SOIL BIOGENICITY IN THE RHIZOSPHERE OF DIFFERENT WHEAT GENOTYPES UNDER THE IMPACT OF FERTILIZATION TREATMENT

Svetlana M. Roljević Nikolić[1*], Željko K. Dolijanović[2], Dušan Đ. Kovačević[2], Snežana I. Oljača[2] and Helena J. Majstorović[1]

[1]Research and Development Institute Tamiš,
Novoseljanski put 33, Pančevo, Serbia
[2]University of Belgrade, Faculty of Agriculture,
Nemanjina 6, Belgrade, Serbia

Abstract: The rhizosphere is a dynamic environment in which many parameters may influence biogenicity. The important factors determining the microbial community in the rhizosphere are plant and soil nutrient supply. The aim of this paper was to determine the abundance of basic microbiological groups in the rhizosphere of four wheat subspecies, in three fertilization treatments in the organic farming system. A field experiment was conducted using a randomized complete block design with four replicates. It was carried out on the leached chernozem soil type. There was significant variability in the abundance of the studied physiological groups of microorganisms between the wheat subspecies, as well as between the fertilization treatments. The rhizosphere of common wheat had the greatest abundance of fungi (24.37×10^3 g^{-1}). The rhizosphere of compactum wheat had the largest abundance of oligonitrophilic bacteria (361.47×10^5 g^{-1}) and amonificators (119.27×10^5 g^{-1}). There were no significant differences in the abundance of actinomycetes between the cultivars of common, compactum and durum wheat, but their lowest number was found in the spelt wheat cultivar (11.25×10^3 g^{-1}). The combined application of biofertilizer and organic fertilizer resulted in a significantly greater abundance of amonificators (56.6%), fungi (28.2%) and oligonitrophiles (14.6%) than in the control treatment. The results show that the crop variety and application of appropriate fertilizer formulations can influence the abundance of the studied groups of microorganisms. This is particularly the case in organic farming, which relies completely on natural resources and processes.

Key words: wheat, organic farming, biohumus, biofertilizer, fungi, actinomycetes, amonificators, oligonitrophiles.

---

[*]Corresponding author: e-mail: roljevic@institut-tamis.rs

Introduction

Intensive farming causes soil degradation (Purwanto and Alam, 2020), excessive water consumption (Pfister et al., 2011), and greenhouse gas emissions (Shakoor et al., 2021), failing to provide the necessary sustainability of food production. The concern for natural resources, high costs and a decrease in oil and gas reserves used in the Haber-Bosch process that produces nitrogen fertilizers industrially has brought some essential changes in agricultural practices based on sustainable management (Singh et al., 2011). Consequently, over the last decades, studies in the field of agriculture have been directed at the development and application of alternative solutions that can potentially provide satisfactory yields without negative consequences on the environment (Ye et al., 2020). Therefore, it is very important to examine the rhizosphere microbial communities and their impact on crop productivity and ecological implications of their application in agriculture (Gqozo et al., 2020; Karličić et al., 2016). Previous researches have shown that the application of microorganisms in crop production increases the accessibility and efficiency of nutritive matter, which decreases the requirements for mineral fertilization by 50% while not lowering the plant yield (Hayat et al., 2010; da Costa et al., 2013).

The rhizosphere community consists of different types of microbes which have beneficial effects on the plant growth and development, including the ones which are capable of atmospheric nitrogen intake, fungi, protozoa and rhizomicrobes promoting plant growth and conducting biocontrol (Zhao et al., 2018). The presence of fungi in soil provides numerous services to crops including improved soil physical properties, mineralization of organic matter and synthesis of humus, efficient use of fertilizer and soil nutrients, protection against drought stress and diseases (Singh et al., 2012). On the other side, actinomycetes perform not only a decomposition of organic matter in the soil, but also perform nitrogen fixation (15% of total fixation) and phosphate solubilization (AbdElgawad et al., 2020). They produce various antibiotics (chloramphenicol, neomycin, streptomycin), biologically active matter such as B vitamins, auxines and others (Jarak et al., 2006). Studies on wheat and rice have shown that reduction of N fertilizer by 20% and replacement of 50% of N fertilizer by organic manure increased the number of actinomycetes by 11–153%, without significantly reducing crop yields (Guan et al., 2011).

The free-living diazotrophic bacteria are known to affect, directly or indirectly, plant growth. This occurs as a result of the synthesis and export of organic compounds such as phytohormones (e.g., indole-3-acetic acid) that enhance root growth and through a contribution of biological nitrogen fixation to nitrogen acquisition by the plant (Venieraki et al., 2011). Oligonitrophilic bacteria represent a specific group of microorganisms capable of reducing the molecular

form of nitrogen from the atmosphere and converting it into the organic ammonia form, using very small quantities of mineral nitrogen content from soil (Rasulić et al., 2021).

Specific characteristics of a microbial community are affected by physical and chemical soil properties, grown plant species, fertilizer use and other agrotechnical measures (Sivojiene et al., 2021). Organic matter is a vital component of soil quality and fertility. At the same time, it represents the main substrate and energy source for microorganisms (Xu et al., 2013), as well as the limiting factor for the abundance and diversity of the microbial population (Fließbach et al., 2007). It has been determined that the increase in the organic matter content leads to the increase in the weight and diversity of heterotrophic microorganisms (Ding et al., 2016), which consequently results in greater soil respiration (Araújo et al., 2009). Numerous examinations have shown that the application of organic fertilizers improves physical and chemical properties of the rhizosphere soil (Bibhuti and Dkhar, 2011), and consequently increases the biomass and activity of microorganisms (Chang et al., 2007; Mohammadi, 2011).

The plant genotype also has a significant impact on the microbial community in the rhizosphere (Compant et al., 2019). Namely, different plant species have a specific relationship and interaction with microorganisms promoting the plant growth and development, as well as their resistance to stress and diseases (Wei and Jousset, 2017). The examination of the bacterial rhizosphere of *Triticum monococcum* PI 167549, *T. aestivum* cv. CDC Teal and T. *aestivum* cv. Red Fife has shown that *Aureobacter* species differed significantly between cultivars (Germida and Siciliano, 2001). Similarly, significant differences between spelt cultivars were found in the total number of rhizosphere fungi (Korniłłowicz-Kowalska et al., 2022).

In the literature, scanty information is available on the influence of host genotype on the number of different physiological groups of microorganisms in the rhizosphere, so the aim of this research is to study the soil rhizosphere biogenicity of different wheat genotypes under the influence of fertilization treatments.

Material and Methods

The examination of soil biogenicity regarding the abundance of different physiological groups of microorganisms in the rhizosphere of four wheat subspecies, under the influence of fertilization in organic farming, was conducted at the experimental field of the Faculty of Agriculture, Radmilovac. The soil type was a luvic chernozem, with the characteristics: pH-(H_2O) 8.04, total N 0.13%, available K 19.10 mg (K_2O 100 g^{-1}) and P 22.18 mg (P_2O_5 100 g^{-1}), content of SOC 14.2%. According to the content of basic mechanical fractions (sand, silt, clay), the study site belongs to silty clay loam soil (Dolijanović, 2002). The field experiment

was conducted using a randomized complete block design with four replicates in the period 2009–2012. The elementary plot was 6 m².

Figure 1 shows the average monthly temperatures and the amount of precipitation in the long-term period, as well as during the experiment. The average amount of precipitation in the long-term period (1970–2008) amounted to 698.3 mm, while the average monthly air temperature was 12.3°C. However, during the three-year examination period (2009–2012), there were certain deviations from the long-term average values. The average annual amount of precipitation was slightly lower (by 14.9 mm), while the average annual air temperature was greater by 1.2°C in comparison to the long-term average values. The lower amount of precipitation was recorded in April (32.7 mm), August (29.1 mm) and September (33.5 mm), while abundant precipitation was registered in the winter months (December, January and February). Contrary to the tendency of the precipitation regime change, lower average air temperatures were recorded in January (1.0°C) and February (1.2°C), while higher air temperatures were recorded in August (24.8°C) and September (20.6°C), as well as in November (9.3°C) in comparison to the long-term average values.
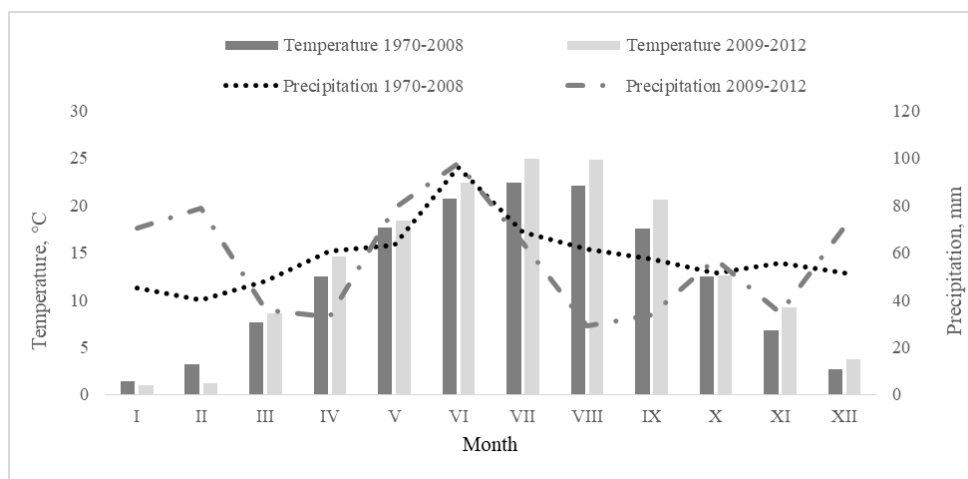

Figure 1. The average monthly mean air temperature (°C) and
the precipitation sum (mm).
Source: RHMS of Serbia

In all three years, the previous crop to wheat was maize (*Zea mays* L.). After the maize harvest, conservation tillage of soil at the depth of 25 cm was performed and the organic fertilizer was plowed in. Presowing preparation was performed using a disc harrow and a spike-tooth harrow. Sowing was done manually at the end of the second decade of October. The original seed from the Institute of Field and Vegetable Crops in Novi Sad was used.

In order to study the abundance of basic microbiological groups in the rhizosphere of different wheat genotypes, three cultivars of alternative wheat subspecies were included in the research (*Triticum aestivum* ssp. *spelta* – cv. Nirvana, *Triticum durum* – cv. Dolap, *Triticim aestivum* ssp. *compactum* – cv. Bambi) and one cultivar of common soft wheat (*Triticum aestivum* ssp. *vulgare* – cv. NS 40S). The seed densities were: NS 40S – 550; Dolap – 600; Bambi – 600; Nirvana – 550 germinating seeds per m^2.

The fertilization treatment involved: T0 – control, without fertilization, T1 – microbiological fertilizer "Slavol"(5.0 l ha^{-1}), T2 – biohumus (3,000 kg ha^{-1}) + microbiological fertilizer "Slavol" (5.0 l ha^{-1}). "Slavol" ("Agrounik" Serbia) is a liquid foliar microbiological fertilizer containing: *Bacillus megaterium* 10^{-6} cm^3, *Bacillus licheniformis* 10^{-6} cm^3, *Bacillus subtilis* 10^{-6} cm^3, *Azotobacter chroococcum* 10^{-6} cm^3, *Azotobacter vinelandii* 10^{-6} cm^3, *Derxia* sp. 10^{-6} cm^3. It was applied during the BBCH 31-33 phenophase.

Biohumus ("Biohumus Royal offert", "Altamed" Serbia) is an organic fertilizer, certified for use in organic farming, and plowed in during the autumn within the primary tillage. The chemical properties of biohumus are as follows: pH 8.63, N 2.2%; P_2O_5 4.8% and K_2O 2.8%.

In all three years, the soil samples for microbiological analyses were taken aseptically at a 0–10 cm depth, in the zone of 0.5 cm from wheat root (Đurić and Jarak, 2006). Soil samples were stored in sterile polyethylene bags. The soil samples were taken at the end of the BBCH 33 phase of wheat, in four replications.

The number of microorganisms was calculated in 1 gram of absolutely dry soil. The number of fungi was determined on the Czapek-Dox medium, and actinomycetes on a synthetic medium by Krasilnikov (1965). The presence of oligonitrophyls was determined on a medium without nitrogen by Fjodorov (Sarić, 1989), and the number of amonificators on the meat peptone agar (Pochon and Tardieux, 1962). The sown media were incubated at the temperature of $28^{o}C$. The incubation depended on the microorganism group and lasted from 3 to 7 days.

The obtained results of the research on the abundance of different physiological groups of microorganisms were analyzed using the analysis of variance (ANOVA) procedure of the Statistical Analysis Software (SPSS software, 19.0). The comparisons among different treatments were made with the least significant difference (LSD) test, at the significance levels of $p<0.01$ and $p<0.05$.

Results and Discussion

Table 1 shows the research results regarding the abundance of physiological groups of microorganisms in the rhizosphere of different wheat subspecies under the influence of fertilization treatments. The analysis of variance shows that the

genotype, treatments, as well as the interaction of these two factors, had a significant impact on the abundance of fungi in the rhizosphere. The greatest number of fungi was recorded in the rhizosphere zone of common wheat (24.37 x 10^3 g^{-1}), which was significantly higher than in spelt (22.25x 10^3 g^{-1}), durum (20.08 x 10^3 g^{-1}) and compactum (20.60 x 10^3 g^{-1}) wheats. The variant with the combined application of organic fertilizer and biofertilizer (26.63 x 10^3 g^{-1}) had a significantly higher number of fungi than the variant with the application of biofertilizers (20.07 x 10^3 g^{-1}) and control (20.78 x 10^3 g^{-1}). The analysis of the interaction between the studied factors, i.e., the analysis of differences in the mean values between treatments, shows that the combined application of fertilizers provided the best results in the spelt wheat cultivar (51.10%).

The greatest difference in the abundance of actinomycetes was determined between durum (21.49 x 10^3g^{-1}) and spelt (11.25 x 10^3g^{-1}) wheats. Although the examined treatments did not have a significant influence on this group of microorganisms, there was an increase at the levels of 30.89% and 16.30% in T1 and T2 in comparison to the control. In addition, there were certain differences between the cultivars regarding their reaction to the applied fertilizers. The greatest differences between T1 and T2 treatments in comparison to the control were registered in the compactum wheat cultivar (90.1% and 58.6%, respectively), while the smallest differences were observed in the durum wheat cultivar (6.8% and 3.1%, respectively).

The number of microorganisms-amonificators was found in the rhizosphere of compactum wheat (119.27 x 10^5g^{-1}) and it was higher compared to the other wheat subspecies. The abundance of amonificators recorded in the treatment with the combined application of organic fertilizer and biofertilizer was higher by 56.6%, while their abundance in the variant with the independent application of biofertilizer was higher by 39.2% than in the control. In all studied wheat subspecies, there was a greater number (p < 0.01) of amonificators in the variants with the applied fertilizers than in the control. The obtained differences were the biggest in spelt wheat – 65.7% and 111.6% in T1 and T2 in comparison to the control.

Within the studied microbial community, oligonitrophiles represent the most abundant group with significant ($p<0.01$) differences between the studied cultivars. The abundance of this group of saprophytes ranged from 229.84 to 361.47 x 10^5g^{-1} in durum and compactum wheat, respectively. The effect of treatment was also significant. Treatment with a combined application of organic fertilizer and biofertilizer (321.21 x 10^5g^{-1}) resulted in an increase in the number of oligonitrophiles by 14.6% compared to the control. The analysis of the differences between the treatments indicates that the fertilizer application in the spelt wheat cultivar increased the number of oligonitrophiles by 22.6% in T1 and by 37.7% in T2, which is significantly more than in other cultivars.

Table 1. The average abundance of the physiological groups of microorganisms in the rhizosphere of different wheat subspecies in the three-year period (2009/2010–2011/2012).

Wheat subspecies/cultivars	T0	T1	T2	Average
Fungi 10^3 g^{-1}				
T. aestivum ssp. *vulgare* – NS 40S	20.40±10.9	23.65±18.7	29.07±21.3	24.37
Triticum durum – Dolap	20.48±11.3	19.27±10.5	20.50±10.9	20.08
T. aestivum ssp. *compactum* – Bambi	24.05±15.7	16.30±9.7	21.45±15.3	20.60
Triticum spelta – Nirvana	18.20±9.4	21.05±13.1	27.50±23.5	22.25
Average	20.78	20.07	26.63	
Actinomycetes 10^3 g^{-1}				
T. aestivum ssp. *vulgare* – NS 40S	15.80±3.2	18.10±4.5	19.75±4.7	17.88
Triticum durum – Dolap	20.80±5.85	22.22±9.73	21.45±9.33	21.49
T. aestivum ssp. *compactum* – Bambi	13.73±3.6	26.10±11.7	21.78±7.6	20.54
Triticum spelta – Nirvana	11.15±2.1	14.05±5.3	8.54±1.84	11.25
Average	15.37	20.12	17.88	
Amonificators 10^5 g^{-1}				
T. aestivum ssp. *vulgare* – NS 40S	92.90±37.3	125.70±53.9	129.60±67.5	116.07
Triticum durum – Dolap	75.40±25.1	91.40±36.7	92.30±38.9	86.37
T. aestivum ssp. *compactum* – Bambi	85.00±30.0	123.20±53.6	149.60±77.0	119.27
Triticum spelta – Nirvana	45.80±26.9	75.90±27.0	96.90±41.7	72.87
Average	74.78	104.05	117.10	
Oligonitrophilic bacteria 10^5 g^{-1}				
T. aestivum ssp. *vulgare* – NS 40S	310.50±81.6	230.82±63.5	230.22±60.6	257.18
Triticum durum – Dolap	219.60±53.7	183.87±49.3	286.05±75.7	229.84
T. aestivum ssp. *compactum* – Bambi	317.35±85.3	375.60±93.7	391.45±103.3	361.47
Triticum spelta – Nirvana	273.85±71.8	335.80±88.2	377.10±96.6	328.92
Average	280.33	281.52	321.21	

*All measurements are the means of three years of testing (± standard deviation) of four replicates.

Microorganisms represent the most numerous component of the soil biological phase, which has a direct impact on the agroecosystem stability (Le Guillou et al., 2019). The research results show that the wheat genotypes significantly affected the biogenicity of the rhizosphere. The similar results were recorded in other crops. The discriminant analysis clearly differentiated rhizosphere microbial communities in relation to the maize genotype (Aira et al., 2010), while in barley, it determined a small but significant host genotype effect on the diversity of root-associated bacterial communities (Bulgarelli et al., 2015). The greatest abundance of fungi was registered in the rhizosphere of the common wheat (NS 40S). Some studies dealt with the diversity of fungal communities in the rhizosphere of the roots in common wheat and spelt (Salamon et al., 2020), but studies of the abundance of fungi in the rhizosphere of different wheat subspecies are very limited. The analysis of the differences between the treatments showed that, in the treatment with the combined application of biohumus and biofertilizer (T2), the abundance of

fungi was greater by 18.5% than in the control. Similarly, Zhu et al. (2020) found that the soil treated with organic fertilizer had a larger number of fungi than the soil where no fertilizer was applied, which could be explained by the balanced content of nutritive matter, primarily organic carbon, nitrogen and potassium (Kumar et al., 2017; Zhu et al., 2020). The differences in the mean values between the treatments showed that the fertilizer application did not significantly increase the abundance of fungi in the rhizosphere of durum wheat and compactum wheat, while the obtained differences were significant for the cultivars of common wheat and spelt wheat. Therefore, understanding the dynamics of the abundance of the fungal population in the rhizosphere represents the first step towards the successful management of the microbial community with the aim of production and yield sustainability (Bever et al., 2012).

Table 2. The analysis of variance of the abundance of the examined physiological groups of microorganisms.

Microorganisms			2009/10 – 2011/12		
			G	T	G*T
Fungi		F	11.747	30.571	12.208
		Sig.	0.000	0.000	0.000
	LSD	0.05	1.386	1.201	2.401
		0.01	1.901	1.646	3.293
Actinomycetes		F	5.434	1.914	0.816
		Sig.	0.005	0.169	0.568
	LSD	0.05	5.098	4.415	8.830
		0.01	6.992	6.055	12.110
Amonificators		F	764.065	929.104	54.906
		Sig.	0.000	0.000	0.000
	LSD	0.05	2.111	1.828	3.656
		0.01	2.895	2.507	5.014
Oligonitrophiles		F	4502.743	867.018	918.446
		Sig.	0.000	0.000	0.000
	LSD	0.05	2.346	2.032	4.064
		0.01	3.218	2.787	5.574

G – genotype, T – treatment.

The genotype represented the key source of the variable abundance of actinomycetes. The greatest number of actinomycetes was found in the rhizosphere of durum wheat ($21.49 \times 10^3 g^{-1}$), followed by compactum wheat ($20.54 \times 10^3 g^{-1}$) and common wheat ($17.88 \times 10^3 g^{-1}$), while their smallest number was recorded in spelt wheat ($11.25 \times 10^3 g^{-1}$). However, the only significant difference in the number of actinomycetes was determined between durum wheat and spelt wheat. Studying the biodiversity of bacteria and their metabolic profile in the rhizosphere of four winter

wheat (*Triticum aestivum* L.) varieties, Wolińska et al. (2020) have established that the number of Actinobacteria was dependent on the wheat variety. Fertilization did not significantly affect the abundance of actinomycetes. Some authors (Liang et al., 2020; Wang et al., 2017) indicate that there is a correlation between the abundance and diversity of the bacterial community in the wheat rhizosphere and pH, nitrates, accessible phosphorus and available potassium. Since the analysis of macromineral accessibility was not conducted in this study, we speculate that one of the factors controlling the bacterial structure and actinomycete abundance is the accessibility of minerals rather than their total content and organic matter content *per se*.

Amonificators are the most represented group of microorganisms in the soil (Rasulić et al., 2021). A significantly greater number of amonificators was recorded in the rhizosphere of compactum wheat than in the rhizosphere of the cultivars of common, durum and spelt wheats. The results reported by Jezierska-Tis et al. (2012) showed that the highest number of proteolytic bacteria was found in the control soil under winter wheat compared to durum winter wheat and spelt winter wheat lines. While analyzing root-associated bacterial and fungal communities in modern wheat cultivars, *Triticum aestivum* ssp. *spelta* and ancestors of wheat (T. *turgidum* ssp. *dicoccum*, T. *monococcum* ssp. *monococcum* and T. *monococcum* ssp. *aegilopoides*), Kinnunen-Grubb et al. (2020) observed a clear separation of bulk soil microbial communities of all wheat accessions. In addition, significant differences between the treatments were registered in this trial. The abundance of amonificators recorded in the treatment with the combined application of biohumus and biofertilizer was greater by more than 50% than in the control, while the greatest differences between the treatments were found in spelt wheat. Some studies found significant differences in the abundance of amonificators between different variants of organic and mineral fertilizer applications (Raičević et al., 2005). The greatest abundance of amonificators in the control was registered in the common wheat rhizosphere, which might indicate its tendency towards forming associations with this bacterial group.

The greatest number of the members of oligonitrophilic bacteria was detected in the rhizosphere of compactum and spelt wheats, as well as in the variant with biofertilizer +biohumus. From the aspect of soil fertility, free-living nitrogen-fixers are extremely important, which underlines the significance of the selection of an appropriate variety within the soil and plant nutritional management.

The research results showed the differences in the abundance of the examined physiological groups of microorganisms in the rhizosphere of the studied species (wheat) which could be used in selecting the genotype adjusted to the specific characteristics of soil and the applied agricultural practices. The same has been indicated by other authors (Abhilash et al., 2012). Nevertheless, this approach to genotype selection has to be supported by crop management practices favoring beneficial microflora.

Conclusion

The obtained results show that the selection of a suitable crop variety, accompanied by the application of appropriate fertilizer formulations, can affect the specific characteristics of the microbial community that represent a significant factor of soil fertility. The greatest abundance of fungi was recorded in the common wheat cultivar (24.37 x 10^3 g^{-1}), while the rhizosphere of compactum wheat had the largest number of amonificators (119.27 x 10^5 g^{-1}) and oligonitrophilic bacteria (361.47 x 10^5 g^{-1}). There was no significant difference in the number of actinomycetes between common, compactum and durum wheats, but their number was the lowest in the spelt wheat cultivar (11.25 x 10^3 g^{-1}). The analysis of differences between the mean values of the examined treatments showed that the combined application of biohumus and biofertilizer had a significant influence on the abundance of fungi, amonificators and oligonitrophiles. The selection of the appropriate variety, along with the suitable manner of nutrient supply, can significantly affect soil biogenicity and, consequently, its fertility. Such an integral approach can represent a basis for the development of innovative technologies within the concept of sustainable development of agriculture, particularly in organic farming, which completely relies on natural resources and mechanisms.

Acknowledgements

References

AbdElgawad, H., Abuelsoud, W., Madany, M.M., Selim, S., Zinta, G., Mousa, A.S., & Hozzein, W.N. (2020). Actinomycetes enrich soil rhizosphere and improve seed quality as well as productivity of legumes by boosting nitrogen availability and metabolism. *Biomolecules*, *10* (12), 1675.

Abhilash, P.C., Powell, J.R., Singh, H.B., & Singh, B.K. (2012). Plant–microbe interactions: novel applications for exploitation in multipurpose remediation technologies. *Trends in biotechnology*, *30* (8), 416-420.

Araújo, A.S., Leite, L.F., Santos, V.B., & Carneiro, R.F. (2009). Soil microbial activity in conventional and organic agricultural systems. *Sustainability, 1* (2), 268-276.

Aira, M., Gómez-Brandón, M., Lazcano, C., Baath, E., & Domínguez, J. (2010). Plant genotype strongly modifies the structure and growth of maize rhizosphere microbial communities. *Soil Biology and Biochemistry*, *42* (12), 2276-2281.

Bever, J.D., Platt, T.G., & Morton, E.V. (2012). Microbial population and community dynamics on plant roots and their feedbacks on plant communities. *Annual Review of Microbiology*, *66*, 265-283.

Bibhuti, B.D., & Dkhar, M.S. (2011). Rhizosphere Microbial Populations and Physico Chemical Properties as Affected by Organic and Inorganic Farming Practices. *American-Eurasian Journal of Agricultural & Environmental Sciences, 10* (2), 140-150.

Bulgarelli, D., Garrido-Oter, R., Münch, P. C., Weiman, A., Dröge, J., Pan, Y., & Schulze-Lefert, P. (2015). Structure and function of the bacterial root microbiota in wild and domesticated barley. *Cell host & microbe*, *17* (3), 392-403.

Chang, E.H., Chung, R.S., & Tsai, Y.H. (2007). Effect of different application rates of organic fertilizer on soil enzyme activity and microbial Population. *Soil Science and Plant Nutrition*, *53,* 132-140.

Compant, S., Samad, A., Faist, H., & Sessitsch, A. (2019). A review on the plant microbiome: ecology, functions, and emerging trends in microbial application. *Journal of Advanced Research*, *19,* 29-37.

da Costa, P.B., Beneduzi, A., de Souza, R., Schoenfeld, R., Kayser Vargas, L., & Passaglia, L.M.P. (2013). The effects of different fertilization conditions on bacterial plant growth promoting traits: guidelines for directed bacterial prospection and testing. *Plant and Soil, 368,* 267-280.

Ding, J.L., Jiang, X., Ma, M.C., Zhou, B.K., Guan, D.W., Zhao, B.S., Zhou, J., Cao, F.M., Li, L., & Li, J. (2016). Effect of 35 years inorganic fertilizer and manure amendment on structure of bacterial and archaeal communities in black soil of northeast China. *Applied Soil Ecology*, *105*, 187-195.

Dolijanović, Ž. (2002). Uticaj aditivnog načina združivanja i prihranjivanja na produktivnost kukuruza i soje. Magistarska teza, Univerzitet u Beogradu, Poljoprivredni fakultet, Zemun.

Đurić, S., & Jarak, M. (2006). The effect of sulphonylurea herbicides on the microbial activity in soil under maize. *Annals of the Faculty of Engineering Hunedoara*, *4*, 93-96.

Fließbach, A., Oberholzer, H.R., Gunst, L., Mäder, P., & Fliessbach, A. (2007). Soil organic matter and biological soil quality indicators after 21 years of organic and conventional farming. *Agriculture, Ecosystems and Environment*, *118*, 273-284.

Germida, J., & Siciliano, S. (2001). Taxonomic diversity of bacteria associated with the roots of modern, recent and ancient wheat cultivars. *Biology and Fertility of Soils*, *33* (5), 410-415.

Gqozo, M.P., Bill, M., Siyoum, N., Labuschagne, N., & Korsten, L. (2020). Fungal diversity and community composition of wheat rhizosphere and non-rhizosphere soils from three different agricultural production regions of South Africa. *Applied Soil Ecology*, *151*, 103543.

Guan, G., Tu, S.X., Yang, J.C., Zhang, J.F., & Li, Y.A.N.G. (2011). A field study on effects of nitrogen fertilization modes on nutrient uptake, crop yield and soil biological properties in rice-wheat rotation system. *Agricultural Sciences in China*, *10*, 1254-1261.

Hayat, R., Ali, S., Amara, U., Khalid, R., & Ahmed, I. (2010). Soil beneficial bacteria and their role in plant growth promotion: a review. *Annals of Microbiology,* 60, 579-598.

Jarak, M., Protić, R., Janković, S., & Čolo, J. (2006). Response of wheat to Azotobacter-actinomycetes inoculation and nitrogen fertilizers. *Romanian Agricultural Research*, *23*, 37-40.

Jezierska-Tys, S., Rachoń, L., Rutkowska, A., & Szumiło, G. (2012). Effect of new lines of winter wheat on microbiological activity in Luvisol. *International Agrophysics*, *26* (1), 33-38.

Karličić, V., Radić, D., Jovičić-Petrović, J., Lalević, B., Jovanović, L., Kiković, D., & Raičević, V. (2016). Isolation and characterization of bacteria and yeasts from contaminated soil. *Journal of Agricultural Sciences (Belgrade)*, *61* (3), 247-256.

Kinnunen-Grubb, M., Sapkota, R., Vignola, M., Nunes, I. M., & Nicolaisen, M. (2020). Wheat domestication has dramatically affected the root-associated microbiome. https://doi.org/10.21203/rs.3.rs-20588/v1

Korniłłowicz-Kowalska, T., Andruszczak, S., Bohacz, J., Kraska, P., Możejko, M., & Kwiecińska-Poppe, E. (2022). The effect of tillage and no-tillage system on culturable fungal communities in the rhizosphere and soil of two spelt cultivars. *Applied Soil Ecology*, *174*, 104413.

Krasilnikov, N.N. (1965). *Biology of some actinomycetes groups.* Science. Moskva.

Kumar, U., Shahid, M., Tripathi, R., Mohanty, S., Kumar, A., Bhattacharyya, P., & Nayak, A.K. (2017). Variation of functional diversity of soil microbial community in sub-humid tropical rice-rice cropping system under long-term organic and inorganic fertilization. *Ecological indicators*, *73,* 536-543.

Le Guillou, C., Chemidlin Prévost-Bouré, N., Karimi, B., Akkal-Corfini, N., Dequiedt, S., Nowak, V., & Ranjard, L. (2019). Tillage intensity and pasture in rotation effectively shape soil microbial communities at a landscape scale. *MicrobiologyOpen*, *8* (4), e00676.

Liang, R., Hou, R., Li, J., Lyu, Y., Hang, S., Gong, H., & Ouyang, Z. (2020). Effects of different fertilizers on rhizosphere bacterial communities of winter wheat in the North China Plain. *Agronomy*, *10* (1), 93.

Mohammadi, K. (2011). Soil Microbial Activity and Biomass as Influenced by Tillage and Fertilization in Wheat Production American-Eurasian. *Journal of Agriculture and Environmental Sciences*, *10* (3), 330-337.

Pfister, S., Bayer, P., Koehler, A., & Hellweg, S. (2011). Projected water consumption in future global agriculture: Scenarios and related impacts. *Science of the total environment, 409* (20), 4206-4216.

Pochon, J., & Tardieux, P. (1962). *Techniques d'analyse en microbiologie du sol.* Paris, France.

Purwanto, B.H., & Alam, S. (2020). Impact of intensive agricultural management on carbon and nitrogen dynamics in the humid tropics. *Soil Science and Plant Nutrition*, *66* (1), 50-59.

Raičević, V., Lalević, B., Ličina, V., Vasić, G., & Antić-Mladenović, S. (2005). Microbiological activity of barley rhizosphere grown on deposol. *Savremena poljoprivreda*, 54 (3-4), 487-491.

Rasulić, N., Delić, D., Stajković-Srbinović, O., Buntić, A., Kuzmanović, Đ., Knežević, M., & Sikirić, B. (2021). Microbiological and basic agrochemical properties of Eutric Cambisols in western and southwestern Serbia. *Zemljište i biljka*, *70* (2), 1-9.

Republic Hydrometeorological Service of Serbia, Meteorological Yearbooks, http://www.hidmet.gov.rs/latin/meteorologija/klimatologija_godisnjaci.php

Salamon, S., Mikołajczak, K., Błaszczyk, L., Ratajczak, K., & Sulewska, H. (2020). Changes in root-associated fungal communities in *Triticum aestivum* ssp. *spelta* L. and *Triticum aestivum* ssp. *vulgare* L. under drought stress and in various soil processing. *Plos one*, 15, e0240037.

Sarić, Z. (1989). *Praktikum iz mikrobiologije*. Naučna knjiga, Beograd.

Singh, A.K., Hamel, C., DePauw, R.M., & Knox, R.E. (2012). Genetic variability in arbuscular mycorrhizal fungi compatibility supports the selection of durum wheat genotypes for enhancing soil ecological services and cropping systems in Canada. *Canadian journal of microbiology*, *58,* 293-302.

Singh, J.S., Pandey, V.C., & Singh, D.P. (2011). Efficient soil microorganisms: a new dimension for sustainable agriculture and environmental development. *Agriculture, Ecosystems & Environment*, *140* (3-4), 339-353.

Sivojiene, D., Kacergius, A., Baksiene, E., Maseviciene, A., & Zickiene, L. (2021). The Influence of Organic Fertilizers on the Abundance of Soil Microorganism Communities, Agrochemical Indicators, and Yield in East Lithuanian Light Soils. *Plants*, *10* (12), 2648.

Shakoor, A., Shakoor, S., Rehman, A., Ashraf, F., Abdullah, M., Shahzad, S. M., & Altaf, M.A. (2021). Effect of animal manure, crop type, climate zone, and soil attributes on greenhouse gas emissions from agricultural soils—A global meta-analysis. *Journal of Cleaner Production*, *278*, 124019.

Venieraki, A., Dimou, M., Pergalis, P., Kefalogianni, I., Chatzipavlidis, I., & Katinakis, P. (2011). The genetic diversity of culturable nitrogen-fixing bacteria in the rhizosphere of wheat. *Microbial Ecology*, *61*, 277-285.

Wang, J., Song, Y., Ma, T., Raza, W., Li, J., Howland, J.G., Huang, Q., & Shen, Q. (2017). Impacts of inorganic and organic fertilization treatments on bacterial and fungal communities in a paddy soil. *Applied Soil Ecology*, *112,* 42-50.

Wei, Z., & Jousset, A. (2017). Plant breeding goes microbial. *Trends in Plant Science*, *22* (7), 555-558.

Wolińska, A., Kuźniar, A., & Gałązka, A. (2020). Biodiversity in the rhizosphere of selected winter wheat (*Triticum aestivum* L.) cultivars-genetic and catabolic fingerprinting. *Agronomy*, *10* (7), 953.

Xu, X., Thornton, P.E, & Post, W.M. (2013). A global analysis of soil microbial biomass carbon, nitrogen and phosphorus in terrestrial ecosystems. *Global Ecology and Biogeography*, *22*, 737-749.

Ye, L., Zhao, X., Bao, E., Li, J., Zou, Z., & Cao, K. (2020). Bio-organic fertilizer with reduced rates of chemical fertilization improves soil fertility and enhances tomato yield and quality. *Scientific Reports*, *10* (1), 1-11.

Zhao, J., Liu, J., Liang, H., Huang, J., Chen, Z., Nie, Y., Wang, C., & Wang, Y. (2018). Manipulation of the rhizosphere microbial community through application of a new bio-organic fertilizer improves watermelon quality and health. *PLoS One. 13* (2), e0192967

Zhu, Z., Bai, Y., Lv, M., Tian, G., Zhang, X., Li, L., & Ge, S. (2020). Soil fertility, microbial biomass, and microbial functional diversity responses to four years fertilization in an apple orchard in North China. *Horticultural Plant Journal, 6* (4), 223-230.

BIOGENOST RIZOSFERNOG SLOJA ZEMLJIŠTA RAZLIČITIH GENOTIPOVA PŠENICE POD UTICAJEM TRETMANA ĐUBRENJA

Svetlana M. Roljević Nikolić[1*], Željko K. Dolijanović[2], Dušan Đ. Kovačević[2], Snežana I. Oljača[2] i Helena J. Majstorović[1]

[1]Istraživačko-razvojni institut Tamiš,
Novoseljanski put 33, Pančevo, Srbija
[2]Univerzitet u Beogradu, Poljoprivredni fakultet,
Nemanjina 6, Beograd, Srbija

R e z i m e

Rizosfera je dinamična sredina na čiju biogenost utiču brojni činioci, među kojima i snabdevenost zemljišta hranljivim materijama i biljka domaćin. Cilj ovog rada bio je da utvrdi brojnost osnovnih grupa mikroorganizama u rizosferi četiri podvrste, odnosno sorte pšenice, u okviru tri tretmana đubrenja u sistemu organske proizvodnje. Poljski ogled je realizovan po metodi potpuno slučajnog blok sistema u četiri ponavljanja, na zemljištu tipa izluženi černozem. Uočena je značajna varijabilnost brojnosti proučavanih fizioloških grupa mikroorganizama između podvrsta, odnosno sorti pšenice, kao i tretmana đubrenja. U rizosferi sorte obične pšenice pronađen je najveći broj mikoriznih gljiva ($24,37 \times 10^3 \ g^{-1}$). Zemljište uzorkovano u zoni rizosfere kompaktum pšenice odlikovalo se najvećim brojem oligonitrofilnih bakterija ($361,47 \times 10^5 \ g^{-1}$) i amonifikatora ($119,27 \times 10^5 \ g^{-1}$). Nije bilo značajnih razlika u brojnosti aktinomiceta između sorti obične, kompaktum i tvrde pšenice, ali je njihov najmanji broj utvrđen kod sorte krupnika ($11,25 \times 10^3 \ g^{-1}$). Na tretmanu kombinovane primene biofertilizatora i organskog đubriva, utvrđen je značajno veći broj gljiva (28,2%), amonifikatora (56,6%) i oligonitrofilnih bakterija (14,6%) u poređenju sa kontrolom. Dobijeni rezultati ukazuju na to da genotip domaćina, uz primenu odgovarajućih formulacija đubriva, može uticati na brojnost mikroorganizama, što je naročito važno u uslovima organske proizvodnje, koja se u potpunosti oslanja na prirodne resurse i procese.

Ključne reči: pšenica, organska proizvodnja, biohumus, biofertilizator, gljive, aktinomicete, amonifikatori, oligonitrofilne bakterije.

* Autor za kontakt: e-mail: roljevic@institut-tamis.rs