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SEASONAL CHANGES OF MICROBIAL POPULATION IN MAIZE AND SOYBEAN RHIZOSPHERE UNDER CONVENTIONAL AND ORGANIC GROWING SYSTEMS

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Abstract

The aim of this study was to compare abundance of microorganisms in the rhizosphere of maize and soybean grown under conventional and organic management. The trial was set up on the chernozem soil at the experimental field of Bački Petrovac, Institute of Field and Vegetable Crops, Novi Sad. Rhizosphere samples were collected in two sampling terms during 2014 (July 7 and August 14) and analysed by the indirect dilution method followed by plating of soil suspension on selective nutritive mediums: soil agar for the total number of microorganisms, meat peptone agar for the number of ammonifiers, Waksman-Carey medium for the number of cellulolytic microorganisms, synthetic medium for the number of actinomycetes, Czapek Dox agar for the number of fungi, and N-free medium for the number of azotobacters and free N-fixers. The results showed significant differences in microbial abundance between plant species, growing systems and sampling terms. Significantly higher number of microorganisms was found in rhizosphere of soybean compared to maize, as well as in organic growing system compared to conventional. Significant differences between sampling terms were recorded for the number of ammonifiers, azotobacters, fungi and actinomycetes, while the number of most tested microbial groups was higher in the second sampling term.

Keywords: *maize, microbial abundance, organic and conventional growing system, rhizosphere, soybean*

Introduction

Agricultural intensification as one of the greatest threats to global biodiversity, leads to large-scale ecosystem degradation and loss of productivity in the long term (Convention on Biological Diversity, 2010). Management practices (tillage, cropping rotation, use of pesticides and mineral fertilizers, irrigation) strongly influence the quality and fertility of agricultural soils and consequently, the size, composition, and function of the soil microbial community (Shannon et al., 2002). In turn, despite of their small volume in soil, microorganisms play a definitive and very useful role in soil fertility through the cycling of carbon, nitrogen, phosphorus, sulfur, and decomposition of organic residues (Nannipieri et al., 2003; Singh et al., 2011). In addition to the effect on nutrient cycling, microorganisms also affect the physical properties of the soil via production of extracellular polysaccharides and other cellular debris, and thereby help in maintaining soil structure as well as soil health (Bastida et al., 2008).

Conventional farming systems have been associated with loss of soil fertility, soil erosion and ground water pollution (Pimentel et al., 2005). Low-input systems such as organic farming, substantially reduce the use of synthetic fertilizers, pesticides, energy and mechanic stress, and mitigate these negative impacts in order to improve sustainable production (Gomiero et al., 2011). Earlier studies have shown that incorporation of organic amendments increase biomass, activity and diversity of soil microorganisms (Gelsomino et al., 2004; Girvan et al., 2004). According to Hartmann et al. (2015), fertilization scheme, the application and quality

of organic fertilizers in particular, is the major determinant of microbial diversity. The addition of animal or green manures on organic plots provides a significantly greater input of organic carbon which increases microbial population (Reeves, 1997).

Microbial processes within the rhizosphere of crop plants are crucial to agriculture. The relation of soil microbial community to cropping system, yield, and soil quality is unclear at present. Seasonal inputs of crop roots, rhizosphere products, and crop residues significantly altered soil microbial biomass and mineralizable C and N of this soil, illustrating the dependence of N dynamics on short-term C inputs and association of soil C/N ratio with changes in microbial community composition across different treatments (Carney and Matson, 2012). Beside management practices and soil environmental factors, the diversity and composition of microbial community in the rhizosphere also depend on several other factors including plant species (Mahmood et al., 2005). Plants can influence composition and stimulate activity of soil microorganisms by producing labile carbon compounds through root exudation (Marschner et al., 2004). Valid evaluation of soil quality requires better understanding of short- and long-term responses of key biochemical and microbiological soil properties to seasonal changes and types of management practice in the cultivation of various crops.

Therefore, the aim of this study was to examine the seasonal changes in rhizosphere microbial population of maize and soybean grown under conventional and organic growing systems.

Materials and Methods

The trial was set up on the chernozem soil at the experimental field of Bački Petrovac, Institute of Field and Vegetable Crops, Novi Sad. Rhizosphere samples were collected in two sampling terms during 2014 (July 7 and August 14) and analysed by the indirect dilution method followed by plating of soil suspension on selective nutritive mediums: soil agar for the total number of microorganisms (dilution 10^7), meat peptone agar for the number of ammonifiers (dilution 10^6), Waksman-Carey medium for the number of cellulolytic microorganisms (dilution 10^5), synthetic medium for the number of actinomycetes (dilution 10^4), Czapek Dox agar for the number of fungi (dilution 10^4), and N-free medium for the number of azotobacters (dilution 10^2) and N-fixers (dilution 10^6) (Jarak and Đurić, 2006). Incubation temperature was 28°C, while incubation time depended on the tested microbial group. All microbiological analyses were performed in three replications, and the average number for all samplings was calculated per 1.0 g of absolutely dry soil. The results were analyzed in accordance with three-way model of analysis of variance (ANOVA) using Statistica software (StatSoft Inc. 2012), followed by mean separation according to Fisher's LSD test (Steel and Torrie, 1980).

Results and Discussion

In a long-term field trial in which organic and conventional growing systems were compared, a significant influence of organic agriculture on microbial biomass, diversity and microbial community structures was reported (Esperschütz et al., 2007). Our research focused on comparison of microbial abundance between rhizosphere of maize and soybean grown under conventional and organic management.

At the first sampling term, the number of examined microbial groups in soybean rhizosphere was higher in the organic farming system. Significant differences between systems were recorded for the total number of microorganisms, number of ammonifiers, free N-fixers and cellulolytic microorganisms. At the second sampling term, higher microbial abundance was also obtained in the organic farming system, except for total and free N-fixers, while significant differences were observed within the number of ammonifiers, azotobacters and cellulolytic microorganisms (Table 1). In study of Das and Dkhar (2012), addition of organic

amendments affected the soil physicochemical properties, which in return affected the microbial characteristics in soybean rhizosphere.

The number of microorganisms in maize rhizosphere, was higher in organic management system at the first term of sampling, while significant differences between the systems were recorded only for the number of ammonifiers.

At the second sampling term, for all tested groups except ammonifiers and free N-fixers exhibited the highest number in the organic management system, while significantly higher number between systems was recorded only for the number of actinomycetes and cellulolytic microorganisms (Table 1). Similar results were reported by Orr et al. (2010), indicating that the larger number of free nitrogen-fixers in conventional system was obtained due to higher concentrations of phosphorus from mineral fertilizers. On the contrary, Buyer and Kaufman (1997) showed that total number and diversity of microorganisms in maize rhizosphere were not significantly different for conventional and low-input systems suggesting that conventional agricultural practices may maintain high indices of microbial diversity in the rhizosphere.

Table 1. Number of microorganisms in rhizosphere of soybean and maize

Microbial group	Number of microorganisms in 1 g of absolutely dry soil (CFU g ⁻¹)				
	Growing system	Organic		Conventional	
	Sampling/Plant	I	II	I	II
Total microbial number x 10 ⁷	Soybean	155.53 ^a	146.22 ^a	76.19 ^{bc}	159.63 ^a
	Maize	105.67 ^{abc}	117.92 ^{ab}	49.62 ^c	65.01 ^{bc}
Ammonifiers x 10 ⁶	Soybean	99.47 ^b	162.13 ^a	40.85 ^{cd}	56.66 ^c
	Maize	60.44 ^c	44.82 ^{cd}	18.49 ^d	51.34 ^{cd}
Azotobacters x 10 ²	Soybean	122.10 ^{bc}	198.34 ^a	90.83 ^{cd}	145.49 ^b
	Maize	25.79 ^c	47.18 ^{de}	7.81 ^e	12.24 ^e
N-fixers x 10 ⁶	Soybean	106.46 ^a	95.43 ^{ab}	58.78 ^{bc}	99.19 ^{ab}
	Maize	72.81 ^{abc}	73.14 ^{abc}	34.52 ^c	73.41 ^{abc}
Fungi x 10 ⁴	Soybean	11.62 ^a	11.88 ^a	6.01 ^{ab}	8.65 ^{ab}
	Maize	3.41 ^b	10.63 ^a	3.14 ^b	6.99 ^{ab}
Actinomycetes x 10 ⁴	Soybean	19.48 ^{abc}	30.87 ^{ab}	2.24 ^c	17.28 ^{abc}
	Maize	6.85 ^{bc}	31.90 ^a	1.58 ^c	2.83 ^c
Cellulolytic microorganisms x 10 ⁵	Soybean	30.39 ^a	31.22 ^a	8.16 ^c	14.95 ^{bc}
	Maize	5.73 ^c	24.46 ^{ab}	5.55 ^c	6.62 ^c

Means with the same letter are not significantly different at the P = 0.05 level of significance

This research showed significant differences in microbial abundance between plant species, growing systems and sampling terms (Table 2). Higher microbial number was recorded in soybean rhizosphere compared to rhizosphere of maize. Significant differences in microbial abundance were found between plant species, for all microbial groups except actinomycetes. These results are in agreement with those of Carney and Matson (2012) who revealed that microbial community composition differed between plant species. Similarly, significant differences in the soil microbial biomass were not visible during the wheat growing season, as a result of application of mineral and organic fertilizers, whereas fertilizer application significantly increased this parameter during the maize growing season (Mahmood et al., 2005).

Growing system demonstrated a significant impact on the total number of microorganisms, number of ammonifiers, free N-fixers, actinomycetes and cellulolytic microorganisms.

Significantly higher number of microorganisms in the organic farming system compared with conventional was also determined by Mrkovački et al. (2012).

However, their study reports the higher number of microorganisms in rhizosphere of maize compared to soybean, which is contrary to our results, and indicates that variations in the number of microorganisms depend on the year of research. Studies of Kong et al. (2011) confirmed the highest total microbial biomass in the organic management, and similar values between the conventional and low-input systems, while Bettiol et al. (2002) obtained similar effects of organic and conventional growing system on soil microbial populations. Various findings confirmed that stimulative effect of organic amendments on biomass, activity and diversity of soil microorganisms depends on numerous factors, such as soil type, plant species, soil management practices and other environmental variables. Franzluebbers et al. (1994) indicated that crop management strategies can affect the short-term dynamics of the active C and N pools of soil organic matter by altering the timing, placement, quantity, and quality of crop root and residue input, as well as nutrient status and environmental conditions. Fließbach and Mäder (2000) also interpreted higher microbial biomass in soils of the organic systems as an enhanced decomposition of the easily-available light fraction pool of soil organic matter with increasing amounts of microbial biomass.

Table 2. Effect of plant species, growing system and sampling term on microbial population

Microbial group	Number of microorganisms in 1 g of absolutely dry soil (CFU g ⁻¹)					
	Plant species		Growing System		Sampling term	
	Soybean	Maize	ORG	CON	I	II
Total microbial number x10 ⁷	134.39	84.59	131.33	87.61	96.75	122.20
	**		**		NSD	
Ammonifiers x 10 ⁶	89.78	43.77	91.72	41.84	54.79	78.73
	***		***		**	
Azotobacters x 10 ²	139.19	23.25	98.35	64.09	61.63	100.81
	***		**		**	
N-fixers x 10 ⁶	89.97	63.47	86.96	66.47	68.14	76.13
	*		NSD		NSD	
Fungi x 10 ⁴	9.54	6.04	9.38	6.20	6.04	9.54
	*		NSD		*	
Actinomycetes x 10 ⁴	17.47	10.79	22.27	5.98	7.54	20.72
	NSD		*		*	
Cel. microorganisms x 10 ⁵	21.18	10.59	22.95	8.82	12.46	19.31
	**		***		NSD	

NSD indicates no significant difference at the P = 0.05 level of significance; *, ** and *** indicates significant differences at the P < 0.05, P < 0.01 and P < 0.001 levels

Significant variations in microbial number in relation to the growing season were recorded for the number of ammonifiers, azotobacters, fungi and actinomycetes, while higher abundance was obtained at second sampling term. Shi et al. (2013) recorded seasonal fluctuations in soil microbial biomass C and N, in dehydrogenase and alkaline phosphomonoesterase activities, and in total phospholipids fatty acid (PLFA) level under different tillage and phosphorus management practices, concluding that soil environmental factors and tillage had a greater effect than fertilization on microorganisms (biomass and activity) and community structure. Bossio et al. (1998) observed sustained increases in microbial biomass resulting from high organic matter inputs in the organic and low-input systems that were significantly different during growing season. Same authors ranked the relative importance of various environmental variables in governing the composition of microbial communities in the following order: soil

type > time > specific farming operation (e.g. cover crop incorporation or sidedressing with mineral fertilizer) > management system > spatial variation in the field.

Conclusion

The increase in the number of microorganisms in rhizosphere of two different crops grown under organic management system confirm the positive effect of this agricultural practice on soil microbial population and biological health of soil compared to conventional management.

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