The influence of some plants from graminaee and vegetables on actinomicaetae quantitative evolution

Borozan Aurica Breica^{1*}, Cojocariu Luminita², Horablaga M.², Misca Corina Dana³, Dogaru Diana³, Bordean Despina³, Moldovan Camelia³

¹Banat's University of Agricultural Sciences and Veterinary Medicine, "King Michael of Romania" Horticulture and Silviculture Faculty; ²Banat's University of Agricultural Sciences and Veterinary Medicine, "King Michael of Romania" Agriculture Faculty; ³Banat's University of Agricultural Sciences and Veterinary Medicine, "King Michael of Romania" Food Technology Faculty

*Corresponding author. Email: borozan_a@yahoo.com

Abstract The actinomicaetae represents a microbial group that are interesting for several domains, including agriculture. These microorganisms were isolated from a eutricambosoil weak gleyed, from Western Romania. Soil samples were taken from experimental barley fields (edafosphere/AS1, rhizosphere /AS7), peas fields (edafosphere/M2, rhizosphere M3), vetch in pods (edafosphere/VS4, rhizosphere /VS6) and barley cultivated after vetch used as green fertilizer (edafosphere/AS5).

After 7 days incubation period, in conditions of pour humidity, there was a significant increase of actinomicaetae from M2 and AS1 variants.

Plants, through root exudats, have a strong effect on soil microbial activity [11], and microorganisms bring benefits to the plants [4].

Although the microbial diversity isn't well known, the soil represents the biggest reservoir of biodiversity [3; 14].

Some authors observed that microorganisms have a essential role in terrestrial ecosystems function because of the macrophytes feedback impact on soil microbiota [1, 17].

For terrestrial ecosystems the main source of organic material with great effect on soil organisms and especially on those from rhizosphere have plants [6; 16].

After Jonas and colab (2004), exudates secreted by roots represents between 1% and 10% from assimilated carbon.

In the present paper studies followed actinomiceatae quantitative evolution as a response to cultivated graminaee and legumes influence.

Material and Methods

The interest microbial group was isolated from a eurotricambosoil weak gleyed, with a very pour humidity factor, from Ghilad, Timis county.

Key words

actinomicaetae, Avena sativa nigrum, Vicia sativa, Pisum sativum, eutricambosoil weak gleyed

Soil samples were taken in the summer time at 0-20cm depth from barley cultivated plots (*Avena sativa nigrum*, edafosphere/AS1 and rhizosphere /AS7), peas (*Pisum sativum*, Amical variety from France, edafosphere/M2 and rhizosphere /M3), vetch in pods (*Vicia sativa*, edafosphere/VS4, rhizosphere /VS6) and barley cultivated after vetch, which was incorporated in soil (edafosphere/AS5).

All 7 soil samples were processed in laboratory conditions.

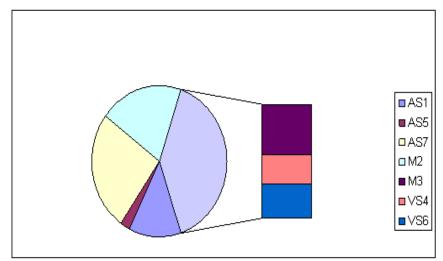
After the humidity degree of each soil sample was investigated, were assembled the experiments in order to determine the quantity of actinomicaete [13].

The specific nutrient medium for actinomicaetae study was Gause no.1, optimal growth temperature was 28°C and incubation time 3 days, respectively 5 days.

Results obtained

Many studies indicated that plants have a great influence on bacterial community from influence plant zone [2; 8; 12], effect that is possible to be determined by species, plant age, depth of root system, root exudates and their composition as well as type of soil [9, 10; 5; 15].

The results obtained after incubation period from working protocol are presented in figure 1 and 2.

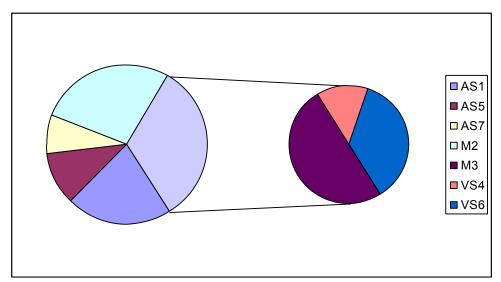


AS1- Avena sativa nigrum (edafosphere); AS7- Avena sativa var. nigrum (rhizosphere); M2-Pisum sativum (edafosphere); M3- Pisum sativum (rhizosphere), VS4-Vicia sativa, (edafosphere); VS6- Vicia sativa (rhizosphere) si AS5- barley grown after vetch (rhizosphere).

Fig. 1 Quantitative evolution of actinomicaetae after 3 days of incubation

As figure 1 shows, there weren't great differences between experimental variants AS1, VS4 and VS6 regarding actinomiceatae number. The greatest number of actinomicaetae was in AS7 variant, the plot where

the first cultivated plant was vetch, and the smallest number of actinomicaetae was in AS5 variant. There were no significant differences between M2 and M3 variants.



AS1- Avena sativa nigrum (edafosphere); AS7- Avena sativa nigrum (rhizosphere) M2-Pisum sativum (edafosphere); M3- Pisum sativum (rhizosphere), VS4-Vicia sativa, (edafosphere); VS6- Vicia sativa (rhizosphere) si AS5-barley grown after vetch (rhizosphere).

Fig. 2 Quantitative evolution of actinomicaetae after 7 days of incubation

As compared to the reduce incubation period (3days), after 7 days of incubation was observed an increase more or less noticeable of actinomicaetae in all experimental variants. The most significant increasing was observed in M2 variant, followed immediately by AS1. The smallest increasing of actinomicaetae was in the AS7 variant. The smallest number of actinomicaetae was isolated in VS6 variant (figure 2).

Conclusions

Although the humidity was very reduced, after 3 days of incubation was highlighted a significant influence of vetch (incorporated in soil) on actinomicaetae from AS7 variant, compared with other studied variants. After 7 days of incubation significant positive modification were observed in peas plot, in the area without root plants influence. After 7 days of

incubation there was a quantitative increasing of actinomicaetae, decreasing from variants M2 and AS1. Comparing with the other studied variants, M3, VS4 and VS6 registered a no significant increasing of actinomicaetae.

On the obtained results, on the type of soil studied in this paper, we can recommend to introduce a rotation of peas and barley cultivated plants.

References

- 1.Brought Lc, Gross KL, 2000,Patterns of diversity in plant in soil microbial communities along a productivity gradient in a Michigan old-field. Oecologia 125:420-427
- 2.Costa, R., Gotz M., Mrotzek N., Lottmann J., Berg G., Smalla K., 2006, Effects of site and plant species on rhizosphere community structure as revealed by molecular analysis of microbial guilds. FEMS Microbiol. Ecol. 56, 236–249.
- 3.Dykhuizen D.E., 1998, Santa Rosalia revisited: Why are there so many species of bacteria? Antonie van Leeuwenhoek 73: 25–33.
- 4.Griffiths, B.S., Ritz K., Ebblewhite N., Dobson. G., 1999, Soil microbial community structure: effects of substrate loading rates. Soil Biol Biochem 31: 145–153
- 5.Hertenberger G., Zampach P., Bachmann G., 2002, Plant species affect the concentration of free sugars and free amino acids in different types of soil. J Plant Nutr Soil Sci 165: 557–565
- 6.Insam H., Domsch K.H., 1988, Relationship between soil organiccarbon and microbial biomass on chronosequences of reclamation sites. Microb. Ecol. 15: 177–188.
- 7.Jones, D.L., Hodge, A., Kuzyakov, Y., 2004, Plant and mycorrhizal regulation of rhizodeposition. New Phytol. 163, 459–480.

- 8.Kowalchuk, G.A., Buma, D.S., de Boer W., Klinkhamer P.G.L., van Veen J.A., 2002, Effects of above-ground plant species composition and diversity on the diversity of soil-borne microorganisms. AV Leeuwenhoek Internat. J. Gen. 9.Mol. Microbiol. 81, 509–520.
- 10.Lupwayi N.Z., Rice W.A., Clayton G.W., 1998, Soil microbial diversity and community structure under wheat as influenced by tillage and crop rotation. Soil Biol Biochem 30: 1733–1741.
- 11.Lynch J.M., Whipps J.M., 1990, Substrate flows in the rhizosphere. Plant Soil 129: 1–10.
- 12.Miethling R., Wielan G., Backhaus H., Tebbe C.C., 2000, Variation of microbial rhizosphere communities in response to crop species, soil origin and inoculation with Sinorhizobium meliloti L33. Microb Ecol 41: 43–56
- 13. Smalla K., Wieland G., Buchner A., Zock A., Parzy J., Kaiser S., Roskot N., Heuer H., Berg G., 2001, Bulk and rhizosphere soil bacterial communities studied by denaturing gradient gel electrophoresis: plant-dependent enrichment and seasonal shifts revealed. Appl. Environ. Microbiol. 67, 4742–4751.
- 14.Stefanic Gh., 2006, Probleme de agrofitotehnie teoretica si aplicata. ICDA Fundulea, XXVIII, pg.1-78 15.Torsvik V., Goksoyr J., Daae F.L., 1990, High diversity in DNA of soil bacteria. Appl. Environ. Microbiol. 56: 782–787.
- 16.Yang C.H., Crowley D.E., 2000, Rhizosphere microbial community structure in relation to root location and plant iron nutritional status. Appl Environ Microbiol 66: 335–351.
- 17. Wardle D.A., 1992, A comparative assessment of factors which influence microbial biomass carbon and nitrogen levels in soil. Biol. Rev. Cambridge Phil. Soc. 67: 321–358.
- 18.Yin B., Crowley D., Sparovek G., De Melo W.J., Borneman J., 2000, Bacterial functional redundancy along a soil reclamation gradient. Appl Environ Microbiol 66: 4361–4365.