

## Effect of Bacterization on the Number of Microorganisms and the Nitrogen Content in Soil under Maize

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**Abstract:** The number of microorganisms and the nitrogen content in soil depended on the strain of bacteria, maize hybrid and the place where the soil samples were taken from. The maize seed bacterization led to increase as well as to decrease of microorganisms number, both in rhizospheric and surrounding soil. Certain amount of nitrogen was also fixed by the investigated microorganisms which is of great importance for the following crop. A bit higher effectiveness of the investigated microorganisms was obtained in the rhizospheric soil. The highest effectiveness was measured in PKB-509 and a bit lower in Srečko-5. This research has showed that the selection of *Azotobacter chroococcum* and *Bacillus megaterium* must be carried out at the level of plant genotype so that we would be able to choose the most effective strains of bacteria for each maize hybrid.

**Key words:** microorganisms, maize, bacterization, nitrogen, soil

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### Introduction

Soil is a natural multicomponent open system created in the process where a large number of factors interacted in which the microorganisms had the most important role. The number and biochemical activity of microorganisms is specific for each type of soil. Fertile soil is a soil with high content of humus which is convenient for the largest number of bacteria and other micro-

organisms. Diazotrophs are found in the layers of soil near the surface but mostly in the rhizospheric soil which was confirmed by many authors (Feodorov, 1954; Krasiljnikov, 1958; Dobereiner and Pupin, 1961; Dobereiner, 1972; Zimna, 1962; Mališkin, 1965; Litovčenko, 1965; Barea, 1978; Govedarica, 1986.). The dynamics of phosphorus mineralization and immobilization, controlled by the microorganisms, is of great importance for plant nutrition (Cross and Schlesinger, 1995). Maize seed inoculation with microorganisms that produce the phosphatase enzyme effects the activity of phosphomonoesterases in their rhizosphere as well as the content of total nitrogen and phosphorus in soil. Importantly, strains of microorganisms that possess phosphomonoesterases need to be selected in order to increase the amount of easily accessible phosphorus in maize rhizosphere and reduce the need for mineral fertilizers as well as the costs of production but avoid the pollution of the environment.

The aim of this research was to investigate the effect of different single strains of diazotrophs and phospho-mineralizing microorganisms as well as their combinations on the number of microorganisms and nitrogen content in soil under maize.

### Materials and Methods

The investigation of the effectiveness of single strains of *Azotobacter chroococcum* and *Bacillus megaterium*, as well as their combinations, was conducted in field conditions on fertile soil in 2000. The following maize hybrids were chosen: PKB-509 and Srečko-5. The maize seed inoculation was performed before sowing. Soil samples were taken at the end of the maize growing season from surrounding soil (between rows at the depth of 0-30 cm) and rhizospheric soil (0,5 -1 cm from the root). The number of some systematic and physiological groups of microorganisms was determined. The standard methods by Pochon and Tardieux (1962) and Krasiljnikov (1965) were used for determination of the number of microorganisms. Nitrogen content in soil was measured by Kjeldahl method (Nelson and Sommers, 1973).

### Results and Discussion

The number of microorganisms and the nitrogen content in soil depended on the strains of *azotobacter* and *bacillus*, maize hybrid and the sampling place. The investigated single strains of *Azotobacter chroococcum* and *Bacillus megaterium*, as well as their combinations had a stimulating and yet inhibitory effect on the number of microorganisms in rhizospheric and surrounding soil, in both maize hybrid. This kind of stimulation and inhibition effects were stated by many authors (Govedarica et. al. 2001; Hajnal, T., 2002). In both maize hybrids, in rhizospheric and surrounding soil, certain amount of nitrogen was found which is of great significance for the following crop in rotation. Maize seed bacterization increased the number of ammonifiers. In PKB-509 hybrid, the most effective bacteria in the rhizosphere were *Bacillus megaterium* strain 7. *Azotobacter chroococcum* strain 16 was the most effective

with Srećko-5. In PKB-509, stimulation was caused by eight variants in the surrounding soil. The most effective was *Azotobacter chroococcum* strain 16. In Srećko-5, extreme inhibitory effect was determined. All the investigated variants of the experiment had a negative effect, decreasing the number of ammonifiers in surrounding soil (Tab.1). Strains of *Azotobacter chroococcum* and *Bacillus megaterium*, single and joined, increased the number of oligonitrophilic bacteria in PKB-509. This effect of stimulation was also determined in Srećko-5 hybrid. The seed bacterization increased the number of oligonitrophilic bacteria in surrounding soil in PKB-509. In Srećko-5, this stimulation was of a smaller extent. The highest increase of this group of microorganisms in relation to the control variant caused the variant 11 (Tab.2). The number of actinomycetes, with PKB-509, was increased by stimulation of nine variants in the rhizosphere. In the other hybrid, the stimulation effect was smaller in the surrounding soil. In PKB-509, seven variants had a positive effect, increasing the number of actinomycetes related to the control variant. This stimulation effect was extremely high in Srećko-5. Almost every single and joined strains of diazotrophs and phospho-minerilizing microorganisms (Tab.3). Increased number of fungus was measured in both investigated hybrids. Maize seed bacterization caused the increase of the number of this group of microorganisms, both in rhizosphere and surrounding soil (Tab.4). *Azotobacter chroococcum* strain 309 and two investigated combinations of *Azotobacter chroococcum* and *Bacillus megaterium* significantly increased the number of azotobacter with PKB-509, in rhizospheric soil. *Bacillus megaterium* strain 10 caused the highest increase of azotobacter number. The other six variants also stimulated the number of azotobacters but to a lesser extent. The effect of inhibition was greater in the surrounding soil of PKB-509. However, stimulation caused by seed bacterization was found in the surrounding soil of Srećko-5 (Tab.5). Nine variants of this experiment had a positive effect, increasing the number of phospho-minerilizing organisms in the PKB-509 rhizosphere. Seven variants stimulated and the other eight inhibited the number of this group of microorganisms in the rhizosphere under Srećko-5. Those effects of stimulation and inhibition were recorded in the surrounding soil of both maize hybrids (Tab.6). The number of phospho-mobilizing organisms was decreased in relation to the control in the rhizosphere of PKB-509. Only five variants stimulated the number of this group of microorganisms in Srećko-5 rhizosphere. The inhibitory effect of all investigated strains of bacteria, was recorded in the surrounding soil of PKB-509. Two strains of *Azotobacter chroococcum* and two strains of *Bacillus megaterium* increased the number of phospho-mobilizing organisms in the surrounding soil of Srećko-5. The other single strains as well as their combinations affected negatively (Tab.7). Increased nitrogen content in the rhizospheric soil of both maize hybrids was found (Tab.8). Nine variants in PKB-509 and eleven variants in Srećko-5, had stimulatory effect. Certain amount of nitrogen was accumulated in the soil. All the investigated variants had stimulatory effect in the surrounding soil of PKB-509. That stimulation was also recorded in the surrounding soil of Srećko-5 caused by all strains of diazotrophs, two strains of *Bacillus megaterium* and two other variants of the experiment as well.

Tab.1. Number of ammonifiers in the soil under maize ( $10^7/g$  soil)

variants (FACTOR C)	hybrids (FACTOR A)			
	PKB-509		SREĆKO-5	
	sampling place (FACTOR B)			
	rhizosp.soil	surroun.soil	rhizosp.soil	surroun.soil
Control	56,3	55,4	360,1	441,3
1. <i>Azotobacter chroococcum</i> strain 16	133,6	136,2	452,3	411,6
2. <i>Azotobacter chroococcum</i> strain 76	61,5	65,3	105,7	99,1
3. <i>Azotobacter chroococcum</i> strain 84	79,8	74,1	250,5	184,5
4. <i>Azotobacter chroococcum</i> strain 209	55,5	55,1	300,2	254,9
5. <i>Azotobacter chroococcum</i> strain 309	84,9	67,1	394,6	405,2
6. <i>Bacillus megaterium</i> strain 3	57,7	60,1	333,3	355,7
7. <i>Bacillus megaterium</i> strain 7	140,1	125,3	106,3	170,9
8. <i>Bacillus megaterium</i> strain 9	49,5	51,3	277,7	333,4
9. <i>Bacillus megaterium</i> strain 10	78,1	67,9	64,7	47,3
10. <i>Bacillus megaterium</i> strain 11	41,2	30,9	393,8	380,3
11. <i>Az. chr.</i> strain 16 + <i>B. meg.</i> strain 3	31,1	33,2	105,9	100,1
12. <i>Az. chr.</i> strain 76 + <i>B. meg.</i> strain 7	43,8	35,6	346,6	385,5
13. <i>Az. chr.</i> strain 84 + <i>B. meg.</i> strain 9	63,1	69,6	306,7	319,7
14. <i>Az. chr.</i> strain 209 + <i>B. meg.</i> strain 10	77,9	50,6	221,2	276,4
15. <i>Az. chr.</i> strain 309 + <i>B. meg.</i> strain 11	60,5	54,7	288,8	387,3
	LSD0,01		LSD0,05	
A	191,3**		145,0**	
B	294,5ns		223,2ns	
C	276,2**		209,3**	
interaction AxB	191,9ns		145,5ns	
interaction AxC	66,95**		50,72**	
interaction BxC	288,7ns		218,7ns	
interaction AxBxC	59,38**		44,94**	

Tab.2. Number of oligonitrophilic bacteria in the soil under maize (  $10^6$ /g soil )

variants (FACTOR C)	hybrids (FACTOR A)			
	PKB- 509		SREČKO-5	
	sampling place (FACTOR B)			
	rhizosp.soil	surroun.soil	rhizosp.soil	surroun.soil
<i>Control</i>	<u>96,3</u>	<u>100,8</u>	<u>113,4</u>	<u>122,1</u>
1. <i>Azotobacter chroococcum</i> strain 16	360,6	342,7	49,8	46,9
2. <i>Azotobacter chroococcum</i> strain 76	180,0	182,3	80,9	58,6
3. <i>Azotobacter chroococcum</i> strain 84	240,5	249,4	28,4	41,0
4. <i>Azotobacter chroococcum</i> strain 209	93,9	184,7	129,8	143,6
5. <i>Azotobacter chroococcum</i> strain 309	205,2	213,1	85,4	76,7
6. <i>Bacillus megaterium</i> strain 3	182,7	160,3	87,8	89,1
7. <i>Bacillus megaterium</i> strain 7	284,7	273,2	73,8	65,9
8. <i>Bacillus megaterium</i> strain 9	170,1	198,6	107,9	90,0
9. <i>Bacillus megaterium</i> strain 10	252,7	222,5	139,2	116,4
10. <i>Bacillus megaterium</i> strain 11	225,6	215,2	134,9	169,4
11. <i>Az.chr.</i> strain 16 + <i>B.meg.</i> strain 3	149,3	198,5	241,2	284,2
12. <i>Az.chr.</i> strain 76 + <i>B.meg.</i> strain 7	76,6	183,2	265,9	272,7
13. <i>Az.chr.</i> strain 84 + <i>B.meg.</i> strain 9	122,5	164,6	371,9	365,0
14. <i>Az.chr.</i> strain 209 + <i>B.meg.</i> strain 10	84,3	81,4	87,0	84,8
15. <i>Az.chr.</i> strain 309 + <i>B.meg.</i> strain 11	110,6	96,4	154,6	129,4
	LSD0,01		LSD0,05	
A	177,8**		134,8**	
B	185,5ns		140,6ns	
C	166,9**		126,5**	
interaction AxB	178,5ns		135,3ns	
interaction AxC	59,64**		45,18**	
interaction BxC	172,7ns		130,8ns	
interaction AxBxC	52,23**		39,52**	

Tab.3. Number of actinomycetes in the soil under maize (  $10^4$ /g soil )

variants (FACTOR C)	hybrids (FACTOR A)			
	PKB-509		SREĆKO-5	
	sampling place (FACTOR B)			
	rhizosp.soil	surroun.soil	rhizosp.soil	surroun.soil
Control	15,0	15,4	12,8	8,4
1. <i>Azotobacter chroococcum</i> strain 16	12,6	14,3	6,8	5,7
2. <i>Azotobacter chroococcum</i> strain 76	24,5	26,3	12,0	9,6
3. <i>Azotobacter chroococcum</i> strain 84	6,6	6,9	16,0	11,4
4. <i>Azotobacter chroococcum</i> strain 209	17,4	16,8	9,5	9,5
5. <i>Azotobacter chroococcum</i> strain 309	27,2	28,0	7,5	8,1
6. <i>Bacillus megaterium</i> strain 3	9,8	5,9	6,4	7,2
7. <i>Bacillus megaterium</i> strain 7	16,1	9,2	18,1	17,7
8. <i>Bacillus megaterium</i> strain 9	27,5	22,4	14,4	21,8
9. <i>Bacillus megaterium</i> strain 10	18,4	18,8	14,7	12,1
10. <i>Bacillus megaterium</i> strain 11	10,8	13,0	6,7	13,1
11. <i>Az. chr.</i> strain 16 + <i>B. meg.</i> strain 3	5,4	9,6	11,2	5,9
12. <i>Az. chr.</i> strain 76 + <i>B. meg.</i> strain 7	15,9	16,7	19,7	11,9
13. <i>Az. chr.</i> strain 84 + <i>B. meg.</i> strain 9	15,7	13,3	13,1	11,6
14. <i>Az. chr.</i> strain 209 + <i>B. meg.</i> strain 10	9,2	10,8	6,6	10,7
15. <i>Az. chr.</i> strain 309 + <i>B. meg.</i> strain 11	18,6	18,6	10,7	9,3
	LSD0,01		LSD0,05	
A	13,45**		10,20**	
B	14,20ns		10,76ns	
C	12,06**		9,138**	
interaction AxB	13,51ns		10,24ns	
interaction AxC	8,789**		6,658**	
interaction BxC	12,42ns		9,406ns	
interaction AxBxC	8,738ns		6,612ns	

Tab.4. Number of fungus in the soil under maize ( 10<sup>4</sup>/g soil )

variants (FACTOR C)	hybrids (FACTOR A)			
	PKB-509		SREČKO-5	
	sampling place (FACTOR B)			
	rhizosp.soil	surroun.soil	rhizosp.soil	surroun.soil
<b>Control</b>	<u>20,9</u>	<u>26,0</u>	<u>27,5</u>	<u>19,1</u>
1. <i>Azotobacter chroococcum</i> strain 16	53,3	69,1	27,7	30,7
2. <i>Azotobacter chroococcum</i> strain 76	18,3	22,7	21,5	22,7
3. <i>Azotobacter chroococcum</i> strain 84	33,0	33,7	83,1	70,6
4. <i>Azotobacter chroococcum</i> strain 209	25,4	21,6	28,4	40,3
5. <i>Azotobacter chroococcum</i> strain 309	41,5	38,6	74,3	67,9
6. <i>Bacillus megaterium</i> strain 3	29,7	35,7	39,7	35,8
7. <i>Bacillus megaterium</i> strain 7	43,6	33,4	65,0	53,1
8. <i>Bacillus megaterium</i> strain 9	54,8	35,5	44,8	33,9
9. <i>Bacillus megaterium</i> strain 10	17,6	25,9	37,4	33,8
10. <i>Bacillus megaterium</i> strain 11	30,1	32,0	28,9	24,9
11. <i>Az.chr.</i> strain 16 + <i>B.meg.</i> strain 3	17,8	25,2	24,6	28,2
12. <i>Az.chr.</i> strain 76 + <i>B.meg.</i> strain 7	41,8	32,2	59,1	42,7
13. <i>Az.chr.</i> strain 84 + <i>B.meg.</i> strain 9	27,7	25,4	39,6	41,8
14. <i>Az.chr.</i> strain 209 + <i>B.meg.</i> strain 10	28,4	29,9	36,8	32,2
15. <i>Az.chr.</i> strain 309 + <i>B.meg.</i> strain 11	24,3	22,1	26,1	25,5
	<b>LSD 0,01</b>		<b>LSD 0,05</b>	
A	33,65**		25,51**	
B	34,61 ns		26,24 ns	
C	26,59**		20,15**	
interaction AxB	33,70 ns		25,55 ns	
interaction AxC	18,50**		14,01**	
interaction BxC	26,78 ns		20,28 ns	
interaction AxBxC	17,84 ns		13,50 ns	

Tab.5. Number of azotobacters in the soil under maize (  $10^2/g$  soil )

variants ( FACTOR C )	hybrids ( FACTOR A )			
	PKB-509		SREĆKO-5	
	sampling place ( FACTOR B )			
	rhizosp.soil	surroun.soil	rhizosp.soil	surroun.soil
Control	10,5	13,6	9,9	9,6
1. <i>Azotobacter chroococcum</i> strain 16	14,6	13,9	9,3	11,4
2. <i>Azotobacter chroococcum</i> strain 76	22,7	21,2	15,7	14,9
3. <i>Azotobacter chroococcum</i> strain 84	11,1	11,0	13,5	12,5
4. <i>Azotobacter chroococcum</i> strain 209	5,4	3,4	9,4	9,8
5. <i>Azotobacter chroococcum</i> strain 309	20,4	20,1	13,3	14,4
6. <i>Bacillus megaterium</i> strain 3	6,5	5,1	11,8	12,5
7. <i>Bacillus megaterium</i> strain 7	5,6	5,2	7,9	7,4
8. <i>Bacillus megaterium</i> strain 9	4,5	3,5	7,5	7,6
9. <i>Bacillus megaterium</i> strain 10	10,5	10,6	19,3	19,3
10. <i>Bacillus megaterium</i> strain 11	16,0	11,9	15,1	14,5
11. <i>Az. chr.</i> strain 16 + <i>B. meg.</i> strain 3	16,8	16,5	6,4	5,9
12. <i>Az. chr.</i> strain 76 + <i>B. meg.</i> strain 7	4,8	4,2	8,5	7,4
13. <i>Az. chr.</i> strain 84 + <i>B. meg.</i> strain 9	7,3	4,8	8,9	9,3
14. <i>Az. chr.</i> strain 209 + <i>B. meg.</i> strain 10	9,4	8,4	11,1	9,5
15. <i>Az. chr.</i> strain 309 + <i>B. meg.</i> strain 11	12,8	10,5	14,5	19,4
	LSD0,01		LSD0,05	
A	106,7ns		80,85ns	
B	106,9ns		81,07ns	
C	70,35**		53,32**	
interaction AxB	107,0ns		81,12ns	
interaction AxC	41,82**		31,68**	
interaction BxC	72,88ns		55,21ns	
interaction AxBxC	41,48ns		31,39ns	



Tab.6. Number of phospho-minerilzing microorganisms in the soil under maize ( $10^4/g$  soil)

variants (FACTOR C)	hybrids (FACTOR A)			
	PKB-509		SREĆKO-5	
	sampling place (FACTOR B)			
	rhizosp.soil	surroun.soil	rhizosp.soil	surroun.soil
Control	48,1	48,5	47,9	37,1
1.Azotobacter chroococcum strain 16	58,3	48,8	28,3	26,1
2.Azotobacter chroococcum strain 76	33,6	38,3	90,7	70,6
3.Azotobacter chroococcum strain 84	23,7	23,2	17,1	13,7
4.Azotobacter chroococcum strain 209	83,6	45,7	21,3	17,8
5.Azotobacter chroococcum strain 309	62,2	24,5	37,5	32,2
6.Bacillus megaterium strain 3	58,8	51,1	59,7	38,2
7.Bacillus megaterium strain 7	35,4	34,5	39,5	29,5
8.Bacillus megaterium strain 9	22,9	47,3	55,0	44,8
9.Bacillus megaterium strain 10	80,5	54,2	81,3	33,8
10.Bacillus megaterium strain 11	92,0	55,7	40,9	43,9
11.Az.chr. strain 16 + B.meg. strain 3	51,9	56,5	31,9	25,9
12.Az.chr. strain 76 + B.meg. strain 7	72,2	63,2	46,9	37,9
13.Az.chr. strain 84 + B.meg. strain 9	47,9	41,1	83,3	27,9
14.Az.chr. strain 209 + B.meg. strain 10	86,2	82,6	95,5	67,9
15.Az.chr. strain 309 + B.meg. strain 11	24,1	18,6	65,8	56,8
	LSD0,01		LSD0,05	
A	49,18ns		37,28ns	
B	47,79**		36,23**	
C	41,53**		31,47**	
interaction AxB	47,62ns		36,10ns	
interaction AxC	33,40**		25,30**	
interaction BxC	39,20ns		29,70ns	
interaction AxBxC	26,25**		19,87**	

Tab.7. Number of phospho-mobilizing microorganisms in the soil under maize  
( $10^4/g$  soil)

variants (FACTOR C)	hybrids (FACTOR A)			
	PKB-509		SREĆKO-5	
	sampling place (FACTOR B)			
	rhizosp.soil	surroun.soil	rhizosp.soil	surroun.soil
Control	84,7	78,1	71,8	56,2
1. <i>Azotobacter chroococcum</i> strain 16	58,3	60,7	46,7	36,4
2. <i>Azotobacter chroococcum</i> strain 76	30,5	38,3	62,7	59,8
3. <i>Azotobacter chroococcum</i> strain 84	44,9	45,3	67,5	45,5
4. <i>Azotobacter chroococcum</i> strain 209	42,9	36,1	80,1	54,6
5. <i>Azotobacter chroococcum</i> strain 309	49,5	37,4	119,3	86,3
6. <i>Bacillus megaterium</i> strain 3	39,7	27,3	72,2	75,2
7. <i>Bacillus megaterium</i> strain 7	26,9	19,6	25,0	23,6
8. <i>Bacillus megaterium</i> strain 9	32,9	39,0	56,8	37,5
9. <i>Bacillus megaterium</i> strain 10	47,0	37,7	99,8	60,4
10. <i>Bacillus megaterium</i> strain 11	61,9	28,5	39,8	28,5
11. <i>Az. chr.</i> strain 16 + <i>B. meg.</i> strain 3	38,0	16,8	54,5	38,8
12. <i>Az. chr.</i> strain 76 + <i>B. meg.</i> strain 7	47,9	40,6	54,1	51,0
13. <i>Az. chr.</i> strain 84 + <i>B. meg.</i> strain 9	56,8	66,4	35,7	33,7
14. <i>Az. chr.</i> strain 209 + <i>B. meg.</i> strain 10	61,2	44,3	82,1	48,8
15. <i>Az. chr.</i> strain 309 + <i>B. meg.</i> strain 11	53,3	46,6	68,3	34,8
	LSD0,01		LSD0,05	
A	44,38**		33,64**	
B	44,28**		33,57**	
C	39,71**		30,10**	
interaction AxB	42,47ns		32,19ns	
interaction AxC	29,25**		22,16**	
interaction BxC	37,82ns		28,65ns	
interaction AxBxC	23,49ns		17,77ns	

Tab.8. Nitrogen content in soil ( % )

variants (FACTOR C)	hybrids (FACTOR A)			
	PKB-509		SREĆKO-5	
	sampling place (FACTOR B)			
	rhizosp.soil	surroun.soil	rhizosp.soil	surroun.soil
Control	<u>0,171</u>	<u>0,169</u>	<u>0,190</u>	<u>0,181</u>
1. <i>Azotobacter chroococcum</i> strain 16	0,186	0,171	0,212	0,187
2. <i>Azotobacter chroococcum</i> strain 76	0,168	0,175	0,197	0,185
3. <i>Azotobacter chroococcum</i> strain 84	0,169	0,174	0,188	0,191
4. <i>Azotobacter chroococcum</i> strain 209	0,169	0,171	0,207	0,188
5. <i>Azotobacter chroococcum</i> strain 309	0,173	0,184	0,214	0,190
6. <i>Bacillus megaterium</i> strain 3	0,163	0,178	0,203	0,199
7. <i>Bacillus megaterium</i> strain 7	0,179	0,178	0,173	0,099
8. <i>Bacillus megaterium</i> strain 9	0,179	0,178	0,190	0,179
9. <i>Bacillus megaterium</i> strain 10	0,174	0,180	0,193	0,179
10. <i>Bacillus megaterium</i> strain 11	0,186	0,180	0,191	0,184
11. <i>Az.chr.</i> strain 16 + <i>B.meg.</i> strain 3	0,170	0,186	0,199	0,175
12. <i>Az.chr.</i> strain 76 + <i>B.meg.</i> strain 7	0,170	0,178	0,192	0,180
13. <i>Az.chr.</i> strain 84 + <i>B.meg.</i> strain 9	0,180	0,177	0,192	0,184
14. <i>Az.chr.</i> strain 209 + <i>B.meg.</i> strain 10	0,181	0,181	0,352	0,181
15. <i>Az.chr.</i> strain 309 + <i>B.meg.</i> strain 11	0,186	0,171	0,167	0,187
	LSD0,01		LSD0,05	
A	130,5ns		98,94ns	
B	22,71**		17,21**	
C	136,1ns		103,2ns	
interaction AxB	14,50**		10,99**	
interaction AxC	142,2ns		107,7ns	
interaction BxC	22,41ns		16,97ns	
interaction AxBxC	9,786**		7,405**	

### Conclusions

The number of microorganisms and the content of nitrogen in soil depended on the strain of *Azotobacter chroococcum* and *Bacillus megaterium*, maize hybrid and the sampling place.

Maize seed bacterization with single and joined strains of *Azotobacter chroococcum* and *Bacillus megaterium* increased but also decreased the number of microorganisms in soil under both maize hybrids.

This research has shown that certain amount of nitrogen accumulated in soil under both maize hybrids investigated.

Most of the investigated strains of *Azotobacter chroococcum*, *Bacillus megaterium* and their combination, in the average, increased the number of ammonifiers, oligonitrophilic bacteria, actinomycetes, fungus, phosphomining microorganisms and the nitrogen content in soil but decreased the number of azotobacter and phospho-mobilizing organisms, both in rhizospheric and surrounding soil of PKB-509 hybrid.

The single and joined strains of *Azotobacter chroococcum* and *Bacillus megaterium*, in average, increased the number of fungus and the content of nitrogen in soil and decreased the number of ammonifiers, oligonitrophilic bacteria, actinomycetes, azotobacter, phospho-mineralizing and phospho-mobilizing microorganisms both in rhizospheric and surrounding soil under Srećko-5 hybrid.

The number of microorganisms and nitrogen content in soil was higher in the rhizosphere of both maize hybrids.

This research has shown that the selection of *Azotobacter chroococcum* and *Bacillus megaterium* must be carried out at the level of plant genotype so that we would be able to choose the most effective strains of bacteria for each maize hybrid.

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## UTICAJ BAKTERIZACIJE NA BROJNOST MIKROORGANIZAMA I SADRŽAJ AZOTA U ZEMLJIŠTU POD USEVOM KUKURUZA

-originalni naučni rad-

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### Rezime

Brojnost i biohemijska aktivnost mikroorganizama specifičan je za svaki tip zemljišta. U ovom radu je ispitivan uticaj različitih sojeva diazotrofa i fosfomineralizatora, kao i njihovih kombinacija, na brojnost mikroorganizama i sadržaj azota u zemljištu pod usevom kukuruza. Ispitivanje uticaja pojedinačnih sojeva *Azotobacter chroococcum* i *Bacillus megaterium*, kao i njihovih kombinacija, obavljeno je u poljskim uslovima u toku 2000. godine. Za ova istraživanja odabrano je dva hibrida kukuruza : PKB-509 i Srečko-5. Određivana je brojnost pojedinih sistematskih i fizioloških grupa mikroorganizama i sadržaj azota u zemljištu.

Brojnost mikroorganizama i sadržaj azota u zemljištu zavisila je od soja azotobaktera i bacilusa, hibrida kukuruza i mesta uzimanja uzoraka. Ispitivani pojedinačni sojevi *Azotobacter chroococcum* i *Bacillus megaterium*, kao i njihove kombinacije, delovali su stimulatивно, ali i inhibitorno na brojnost mikroorganizama u rizosfernom i okolnom zemljištu, kod oba hibrida kukuruza. Kod oba hibrida kukuruza je konstatovano povećanje sadržaja azota u rizosfernom zemljištu.

Brojnost mikroorganizama i sadržaj azota u zemljištu je kod oba hibrida kukuruza bila veća u rizosfernom zemljištu.

Veća efektivnost bakterizacije dobijena je kod hibrida PKB-509, a nešto manja kod hibrida Srečko-5.