley rhizosphere microbiome under different fertiliser systems in typical chernozems. The study determined that the type of fertiliser affects the composition of microbial

communities, which is relevant for an increase in soil fertility and crop yields.

Microbial diversity and dynamics of potato rhizosphere communities during cultivation were assessed in a study by Q. Hou *et al.* (2020). The study determined that the potato microbiome undergoes significant changes depending on agronomic factors, which affect its health and productivity. Additionally, the study demonstrated that the most pronounced changes in microbial communities occurred in the early stages of plant development, while after flowering, the structure of the microbiome became relatively more stable. P. Lu *et al.* (2023) studied the metagenomic analysis of the tobacco rhizosphere. The study demonstrated changes in microbial communities under the influence of root nematodes, confirming the influence of the microbiome on the regulation of plant stress resistance. The study also noted that the structure and functional potential of the rhizosphere bacterial community statistically correlated with the degree of damage by root nematodes. Changes in the microbial community in different underground compartments of potatoes, which affect crop yield and quality, were evaluated in a study by G. Chen *et al.* (2022). The study proved that changes in the microbiome can directly correlate with the agronomic characteristics of potatoes. A clear difference in microbiota between compartments (rhizosphere, tuber surface, soil) and regions was also shown, with soil nutrients and pH being the key factors of variation. A review of current metagenomic approaches to studying microbial diversity in the rhizosphere was conducted by B. Rajguru *et al.* (2024). The study considered the use of metagenomic technologies to assess the functional capabilities of the microbiome, which provides a complete overview of its impact on plants. The advantages and limitations of the approaches (shotgun metagenomics vs. 16S profiling) and their suitability for interpreting the functions of the microbiome, particularly in the context of nutrition and disease suppression, were systematised separately.

The assessment of the potato rhizosphere microbiome during bacteriophage therapy was conducted by S. Mousa *et al.* (2022). During the analysis, scientists discovered the possibility of modifying the microbial community to improve



plant health. Additionally, the study demonstrated that phage cocktails after infection with bacterial pathogens provided a better effect in reducing disease manifestations compared to monophages, confirming the controllability of rhizosphere microbiota as an element of biocontrol. N. Imam *et al.* (2021) determined that the properties of local microbiome networks in the soil are predictive factors for potato yield. This statement emphasises the role of the microbiome in agronomic performance. The study demonstrated that combining NGS data and bioinformatics with the Random Forest model provided high accuracy (84.6%) in distinguishing between low/high yield plots, with the network characteristics of fungal communities having higher predictive power than those of bacterial communities. The impact of different crop rotation systems on the potato rhizosphere microbiome was investigated by J. Qin *et al.* (2022). The study emphasised the significance of agronomic practices for microbiome management and yield improvement. Additionally, the study demonstrated that during long-term continuous cultivation, the incidence of diseases (in particular, black scurf) increased, and crop rotation and continuous cultivation regimes differently altered the diversity of bacterial and fungal communities in the soil and rhizosphere. Research into the microbial environment of the potato rhizosphere occupies a prominent place in agrobiotechnology, as the rhizosphere microbiome directly affects plant health, growth and productivity. Many authors have confirmed that changes in the composition of the microbial community can significantly improve the efficiency of agrochemicals and contribute to increasing plant resistance to diseases and stress factors. In particular, the use of biological preparations that stimulate the activity of beneficial microorganisms is a promising direction in agriculture for optimising the soil ecosystem and increasing crop yields. The study aimed to evaluate the effect of microbial preparations on the structural and functional characteristics of the potato rhizosphere metagenome. The objectives of the study were: 1) to analyse changes in the taxonomic composition of the rhizosphere microbiome under the influence of various microbial preparations; 2) to assess the relationship between changes in the microbiome and agronomic indicators of potatoes.

MATERIALS AND METHODS

The study was conducted in a field experiment with potatoes (*Solanum tuberosum* L.) of the mid-season variety 'Slovyanika' during the growing season from April to September 2025 in Ukraine, Kyiv region, in a temperate climate zone on sod-podzolic/chernozem soil (pH 6.2-6.5, humus content 2.5-3.0%). In addition, the agrochemical and agrophysical indicators of the soil were characterised, in particular the content of mineral nitrogen (N-NO_3^- , N-NH_4^+), mobile forms of phosphorus and potassium (P_2O_5 , K_2O), micro-nutrient availability (Fe, Mn, Zn, Cu, B), as well as field moisture and soil temperature during vegetation (at the depth of the root-containing layer). The predecessor of potatoes was winter wheat, which provided a typical background for evaluating the effect of microbial preparations without excessive accumulation of organic residues of leguminous crops. The choice of crop (potatoes) and the 'Slovyanika' variety was justified by their prevalence in the forest-steppe zone of Ukraine, stable adaptability to the soil and climatic conditions of the Kyiv region, and suitability for comparative assessment of the effect of microbial inoculants on growth indicators, yield and rhizosphere microbiome parameters under typical technological conditions. The study included five variants (control, M1, M2, M3, M1+M2) and was conducted on plots of 10-12 m² for each variant, with a planting pattern of 70×25 cm, incorporating technological tracks and protective strips around the perimeter. Planting was conducted manually with calibrated tubers of standard size with visually healthy characteristics, to a depth of 6-8 cm, in pre-prepared soil without excessive compaction. Experimental studies of plants, including the collection of plant material, complied with institutional and national guidelines. The study adhered to the standards of the Convention on Biological Diversity (1992).

The experimental design consisted of five variants: control without treatment (C), three variants with separate microbial preparations (M1, M2, M3) and combined treatment with preparations M1+M2. In variant M1, the preparation "Azotofit" based on strains of nitrogen-fixing rhizobacteria *Azotobacter* spp. was used; in variant M2, the phosphate-mobilising Fosfoenter preparation based on *Bacillus* spp. and *Pseudomonas* spp. was



used; in variant M3, the complex biological Bio-Complex-Rhizo preparation was used, which included strains of *Rhizobium* spp., *Azospirillum* spp. and associated rhizobacteria capable of synthesising phytohormone-like compounds. In the combined variant M1+M2, these preparations were applied together in the same proportions as when used separately. The choice of these preparations was justified by their different PGPR mechanisms of action and the expected complementary effect on the rhizosphere microbiome and mineral nutrition of potatoes: M1 was chosen as an inoculant with the potential to increase nitrogen supply and stimulate root formation; M2 – as a preparation aimed at mobilising hard-to-reach forms of phosphorus and enhancing phosphorus nutrition; M3 – as a complex consortium combining nitrogen fixation, phosphate mobilisation and phytohormone-like growth stimulation. The combined option M1+M2 was included to test the possible synergistic effect of simultaneous enhancement of nitrogen and phosphorus nutrition and to assess whether the combination of functional groups of microorganisms leads to more pronounced changes in the taxonomic and functional structure of the rhizosphere microbiome compared to mono-inoculation. The microbial preparations belonged to a group of biological agents based on rhizosphere bacteria with a declared ability to fix nitrogen, mobilise phosphorus and synthesise biologically active metabolites. The treatment was conducted before planting by inoculating the tubers with working suspensions of the preparations in the concentrations recommended by the manufacturer, ensuring uniform application over the entire surface of each tuber (the same rate of working solution per unit of mass/number of tubers), with uniform wetting of the tubers and holding until drying, after which planting was conducted on the experimental plots.

The experiment was conducted using a randomised block design in three replicates, with each variant presented as a separate plot using standard potato cultivation techniques. For metagenomic analysis, five rhizosphere samples were selected from each variant (one sample from individual plants from different plots of the repetition), which provided 25 biological replicates. Samples from different replicates were not mixed but were processed and sequenced separately

as independent biological replicates (each sample formed a separate library/separate data file for further taxonomic and functional analysis). Rhizosphere soil was collected during the period of active plant growth, after carefully extracting the tuberous plant and separating the soil adhering to the root system. The samples were immediately cooled in thermal containers with cooling elements ($\approx +2...+6^{\circ}\text{C}$) and transported to the laboratory within 4-6 hours, where they were stored at -80°C until DNA (deoxyribonucleic acid) extraction. During sample preparation in the laboratory, standard microclimatic conditions were maintained ($t\ 20-22^{\circ}\text{C}$; relative humidity 40-60%), which minimised the risk of condensation and secondary moistening of the samples.

Genomic DNA from rhizosphere soil was extracted using a soil sample kit (DNeasy PowerSoil Kit, QIAGEN, Germany) according to the manufacturer's instructions. The quality and concentration of DNA were monitored using a NanoDrop spectrophotometer (Thermo Fisher Scientific, USA) and a Qubit fluorometer (Thermo Fisher Scientific, USA). For metagenomic analysis, random fragmentation libraries were prepared and subsequently sequenced using paired-end technology on an Illumina platform (NovaSeq 6000, USA), which provided an average volume of approximately 0.49 million reads per sample.

Primary processing of sequencing data was performed using a standard pipeline, which included quality control, adapter sequence trimming, and quality threshold filtering. Taxonomic annotation was performed based on comparison with reference databases of bacterial genomes, forming OTUs (Operational Taxonomic Units)/ASVs (Amplicon Sequence Variants) and generalising them to the level of types, families and genera. The functional profile of the metagenome was formed based on the prediction of functions from 16S data using PICRUSt2 (Phylogenetic Investigation of Communities by Reconstruction of Unobserved States, version): predicted KEGG (Kyoto Encyclopedia of Genes and Genomes) orthologs were aggregated into functional categories and metabolic pathways related to plant nutrition (nitrogen fixation, phosphorus mobilisation, potassium transport, sulphur assimilation) and stress resistance (biosynthesis of antibiotic-like compounds and siderophores, antioxidant enzymes,

resistance induction). The morphological and productive indicators of potatoes were determined on a representative sample of plants from each variant (at least 10 plants per repetition). Plant height was measured with a tape measure, tuber weight was measured on laboratory scales, and the number of tubers was measured by direct counting. The fractional composition of the harvest (small, medium, large tubers) was determined by weight and calibre, with the proportion of each fraction calculated as a percentage.

Intragroup diversity indices (Shannon, Simpson, Chao1) were calculated based on OTUs/ASVs tables. Intergroup differences in microbiome structures were assessed using Bray-Curtis taxonomic distance matrices followed by ordination (e.g., principal coordinates) and clustering of samples. Correlation analysis (Pearson's or Spearman's coefficients, depending on the data distribution) was used to analyse the relationships between microbiome indicators and productivity, controlling for the influence of external environmental factors (soil temperature and moisture) by partial correlation/inclusion of these indicators as covariates. The normality of the distribution was tested using the appropriate criterion, and differences between variants were assessed using parametric or non-parametric tests for independent samples with a statistical significance level of $p < 0.05$ and, if necessary, multiple comparison control. The integral indicator of biotechnological potential was calculated by normalising structural, functional and agronomic parameters to a dimensionless

scale and then aggregating them into a single index with equal weights of blocks. All calculations were performed using specialised statistical and metagenomic analysis software packages.

RESULTS AND DISCUSSION

General characteristics of the metagenome of potato rhizosphere microorganisms

Within the scope of the study, whole-genome metagenomic profiles of rhizosphere samples of potatoes were obtained from five variants: control (C), treatment with microbial preparation 1 (M1), microbial preparation 2 (M2), microbial preparation 3 (M3) and combined treatment with preparations 1+2 (M1+M2). The total number of sequenced genera that passed the basic quality filtration was 11.8 million, with an average of 0.49 million genera per sample. In the control variant, 2.1 million genera were obtained, in variants M1, M2 and M3 – 2.4, 2.3 and 2.5 million genera, respectively, and in variant M1+M2 – 2.5 million genera. As a result of taxonomic annotation, 2,950 OTUs/ASVs were identified, belonging to 17 types, 46 classes, 118 families and 247 genera of prokaryotic microorganisms. In the control variant, the number of OTUs/ASVs averaged 820 ± 60 per sample, in variants M1, M2 and M3 – 910 ± 55 , 880 ± 50 and 940 ± 65 , respectively, and in variant M1+M2 – 960 ± 70 OTUs/ASVs per sample. The ratio between the number of genera and the number of OTUs/ASVs remained stable in most variants, reflecting a comparable level of taxonomic diversity coverage (Table 1).

Table 1. Summary indicators of sequencing and basic diversity of the potato rhizosphere metagenome

Variant	Number of births, million	Average number of OTUs/ASVs per sample	Observed richness, average, OTUs/ASVs	Shannon index, H'
K (control)	2.1	820	805	4.82
M1	2.4	910	905	5.05
M2	2.3	880	895	4.96
M3	2.5	940	935	5.12
M1+M2	2.5	960	945	5.18

Source: compiled by the authors based on research

Analysis of basic diversity indicators showed that the total number of taxa (OTUs/ASVs) at the sample and variant levels remained comparable, although an increase in species richness was

observed in the variants with microbial preparations compared to the control. The mean values of observed richness at the OTUs/ASVs level were 805 for the control, 895-935 for individual

preparations, and 945 for the M1+M2 combination. Diversity indices that considered both richness and evenness (in particular, the Shannon index) ranged from 4.8 to 5.3 bits for most variants, with minimal differences between them (Table 1). The taxonomic spectrum of rhizosphere microbiomes in all variants was formed mainly by representatives of the Proteobacteria, Actinobacteriota, Bacteroidota, and Firmicutes types. The total share of these types in the overall metagenome struc-

ture ranged from 82.3% in the control to 87.5% in the M1+M2 variant. In the control variant, Proteobacteria (43.1%) and Actinobacteriota (22.4%) had the highest relative abundance, while in the variants with microbial preparations, the proportion of Proteobacteria ranged from 45.6 to 49.2% and Actinobacteriota from 20.1 to 23.8%. The proportion of Bacteroidota varied from 9.5% (control) to 11.7% (M3), and Firmicutes from 7.3% to 9.4%, depending on the variant (Fig. 1).

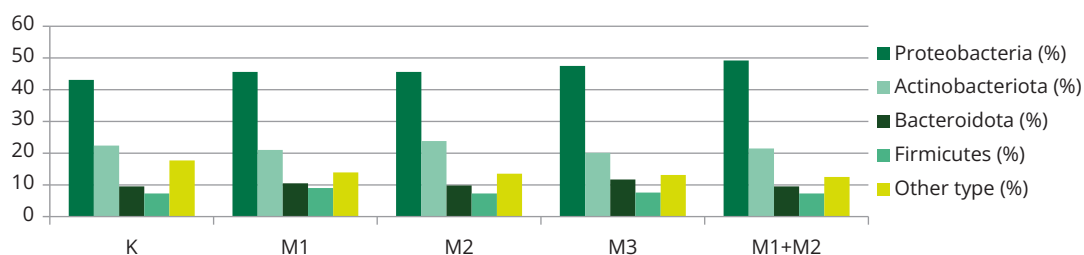


Figure 1. Relative abundance of dominant bacterial types in the potato rhizosphere under different microbial treatment options

Source: compiled by the authors based on research

This reflected a predominantly even distribution of abundance between dominant and sub-dominant taxa in all variants. A core microbiome of the potato rhizosphere was identified, consisting of taxa found in most samples regardless of variant. The core included representatives of the genera *Pseudomonas*, *Bacillus*, *Streptomyces*, *Flavobacterium*, *Rhizobium*, and *Sphingomonas*, whose total relative abundance was 41.2% in the control and 43.5-47.8% in the variants with microbial preparations. The proportion of core genera at the type level was distributed mainly between Proteobacteria (24.3-27.9%) and Actinobacteriota (10.8-12.6%).

The results of the study are consistent with the conclusions of J.K. Kiige *et al.* (2025), noting an increase in the diversity of the potato microbiome when treated with microbial preparations. Changes in the metagenome confirm the effect of such preparations on the stability of rhizosphere microbiomes. The study by M. Wang *et al.* (2025) also demonstrated the influence of agrotechnical conditions on the potato rhizosphere microbiome, which is reflected in the study on the influence of microbial preparations. In the variant with combined treatment with preparations, an

increase in the proportion of genera that promote plant growth was noted. The results obtained in this work confirm the conclusions of J. Song *et al.* (2021) regarding the positive effect of biological preparations on the rhizosphere microbiome, which is associated with an improvement in the quality of potato tubers. In this study, as in the work of scholars, an increase in the diversity of the microbiome was accompanied by an improvement in agronomic indicators.

The generalisation of the results obtained made it possible to characterise the rhizosphere metagenome of potatoes as a taxonomically diverse bacterial community with a comparable level of sequencing depth between variants and a stable ratio of genera and OTUs/ASVs. In all variants, representatives of the Proteobacteria, Actinobacteriota, Bacteroidota and Firmicutes types dominated, accounting for more than 80% of the total metagenome structure, while the contribution of other types remained relatively limited. Variants with microbial preparations were characterised by higher species saturation compared to the control in terms of observed richness and average number of OTUs/ASVs per sample, while maintaining similar Shannon index values. The core microbiome of



the potato rhizosphere included the genera *Pseudomonas*, *Bacillus*, *Streptomyces*, *Flavobacterium*, *Rhizobium*, and *Sphingomonas*, which were present in most samples regardless of the variant, ensuring the stability of the basic taxonomic core when using different microbial preparations.

Dynamics of α -diversity of the rhizosphere microbiome under the influence of drugs

The indicators of intragroup diversity of the potato rhizosphere microbiome were assessed using the Shannon, Simpson, and Chao1 indices for all experimental variants (Table 2).

Table 2. α -diversity indices of the rhizosphere microbiome of potatoes

Variant	Shannon index, H' (mean $\pm$ SD)	Simpson index (mean $\pm$ SD)	Chao1, OTUs/ASVs (average $\pm$ SD)
K (control)	4.82 $\pm$ 0.03	0.912 $\pm$ 0.003	830 $\pm$ 8.5
M1	5.05 $\pm$ 0.03	0.928 $\pm$ 0.003	940 $\pm$ 8.5
M2	4.96 $\pm$ 0.03	0.921 $\pm$ 0.003	925 $\pm$ 8.5
M3	5.12 $\pm$ 0.03	0.931 $\pm$ 0.003	960 $\pm$ 8.5
M1+M2	5.18 $\pm$ 0.03	0.935 $\pm$ 0.003	975 $\pm$ 8.5

Source: compiled by the authors based on research

A comparison of the experimental variants showed that the use of microbial preparations was accompanied by an increase in both taxon richness and the evenness of their relative abundance distribution compared to the control. The lowest values of Chao1, Shannon, and Simpson indices were recorded in the control variant, while all experimental variants were characterised by higher species saturation. The most pronounced increase in the assessed indicators was recorded in the combined treatment variant M1+M2, where the Chao1 and diversity index values exceeded those of the control and individual single-component treatments. In variants M1, M2 and M3, α -diversity also exceeded the control level, but the differences between individual preparations were less pronounced than between the control and combined treatment. Analysis of the richness (Chao1) and evenness (Shannon and Simpson indices) indices showed that the increase in α -diversity in the variants with microbial preparations was mainly due to an increase in the number of rare OTUs/ASVs while maintaining a high proportion of dominant taxa. Rare taxa were considered a “reservoir” of functional potential of the rhizosphere, since even at low relative abundance they may contain genes associated with key ecosystem functions (mobilisation of nutrients, synthesis of siderophores and antimicrobial metabolites, participation in hormone-like regulation and induction of systemic resistance). The increase in the proportion of rare OTUs/ASVs in the treatment groups was interpreted as a potential expansion of the functional niche of the microbiome and an increase in

its functional redundancy, which may contribute to the stability of the microbial community and support plant productivity under changing environmental conditions. Elevated Chao1 values in the M3 and M1+M2 variants indicated a broader spectrum of taxa in the microbial community, while the increase in the Simpson index reflected a more even distribution of relative abundance among them. This combination of greater richness and evenness of the microbiome structure was considered an indicator of increased structural complexity and potential functional capacity of the rhizosphere community. In the context of microbial community stability, increased α -diversity values in the experimental variants, particularly in the combined treatment M1+M2, indicated the formation of a more diverse and evenly structured microbiome capable of supporting a wider range of metabolic functions due to the presence of both dominant and rare taxa. Within the scope of this study, this configuration of intragroup diversity was identified as the basis for further analysis of the relationship between α -diversity, functional characteristics of the metagenome, and agrobiological indicators of potato plants.

The results of the study of α -diversity of the potato rhizosphere microbiome are consistent with the study by J. Ha *et al.* (2021) also showed that treating plants with microbial preparations leads to an increase in microbiome diversity. Both studies observed an increase in the number of rare OTUs/ASVs, indicating an expansion of microbiological diversity. The results of B.R. Martins *et al.* (2024) also confirmed that an increase in



microbiome diversity may be associated with improved agronomic characteristics of plants. Similar to their conclusions, the highest increase in diversity indices was observed in the combined treatment with preparations M1+M2. The conclusions of P. Gao *et al.* (2025) on the influence of environmental factors on the microbiome supported the data obtained in this study on the adaptation of the microbiome to changes in the environment, in particular after treatment with microbial preparations.

Comparison of the structure of potato rhizosphere microbiomes between variants based on taxonomic distance matrices showed pronounced differentiation of microbial communities under conditions of microbial preparation application. On the ordination diagram, the first axis summarised 38.2% of the variation in species composition, and the second axis summarised 19.4%. The centroids of the control variant samples were shifted to a separate area of the plane, while the variants with microbial preparations were grouped in other sectors. Samples M1 and M2 were located at a moderate distance from the control, demonstrating partial preservation of the microbiome structure with a simultaneous change in the relative contributions of individual taxa. For variants M3 and M1+M2, a more pronounced departure from the control centroids along the first axis was observed, reflecting a greater degree of taxonomic restructuring of the community. The study by B.R. Martins *et al.* (2024) confirms that different options for treating potatoes with microbial preparations can significantly alter the rhizosphere microbiome, which is reflected in its structure and richness. According to their results, variants treated with microbes often show an increase in species richness and a change in the ratio of taxa, which was also observed in this study, particularly in variants M1, M3 and M1+M2.

Analysis of the cluster structure based on distance matrices identified two main clusters of rhizosphere microbiomes. The first cluster was formed by the control variant and variant M2, for which the average pairwise distance between samples remained minimal. The second cluster combined variants M1, M3 and M1+M2, within which a subcluster with M3 and M1+M2 with lower intra-group dispersion was additionally identified. The average distance between the control variant and the M1+M2 variant was the maximum among all

comparisons, indicating the greatest difference in the structure of the microbial community under combined treatment conditions. For variants M1 and M2, the values of intergroup distances relative to the control were lower than for M3 and M1+M2, which corresponded to the intermediate nature of structural changes. The results of the study of β -diversity of the potato rhizosphere microbiome confirm the conclusions of R.W.P.M. Rajapaksha *et al.* (2024), which showed that the microbiomes of different parts of the plant can vary significantly in structure and diversity depending on agronomic conditions. In this study, the variants with microbial preparations demonstrate a pronounced structural differentiation of microbial communities, reflecting the redistribution of dominant and subdominant taxa in response to treatment. Similar to a study by Z. Wang *et al.* (2021), which determined significant changes in the composition of the rhizosphere microbiome under the influence of microbial consortia, this study also observed that combined treatments M1+M2 led to the greatest changes in the structure of the microbial community. Z. Wang *et al.* (2021) found that increased diversity was associated with improved metabolic processes, which was also reflected in the increase in taxonomic restructuring in this study in variants with microbial preparations.

The structural differentiation of rhizosphere microbiomes in the experimental variants was interpreted as a result of the redistribution of dominant and subdominant taxa in response to the action of microbial preparations. The inclusion of M3 and especially the combination of M1+M2 was accompanied by the formation of configurations that differed from the control not only in species richness but also in the ratio of taxa that contributed most to intergroup diversity. The identified clusters reflected the presence of variants with a preserved microbial community structure (control, M2) and variants with a reformed community (M1, M3, M1+M2), which provided a basis for further analysis of the relationship between β -diversity, the functional profile of the metagenome, and the agrobiological parameters of plants.

Taxonomic profile of rhizosphere microorganisms under the influence of microbial preparations

Taxonomic analysis at the type level showed that

representatives of Proteobacteria, Actinobacteriota, Bacteroidota, and Firmicutes dominated in all variants of the experiment. In the control variant, the proportion of Proteobacteria was 43.1%, Actinobacteriota – 22.4%, Bacteroidota – 9.5%, Firmicutes – 7.3%, while the total contribution of other types to the metagenome structure was 17.7%. Under the conditions of treatment with microbial preparations, an increase in the relative abundance of Proteobacteria to 45.6–49.2% was observed in variants M1, M2, M3 and M1+M2. The maximum value of this indicator was recorded in the combined treatment variant M1+M2 (49.2%), accompanied by a simultaneous decrease in the proportion of “other” types to 12.5%. The proportion of Actinobacteriota in the experimental variants ranged from 20.1 to 23.8%, with slightly higher values in variant M2 (23.8%) compared to the control. For Bacteroidota, an increase in the proportion was noted in the variants with preparations M1 and M3: from 9.5% in the control to 10.5% in M1 and 11.7% in M3. In variants M2 and M1+M2, the proportion of Bacteroidota was at the level of 9.5–9.8%, close to the control values. The contribution of Firmicutes under the action of the preparations changed less significantly: in the control, it was 7.3%, in the M1 variant, 9.0%, in the M2, M3 and M1+M2 variants, 7.3–7.6%. Thus, the use of microbial preparations was accompanied by a shift in the taxonomic profile towards an increase in the proportion of Proteobacteria and, in some variants, Bacteroidota, while maintaining comparable proportions of Actinobacteriota and Firmicutes. Dominant types retained their leading role in the structure of the microbial community, and changes in their relative abundance determined the main differences between the control and experimental variants. The results of the taxonomic profile of potato rhizosphere microorganisms correlate with the study by F. Rasche *et al.* (2006), demonstrating that the use of transgenic potatoes with antibacterial properties changes the composition of the rhizosphere microbiome, in particular, increasing the proportion of beneficial bacteria such as *Pseudomonas* and *Bacillus*. Similar to their study, in this work, the use of microbial preparations led to an increase in the proportion of these genera in the structure of the microbiome, indicating the activation of components that promote plant growth.

At the family and genus level, a group of taxa associated with plant growth and nutrition was identified, including representatives of Plant Growth Promoting Rhizobacteria (PGPR), nitrogen fixers, phosphate-mobilising microorganisms, and phytohormone producers. The core group included the genera *Pseudomonas*, *Bacillus*, *Streptomyces*, *Flavobacterium*, *Rhizobium*, and *Sphingomonas*, which were present in most samples in all variants. In the control variant, the total relative abundance of these genera was 41.2%: *Pseudomonas* – 12.3%, *Bacillus* – 8.1%, *Streptomyces* – 6.2%, *Flavobacterium* – 4.0%, *Rhizobium* – 3.5%, *Sphingomonas* – 2.9%. In variant M1, there was an increase in the proportion of *Pseudomonas* to 14.5% and *Bacillus* to 9.8%, while the proportion of *Streptomyces* remained at 6.5%. The total contribution of these genera to the microbiome structure reached 44.9%, reflecting the increased representation of the PGPR component compared to the control. In variant M2, the growth was mainly concerned Actinobacteriota: the proportion of *Streptomyces* increased to 7.1%, while *Pseudomonas* and *Bacillus* remained at 13.0% and 8.5%, respectively. In variant M3, an increase in the relative abundance of *Flavobacterium* to 5.2% and *Rhizobium* to 4.3% was combined with an increase in the proportion of *Pseudomonas* to 15.0%, reflecting an increase in the participation of both PGPR and nitrogen-fixing components in the microbiome structure. In the combined treatment option M1+M2, the largest total contribution was recorded for the genera *Pseudomonas*, *Bacillus* and *Streptomyces*, which amounted to 30.8% (15.7%, 9.9% and 5.2%, respectively). In addition, this variant showed increased relative abundance of *Rhizobium* (4.0%) and *Sphingomonas* (3.0%). The total share of core genera in the M1+M2 variant reached 47.8%, which exceeded the control values (Fig. 2). A.C.F. Dias *et al.* (2013) emphasised that genetically modified potatoes contribute to changes in the composition of the rhizosphere microbiome compared to traditional varieties, which is also reflected in this study. In the combined treatment M1+M2, the largest increase in the proportion of the genera *Pseudomonas*, *Bacillus*, and *Streptomyces* was observed, indicating changes in the composition of rhizosphere bacteria associated with plant growth and development.

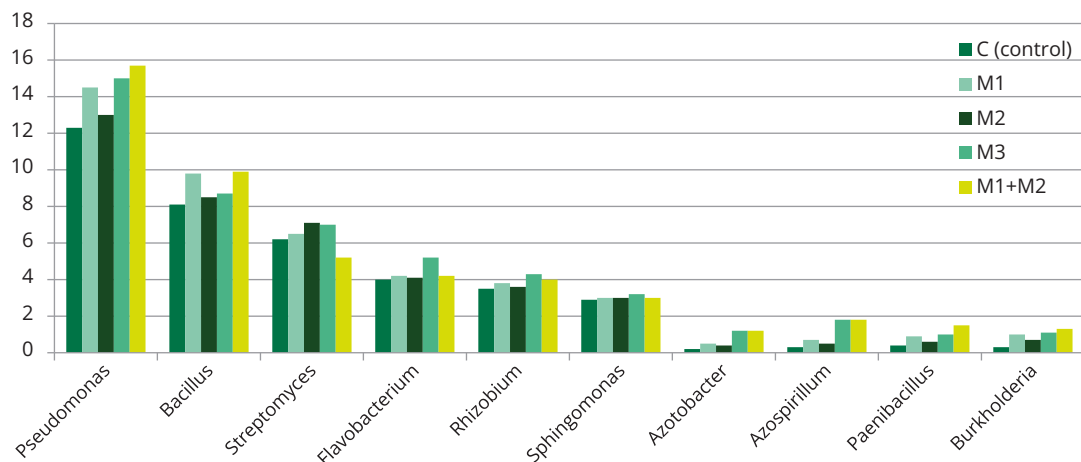


Figure 2. Relative abundance of key genera associated with potato growth, % of total bacterial community

Source: compiled by the authors based on research

A separate group consisted of genera that were absent or had a share of less than 0.5% in the control but reached noticeable values in the experimental variants. These included *Azotobacter*, *Azospirillum*, *Paenibacillus*, and *Burkholderia*. In variant M3, the proportion of *Azospirillum* reached 1.8% and *Azotobacter* 1.2%, while in the control, these genera were recorded at <0.5%. In variant M1+M2, the proportion of *Paenibacillus* was 1.5%, and *Burkholderia* was 1.3%, accompanied by an increase in the total proportion of nitrogen-fixing and phosphate-mobilising microorganisms. These changes indicated a reformatting of the functionally significant part of the microbial community due to the involvement of additional PGPR components and previously underrepresented taxa. A comparative analysis showed that under the conditions of treatment with microbial preparations, not only the ratio of dominant types changed, but also the structure of key families and genera associated with providing plants with nutrients and regulating growth processes. The increase in the proportion of *Pseudomonas*, *Bacillus*, *Streptomyces*, as well as the appearance or intensification of *Azotobacter*, *Azospirillum*, *Paenibacillus* and *Burkholderia* formed distinct taxonomic profiles of the experimental variants compared to the control and created prerequisites for further analysis of the functional potential of the potato rhizosphere metagenome. A. Boke (2024) also confirmed that the proportion

of microorganisms that can suppress pathogens, in particular the genera *Burkholderia* and *Azotobacter*, increases in the rhizosphere of potatoes, which was found in this study after the combined use of microbial preparations. The observed increase in the relative abundance of these genera in the M1+M2 variant indicates the positive effect of microbial preparations on the formation of a healthy microbial community, which can potentially improve plant resistance to diseases.

Changes in the functional potential of the metagenome of rhizosphere microorganisms

Functional annotation of metagenomic sequences revealed the presence of a wide range of genes involved in providing plants with mineral nutrients. In all variants, genes for nitrogen fixation (*nifH*, *nifD*, *nifK*), phosphorus mobilisation and transport (*phoD*, *pstS*, *pstA*), potassium transport (*kdpA*, *kdpB*) and sulphur assimilation (*cysD*, *cysN*, *cysK*) were identified. The total relative share of these functional categories was 6.8% of the total number of functionally annotated genes in the control and 8.1-10.4% in the variants with microbial preparations. In the M1+M2 variant, this indicator reached 10.4%, which was the maximum value among all variants. Figure 3 shows the contribution of individual functional categories to this total indicator (the proportion of each category separately).

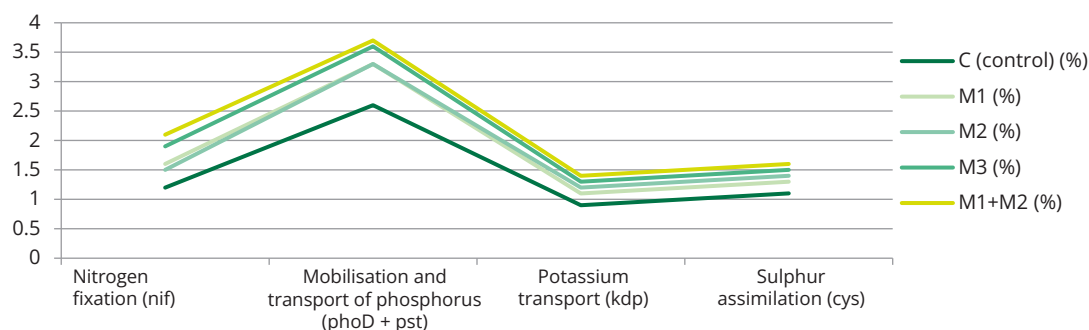


Figure 3. Relative proportion of individual functional categories of genes associated with plant nutrition, % of the total number of functionally annotated genes

Note: each column reflects the contribution of a separate category; the 0-4% scale is presented in percentages

Source: compiled by the authors based on research

Nitrogen fixation genes (nif complex) in the control variant accounted for 1.2% of the total number of functional annotations, while in variants M1, M2 and M3 their share was 1.6, 1.5 and 1.9%, respectively. In variant M1+M2, the relative proportion of nif genes reached 2.1%. The number of nifH annotations per 10^7 genera was 310 in the control, 410-430 in variants M1 and M2, 480 in variant M3, and 520 in variant M1+M2. This reflected an increase in the potential for biological nitrogen fixation under conditions of microbial preparation application, especially in the combined variant. For phosphorus-binding and phosphate-mobilising genes, the proportion of phoD and other organic phosphorus markers in the control was 1.5%, while in variants M1, M2 and M3 it was 1.9, 1.8 and 2.0%, respectively, and in variant M1+M2 it was 2.2%. The relative number of genes of highly related phosphate transport systems (pstS, pstA) increased from 1.1% in the control to 1.4-1.6% in the variants with preparations, with a maximum of 1.6% in variant M3. For potassium transport systems (kdpA, kdpB), the proportion of corresponding genes in the control was 0.9%, in variants M1, M2, M3 – 1.1-1.3%, and in M1+M2 – 1.4%. The total proportion of genes associated with sulphur assimilation (cysD, cysN, cysK) ranged from 1.1% in the control to 1.5% in M3 and 1.6% in the M1+M2 variant. The results of functional annotation of the potato rhizosphere metagenome confirm the conclusions of T.T. Alawiyeh & O.O. Babalola (2021), noting that sunflower rhizosphere microbiomes contain various functional gene groups that provide plants with essential nutrients. The study observed an increase in

the relative number of genes involved in nitrogen fixation, phosphorus mobilisation, and potassium transport in variants with microbial preparations, indicating an expansion of the functional potential of the potato rhizosphere microbiome.

A comparison of the control and experimental variants showed that the use of microbial preparations was accompanied by an increase in the relative number of genes responsible for biological nitrogen fixation, mobilisation of mineral and organic phosphorus, and transport of potassium and sulphur. The highest values for most functional categories were recorded in variants M3 and M1+M2, which combined increased content of nif-, pho- and cys-genes. This reflected the expansion of the potential of rhizosphere microbial communities to provide plants with essential nutrients by changing the functional profile of the metagenome under the influence of microbial preparations.

Analysis of functional annotations related to stress resistance and phytoprotection revealed the presence of genes responsible for the synthesis of antibiotic-like compounds, siderophores, antioxidant enzymes, and systemic resistance inducers in the potato rhizosphere metagenome. In all variants, genes encoding enzymes for the biosynthesis of several non-specific polyketides and non-peptide polyketide synthases (NRPS/PKS-type clusters) were identified, as well as markers for the biosynthesis of phenazino-like compounds and lipopeptides. The total proportion of genes of potential phytoprotection was 4.5% of the total number of functional annotations in the control and 5.4-7.2% in variants with microbial preparations.

In the control variant, the proportion of genes associated with the biosynthesis of antibiotic-like compounds (in particular, individual NRPS/PKS clusters) was 1.8%, in variants M1, M2 and M3 – 2.2%, 2.1% and 2.6%, respectively, and in variant M1+M2 – 2.8%. For siderophore biosynthesis markers (including enterobactin and pyoverdinin-type systems), the proportion of

functional annotations increased from 1.2% in the control to 1.5-1.7% in variants M1 and M2 and to 1.9-2.0% in variants M3 and M1+M2. Antioxidant enzyme genes (catalase, superoxide dismutase, glutathione peroxidase) accounted for 1.1% in the control, while in the variants with microbial preparations, 1.3-1.6%, with maximum values in M3 and M1+M2 (1.6%) (Fig. 4).

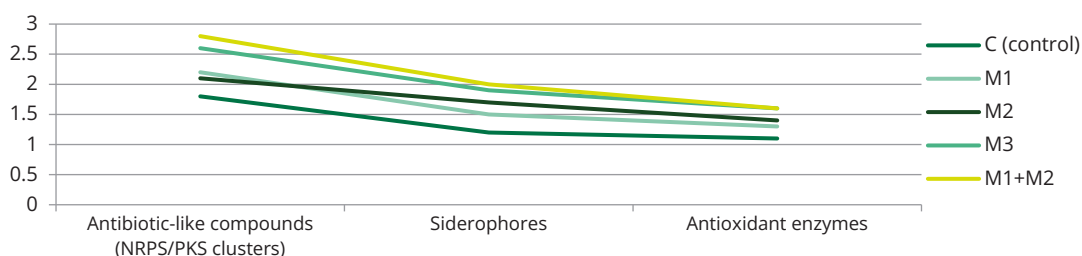


Figure 4. Relative abundance of functional groups of stress resistance and phytoprotection genes, % of the total number of functionally annotated genes

Source: compiled by the authors based on research

Genes associated with the induction of systemic resistance and regulation of plant stress responses were also identified, genes encoding 1-aminocyclopropane-1-carboxylate deaminase (*acdS*) activity and markers of the synthesis of compounds involved in the regulation of signaling pathways (in particular, phenolic metabolites). In the control, the relative proportion of such genes was 0.4%, while in variants M1, M3, and M1+M2, it was 0.6, 0.7, and 0.8%, respectively. In variant M2, the value remained at 0.5%, close to the control. Similar to R. Molefe *et al.* (2021), who found an increase in the proportion of functional genes in corn rhizosphere microbiomes after treatment, this study also noted an increase in functional genes associated with phytoprotection, in particular the biosynthesis of antibiotic-like compounds and siderophores. The largest increase in the proportion of these genes was recorded in variants M3 and M1+M2, indicating a shift in the functional profile of the microbiome in favour of components that help plants withstand biotic and abiotic stresses.

A comparison of functional markers of stress resistance between the variants showed that the use of microbial preparations caused an increase in the relative number of genes associated with the production of siderophores, antibiotic-like

compounds and antioxidant enzymes, as well as an increase in the representation of genes potentially involved in the induction of systemic plant resistance. The most pronounced increase in the total share of these functional categories was observed in variants M3 and M1+M2. Within the scope of this study, this configuration of the functional profile of the rhizosphere metagenome was interpreted as an increased potential of microbial communities to create conditions that reduce the risk of biotic and abiotic stresses for potato plants.

The relationship between structural and functional changes in the microbiome and potato growth and productivity

A comparison of morphological and productive indicators showed that the variants with microbial preparations differed from the control both in terms of plant growth parameters and tuber yield structure (Table 3). The control variant recorded the lowest values for plant height (48.2 cm), tuber weight per plant (420 g) and number of tubers (7.8), as well as an increased proportion of small tubers (28.5%) with a relatively low proportion of large tubers (20.2%), which corresponds to the typical background without inoculation. In variant M1 (*Azotobacter* spp.), the indicators increased to 51.0 cm, 455 g, and 8.4 pcs., and the

proportion of small tubers decreased to 24.7% with an increase in large tubers to 21.5%, which is consistent with the effect of improved nitrogen supply and growth stimulation. In variant M2 (*Bacillus* spp., *Pseudomonas* spp.), the values increased to 52.6 cm, 470 g and 8.7 pcs., and the fractional structure shifted towards medium/large (54.5% and 22.0%) with a decrease in small tubers to 23.5%, which may reflect increased phosphorus nutrition and tuber filling. In variant M3 (complex consortium), some of the highest indicators were observed: 54.3 cm, 495 g and 9.1 pcs., with a minimum proportion of small tubers of 18.5% and an increase in medium/large tubers to 57.5%

and 24.0%, which corresponds to the complex effect on nutrition and physiological stability of plants. In the combined M1+M2, the maximum values of height (55.1 cm), weight (510 g) and number of tubers (9.3 pcs.) were combined with the highest proportion of large fraction (25.1%) at 23.4% small, which is consistent with the complementarity of nitrogen and phosphorus supply. In general, in the variants with the preparations, the weight of tubers per plant increased from 420 g (control) to 455-510 g, and the number of tubers increased from 7.8 to 8.4-9.3 pieces, with a tendency to increase the proportion of large tubers to 21.5-25.1% compared to 20.2% in the control.

Table 3. Morphological and productive indicators of potatoes by variants

Variant	Plant height, cm (mean ± SD)	Tuber weight per plant, g (mean ± SD)	Number of tubers, pcs/plant (mean ± SD)	Percentage of tubers by fraction, % (small/medium/large)
C (control)	48.2 ± 1.5	420 ± 25	7.8 ± 0.5	28.5 / 51.3 / 20.2
M1	51.0 ± 1.6	455 ± 27	8.4 ± 0.6	24.7 / 53.8 / 21.5
M2	52.6 ± 1.7	470 ± 28	8.7 ± 0.6	23.5 / 54.5 / 22.0
M3	54.3 ± 1.8	495 ± 30	9.1 ± 0.6	18.5 / 57.5 / 24.0
M1+M2	55.1 ± 1.8	510 ± 32	9.3 ± 0.6	23.4 / 51.5 / 25.1

Source: compiled by the authors based on research

Analysis of the relationship between α -diversity indices of the rhizosphere microbiome and potato yield characteristics revealed positive correlations between the Shannon index and tuber weight per plant ($r=0.62$) and the proportion of medium and large fractions ($r=0.58-0.65$). These correlations can be explained by an increase in the proportion of functionally significant PGPR groups (in particular, nitrogen-fixing and phytohormone-producing bacteria, phosphate-mobilising taxa, as well as phytopathogen antagonists such as *Bacillus* spp. and *Pseudomonas* spp.), which enhance mineral nutrition and reduce stress on plants. In parallel, the increase in α -diversity could be accompanied by an increase in predicted functional gene categories (KEGG/KO) associated with nitrogen and phosphorus nutrition (nitrogen fixation, phosphorus mobilisation/transport, ion transport) and stress resistance mechanisms (synthesis of siderophores, antibiotic-like metabolites, antioxidant enzymes, induction of systemic resistance). Collectively, these factors could increase the availability of nutrients and stabilise the physiological state of plants during vegetation, which was manifested by an

increase in tuber weight and an increase in the proportion of medium and large fractions. In variants with higher Shannon and Simpson indices (M3, M1+M2), higher average tuber weight and number of tubers per plant were also recorded. For the Chao1 index, a moderate correlation was found between the number of tubers ($r=0.54$), reflecting the contribution of taxon richness to productivity. At the same time, no excessive variability in α -diversity was observed between variants, and the influence of intragroup diversity was manifested mainly through a combination of richness and evenness of the community. A comparison of β -diversity between variants, incorporating their productive characteristics, showed that the variants most distant from the control in terms of microbiome structure (M3, M1+M2) corresponded to variants with higher tuber weight and a greater contribution of medium and large fractions to the yield structure. A correlation ($r=0.59$) was established for the average pairwise distance between the microbiome profiles and yield indicators, which indicated an association between the structural reorganisation of the rhizosphere community and an increase in

productive characteristics. Variants K and M2, which formed a common cluster on the ordination diagram, had similar values of yield and distribution of tubers by fractions.

A comparison of the relative abundance of key functional groups of microorganisms with the agrobiological characteristics of plants showed that an increase in the proportion of the genera *Pseudomonas*, *Bacillus*, *Rhizobium*, *Azotobacter*, *Azospirillum*, *Paenibacillus* and *Burkholderia* was associated with an increase in tuber weight per

plant ($r = 0.60$ - 0.72 for the total proportion of PGPR genera) and a decrease in the proportion of small-sized tubers ($r = -0.55$). For the total proportion of nitrogen-fixing genes (*nif*) and genes associated with phosphorus mobilisation (*phoD* + *pst*), correlations with tuber weight were recorded ($r = 0.63$ and $r = 0.66$, respectively), while the proportion of potassium transport genes (*kdp*) and sulphur assimilation genes (*cys*) correlated mainly with tuber number and the proportion of the medium fraction ($r = 0.48$ - 0.57) (Fig. 5).



Figure 5. Correlation coefficients between microbiome indicators and potato yield

Source: compiled by the authors based on research

In the group of stress resistance and phyto-protection genes, the total relative proportion of markers for the biosynthesis of antibiotic-like compounds, siderophores, and antioxidant enzymes showed positive correlations with plant height ($r = 0.51$), tuber weight ($r = 0.58$) and the proportion of medium and large fractions ($r = 0.55$ - 0.61). The relative number of genes associated with the induction of systemic resistance (including *acdS*) correlated with the number of tubers per plant ($r = 0.49$) and the proportion of the large fraction ($r = 0.52$). This reflected the participation of functional components of the metagenome not only in providing nutrients, but also in creating conditions conducive to stable growth under the influence of potential stress factors. The results of the study of the functional potential of the potato rhizosphere metagenome

are consistent with the conclusions of T. Zhao *et al.* (2024), noting that the interaction between the microbiome and the potato plant contributes to increased yield by improving plant nutrition and stress resistance. In this study, an increase in the proportion of genes responsible for biological nitrogen fixation and phosphorus, potassium and sulphur mobilisation was observed in variants with microbial preparations, which probably contributed to improved potato growth and productivity. M. Hemkemeyer *et al.* (2024) also emphasised the importance of the microbiome for improving the quality and quantity of potato yields, which is confirmed by the results of this study, where variants with microbial preparations, in particular M1+M2, showed a significant increase in tuber weight and the proportion of large fractions. According to the conclusions,



changes in the composition of the microbiome may be associated with better adaptation of plants to different agronomic conditions, which is reflected in the changes in the structure of the microbiome found in this study. A summary of the results showed that variants M3 and M1+M2 were characterised by a combination of increased α -diversity, pronounced structural differentiation of the microbiome relative to the control, an increased proportion of PGPR genera and functional genes associated with nutrition and stress resistance, with increased potato growth and productivity. Within the study, these variants were considered as configurations in which an optimal combination of parameters, “metagenome structure – functional potential – productivity”, was formed, reflecting the consistency of taxonomic and functional changes in the rhizosphere microbiome with the agrobiological response of plants.

Analysis of the taxonomic structure of the rhizosphere metagenome identified a group of taxa consistently associated with the action of individual microbial preparations. For variant M1, a systematic increase in the proportion of the genera *Pseudomonas* and *Bacillus* was recorded, for variant M2 – an increased relative abundance of *Streptomyces*, and for variant M3 – a combination of an increased proportion of *Flavobacterium* and *Rhizobium*. In variant M1+M2, a complex of bioindicator genera was formed, which, in addition to *Pseudomonas* and *Bacillus*, included *Paenibacillus* and *Burkholderia*. *Azotobacter* and *Azospirillum* were found to be markers mainly for variant M3. The combination of these taxa formed characteristic “signatures” of the microbiome, according to which rhizosphere samples could be assigned to the corresponding treatment variant. At the level of functional potential, specific groups of genes characteristic of individual variants were identified. For M3, the maximum representation of *nif* genes and siderophore clusters was recorded, which was consistent with the increased proportion of *Rhizobium*, *Azotobacter* and *Azospirillum*. Variant M1 was characterised by enrichment of the metagenome with phosphorus mobilisation genes (*phoD*, *pst*) and individual NRPS/PKS clusters, while M2 was characterised by an increase in genes involved in the metabolism of organic forms of sulphur and actinobacterial clusters of secondary metabolism. The most comprehensive

set of functional biomarkers was characteristic of the M1+M2 variant, where the total proportion of nitrogen fixation genes, phosphate mobilisation, potassium and sulphur metabolism, as well as genes associated with the biosynthesis of antibiotic-like compounds, siderophores, antioxidant enzymes and the induction of systemic resistance. The results of the functional analysis of the potato rhizosphere metagenome are consistent with the study by E. Chica *et al.* (2019), which showed that the presence of specific taxa, such as *Pseudomonas* and *Bacillus*, is associated with improved plant growth and health. In the presented study, these genera also showed an increased proportion in variants with microbial preparations, confirming their role in improving the functional potential of the potato rhizosphere microbiome. A study by X. Zhao *et al.* (2021) highlighted the importance of integrated metagenome and metabolomics analysis for identifying microbes with high biotechnological potential. Similar to their findings, this study recorded the maximum growth of functional genes associated with nitrogen fixation, phosphate mobilisation, and antibiotic-like compound synthesis in variants M3 and M1+M2, which contributed to improved agronomic characteristics of potatoes.

To summarise the data, an integral indicator of the biotechnological potential of the rhizosphere metagenome was formed, combining the structural parameters of the microbiome (α - and β -diversity, the proportion of dominant and PGPR genera), functional markers (nutrition and stress resistance genes) and indicators of potato growth and productivity. The value of the integral index was 0.48 for the control, 0.61 and 0.64 for M1 and M2, 0.72 for M3 and 0.75 for the combined variant M1+M2. Thus, all variants with microbial preparations exceeded the control in terms of a set of structural, functional and agronomic characteristics, with M3 and M1+M2 occupying the highest positions in the ranking. In terms of biotechnology, PGPR genera *Pseudomonas*, *Bacillus*, *Rhizobium*, *Paenibacillus*, *Burkholderia*, *Azotobacter* and *Azospirillum*, consistent with an increased content of genes for nitrogen fixation, phosphate mobilisation, siderophore synthesis and antibiotic-like compounds, were considered key biomarkers suitable for the selection of promising microbial consortia. An integrated assessment confirmed that



variants M3 and M1+M2 provided the optimal combination of a favourable metagenome structure, high functional potential, and increased potato productivity, which identified them as the most promising schemes for the application of microbial preparations under the conditions of the experiment.

CONCLUSIONS

The study determined that the use of microbial preparations was accompanied by modification of the potato rhizosphere metagenome at the taxonomic and functional levels and was associated with increased growth and productivity indicators. At a comparable sequencing depth, 11.8 million sequencing reads (after basic quality filtering) were obtained in all variants, and 2,950 taxonomic units (OTUs/ASVs) were identified. In the variants with preparations, an increase in α -diversity was recorded: the Shannon index increased from 4.82 in the control to 5.05-5.18, and Chao1 – from 830 to 940-975, which reflected the enrichment of the microbiome mainly due to rare OTUs/ASVs. Analysis of intergroup diversity showed the separation of some variants from the control profile and a restructuring of community structure. The taxonomic profile shifted towards the enrichment of PGPR genera (*Bacillus*, *Pseudomonas*, *Azotobacter*, *Rhizobium*/*Azospirillum*) and the strengthening of the role of taxa that were underrepresented in the control. The probable mechanisms were phytohormone-like metabolites, bioavailability of N and P, and local suppression of phytopathogens through siderophores.

At the functional level, the total share of gene categories associated with plant nutrition increased from 6.8% in the control to 8.1-10.4% in the variants with preparations; the maximum was recorded in M1+M2 (10.4%). At the same time,

categories related to stress resistance (siderophores, antibiotic-like metabolites, antioxidant enzymes, resistance induction) increased. The most pronounced agronomic effects were observed in M3 and M1+M2: plant height increased from 48.2 ± 1.5 cm in the control to 54.3 ± 1.8 cm and 55.1 ± 1.8 cm; tuber weight increased from 420 ± 25 g to 495 ± 30 g and 510 ± 32 g; the number of tubers increased from 7.8 ± 0.5 to 9.1 ± 0.6 and 9.3 ± 0.6 pcs. The proportion of the large fraction increased from 20.2% in the control to 24.0% (M3) and 25.1% (M1+M2), while the small fraction decreased to 18.5% in M3. Correlation analysis confirmed the association between microbiome diversity and productivity: the Shannon index correlated positively with tuber weight ($r = 0.62$) and the proportion of medium and large fractions ($r = 0.58-0.65$), and correlations for the total proportion of beneficial microorganisms and functional genes with yield indicators reached $r \approx 0.6-0.7$. The integral indicator of biotechnological potential increased from 0.48 in the control to 0.61-0.75 in the variants with preparations, with a maximum in M3 and M1+M2. The limitation was that the experiment was conducted within a single agroecological context without long-term observation and without incorporating the transcriptomic level. Further research should address long-term and multi-location trials and testing of selected consortia in production crops.

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CONFLICT OF INTEREST

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Біотехнологічні аспекти формування метагеному ризосферних мікроорганізмів картоплі під дією мікробних препаратів

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Анотація. Метою дослідження було оцінити вплив мікробних препаратів на структурно-функціональні характеристики ризосферного метагеному картоплі та пов'язані з цим зміни росту і продуктивності рослин. У межах вегетаційного досліду було отримано повногеномні метагеномні профілі ризосфери картоплі за п'яти варіантів: без обробки, три окремі мікробні препарати та їхня комбінація. Було отримано 11,8 млн секвенувальних родів, що пройшли базову якісну фільтрацію; ідентифіковано 2 950 таксономічних одиниць, виконано таксономічну й функціональну анотацію, розраховано показники різноманіття та проведено кореляційний аналіз із морфологічними й врожайними показниками. Встановлено, що у всіх варіантах домінували представники типів Proteobacteria, Actinobacteriota, Bacteroidota та Firmicutes, сумарна частка яких перевищувала 80 % структури метагеному, тоді як застосування мікробних препаратів супроводжувалося підвищенням видового багатства і різноманіття: індекс Шеннона зростав з 4,82 у контролі до 5,12-5,18 у дослідних варіантах, а оцінка багатства за Chao1 – з 830 до 960-975 таксонів. Було виявлено зростання частки родів, асоційованих із ростом рослин, а також відносної кількості генів, пов'язаних з азотфіксацією, мобілізацією фосфору, транспортуванням калію, засвоєнням сірки та ознаками стресостійкості, з максимальними значеннями у варіантах з третім препаратом і його комбінацією з першим. Ці варіанти забезпечували підвищення маси бульб з рослини до 495-510 г і збільшення частки середньої та крупної фракцій врожаю, причому коефіцієнти кореляції між сумарною часткою корисних мікроорганізмів, функціональними генами і продуктивністю досягали 0,6-0,7. Отримані результати засвідчили, що цілеспрямована мікробна обробка здатна формувати ризосферний метагеном із підвищеним біотехнологічним потенціалом і може бути використана агрономами-практиками, розробниками мікробних препаратів, селекціонерами картоплі та фахівцями з інтегрованого управління родючістю ґрунтів для оптимізації мікробних консорціумів у технологіях вирощування картоплі

Ключові слова: варіант; кількість; тип; рід; азотфіксація; фосфор

