THE VARIATION OF ACTINOBACTERIA SPECIES FROM A *VICIA SATIVA* CULTIVATED SOIL MICROHABITAT

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ABSTRACT
Actinobacteria is a fairly complex group, intermediate between bacteria and filamentous fungi involved in producing some infection, in the case of pathogenic strains and recycling of organic matter, as in the case of nonpathogenic actinobacteria. Literature data have surprised many plant-microorganism interaction, on the one hand making reference to the mineralization processes involving microorganisms by whom plants necessary nutrients are released, and on the other hand underlines the influence of plants on the quantity and quality of microbial population in root area as a result of exudates removed in the natural environment.

Actinobacteria from *Frankia* genus are counted among bacteria being able to fix nitrogen, and those from the genus *Streptomyces* are major producers of antibiotics and numerous secondary metabolites. This paper presents the study of the composition of Streptomyces genus actinobacteria community from a moderately gleyed eutricambosoil, grown with vetch (*Vicia sativa*). The soil is located in the western part of Romania. Biological material sampling was conducted in October, the depth of 0-20 cm. Isolation and studies of this bacterial group were performed "*in vitro*", on Gause 1 culture media. Actinobacteria were collected from four areas (biotopes): the plot uncultivated with *Vicia sativa* (control variant), the far rhizospheric area, the hairy root and root areas of vetch plant. Based on effectuated observations, it was noticed that soil microhabitats contain a variety of actinobacteria and *S. albosporeus, S. aureus, S. griseus, S.albus, S. nigrescens, S. lavenduleroseus, S. helvolus*. Numerically dominant species in tested soil samples are: *S. griseus, S. albus* and *S. albosporeus.*

Keywords: actinobacteria, *Vicia sativa*, hairy root area, the root area, far rhizospheric area

INTRODUCTION

In general, rhizosphere represents a specific group of microflora around the roots of living plants (STEFANI AND SANDOIU, 2011). This area is clearly distinguished from the bulk soil by pH, oxygen quantity, redox potential, and also by availability of nutrients and water (HINSINGER ET AL., 2009). So it is known that plant roots affect the living environment of soil microbiota, interaction that has a great impact on plant development (LAMBERS ET AL., 2009; PINTON ET AL., 2007).

Although the competition for some factors such as for N and water can reduce the microbial activity in rhisosphere, the presence of C in root exudates stimulates the microbial segment (BUTLER ET AL., 2004). According to the literature, in plants rhisosphere the Gram-negative bacteria are more common (PRIHA ET AL., 1999, BUTLER ET AL., 2003; TREONIS ET AL., 2004, PATERSON ET AL., 2007).

Actinomycetes are a complex group of prokaryotes, present in different environments both in vegetative form but also as spores. Some actinomycetes produce terpenoids and pyrazines which can affect the taste and odor of drinking water (ZAITLIN AND WATSON, 2006).

Actinomycetes are of socio-economic important, cause various human infections (BERKOW AND FLETCHER, 1992), are among the few microorganisms capable of degrading hardly biodegradable compounds, are involved in recycling nutrients, nitrogen fixation (HUSS-DANELLA, 1997), production of antibiotics (GOODFELLOW AND O'DONNELL, 1989) and various secondary metabolites.

SHARMA ET AL. (2005) have used molecular techniques to study bacterial community from the rhisosphere of three leguminous species (*Vicia faba* L., *Pisum sativum* L. and *Lupinus albus* L.). The study found that in the rhisosphere of three leguminous the actinomycetes species dominated and were followed by proteobacteria.

Rhizosphere microorganisms mediated by root exudates play an important role in soil carbon flux, but information about active organisms community involved or the influence of environmental conditions on them are limited (RANGEL-CASTRO ET AL., 2005).

Studies referred to the composition of actinobacteria from medium as soil, water, and antibacterial and antifungal activity of actinomycetes strains were made by KITOUNI ET AL. (2005). From actinobacteria strains identified by the authors mentioned above, 93% belong to the *Streptomyces* genus, and 7% were classified in the *Actinomadura* genus.

In this study we followed the qualitative changes in the balance of microbial segment, respectively of *Streptomyces* genus actinobacteria, due to the influence of root exudates of *Vicia sativa* legume species.

MATERIAL AND METHODS

The studied soil is a moderately gleyed eutricambosoil and originates from the western part of Romania. In autumn and spring seasons the soil was covered with species of vetch (*Vicia sativa*). Samples were collected in October, from 0-20 cm depth from the far rhizosphere area, from the hairy root and root areas of legume crop and from a vetch uncultivated parcel (control variant).

Study and identification of actinobacteria species was performed "*in vitro*" on Gause 1 culture media (STEFANIC, 2006), based on the identifying key after Gause. Actinobacteria species have developed after 72 hours at a temperature of 28°C.

The results were statistically analyzed with PAST 2.14 software (HAMMER ET AL., 2001).

RESULTS

Abundance and range of actinobacteria species identified in the four studied distinct soil biotopes are shown in the figures below.

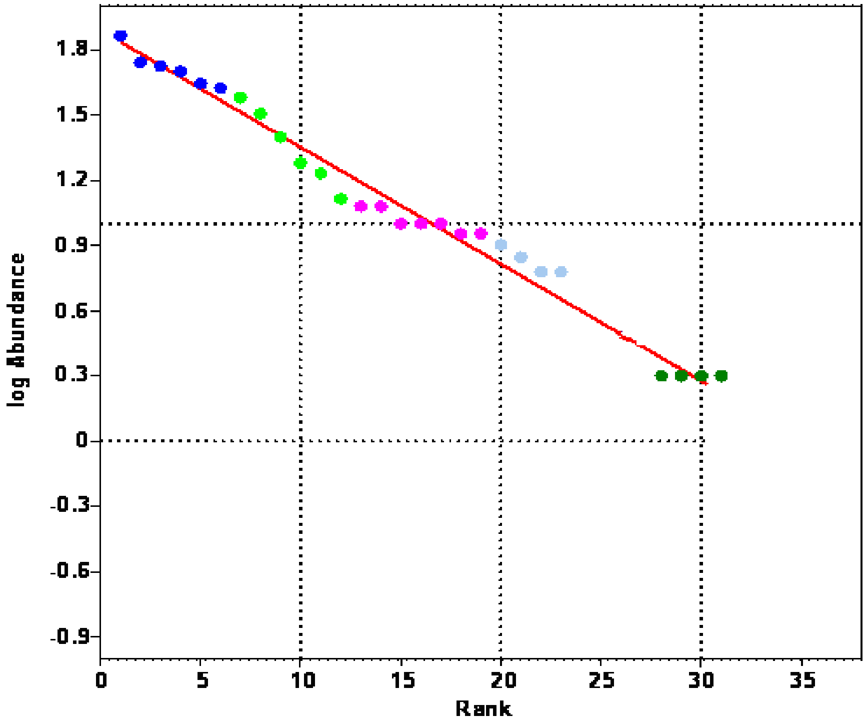

Figure 1. Abundance of actinobacteria species in the studied soil

The largest number of actinobacteria was recorded in the far rhizospheric area removed, followed by the root area, the control variant and the hairy root area (*Figure 1*).

Great abundance of actinomycetes in mature legumes rhizosphere may be linked to the improvement of soil and to the possibility of using legumes as biofertilizers (SHARMA ET AL., 2005).

By summing the species identified in the four areas of soil, *S. albus* dominate, followed by the species *S. albosporeus*. Besides these species, other species are present (arranged in descending order): *S. griseus*, *S. chrysomallus*, *S. aureus*, *S. lavenduleroseus*, *S. helvolus* and *S. nigrescens*.

The species *S. albus* and *S. griseus* are present in control variant, root area, hairy root area and far rhizospheric area.

Rhizosphere microbial community may differ or not compared to the soil microbial load (MOUGEL ET AL., 2006, KANDELER ET AL., 2002). Also, there may be differences between the microflora present in plants rhizosphere, grown on the same soil (MARSCHNER ET AL., 2004, KOWALCHUK ET AL., 2002).

S. nigrescens species was evident only in the hairy root area and *S. chrysomallus* was highlighted in the far rhizospheric area.

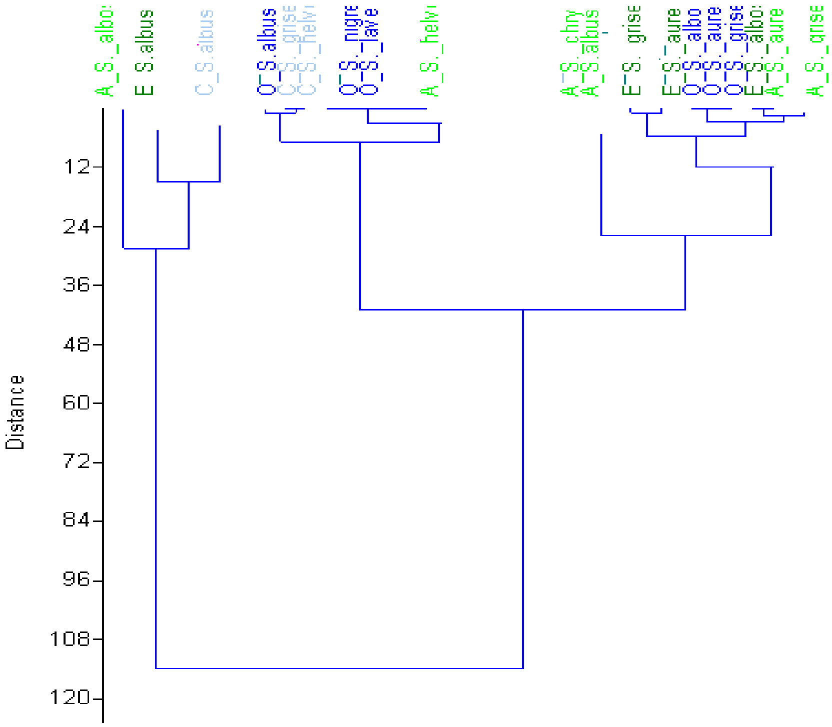

Figure 2. Cluster analysis of actinobacteria species present in analyzed biotopes
(O-hairy root area; A- far rhizospheric area, C-control variant, E-radicular area)

According to the cluster analysis, actinobacteria species were included in two groups. In the first group *S. albosporeus* species is present isolated from the far rhizospheric area and is quantitative different from all species in analyzed biotopes, but also against *S. albus* species, identified in control variant and root area, even if they are included in the same group.

The second group includes the following distinct subgroups:

Subgroup 1a: *S. albus* species (hairy root area) quantitatively dominating other sub-species (*S. griseus* and *S. helvolus*).

Subgroup 1b: *S. helvolus* species along with the species: *S. nigrescens* and *S. lavenduleroseus*.

Subgroup 2a: *S. chrysomallus* and *S. albus* (far rhizospheric area), plus *S. griseus* and *S. aureus* species (root area), the species: *S. albosporeus*, *S. griseus* and *S. aureus* in the hairy root area followed by species: *S. albus* (the root area) and *S. griseus, S aureus* isolated from the far rhizospheric area.

From *Figure 2* results that even if the species are listed together in the same groups and subgroups, they quantitatively differ among them.

Differences between abundance and composition of soil microbial community and rhizosphere, or among different plants rhizosphere is strongly influenced by the quantity and quality of the rhizodeposit (VESTERGARD ET AL., 2008).

CONCLUSIONS

It is known that the actinobacteriile dominate especially in the far rhizospheric area, demonstrated by this study to.

Actinobacteriile are found in abundance in the far rhizospheric area. The lowest number of actinobacteria species was identified in the hairy root area.

The species present in all analyzed biotopes are: *S. albus* and *S. griseus*.

The species quantitatively distinguished when compared with all highlighted species is *S. albus*.

According to the cluster analysis, *S. albosporeus* isolated from the far rhizospheric area, clearly distances from all subgroups where studied species were framed.

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