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INFLUENCE OF DIFFERENT AGRICULTURAL MANAGEMENT PRACTICES ON SOIL MICROBIOME

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Abstract

Microbiomes are the collection of all microbial inhabitants of a given system. At the level of the soil, the microbiome includes four major groups of microorganisms: bacteria, fungi, archaea, and protozoa, as they are the main organisms for essential soil processes such as nutrient cycling, decomposition of organic matter, and plant growth promotion. A healthy soil microbiome is essential for sustainable agriculture and the overall health of terrestrial ecosystems. Some agricultural management practices, i.e. irrigation, can have a significant impact on the soil microbiome. The quality and quantity of irrigation water can affect the abundance and diversity of microorganisms in the soil. For example, excess irrigation can lead to waterlogging, which can create anaerobic conditions that favour the growth of certain types of bacteria. On the other hand, irrigation water in the right amounts can have a positive impact on the soil microbiome and promote plant growth. To test this hypothesis in the agricultural year 2022, a research was carried out on maize and soybean grown under irrigated conditions, to analyse the variations of microbial density during the vegetation period.

Key words*: soil microbiome, soil bacteria communities, soil microbiota.*

INTRODUCTION

Soil microorganisms are essential to the environment, playing an important role in keeping the environment healthy and productive (Chaparro et al., 2012). One of the main activities carried out by microorganisms in the soil is represented by the decomposition of organic matter (Xu et al., 2015). By carrying out this process in the soil, nutrients are released which are then available to be used by plants, but also by other microorganisms (Osorio Vega, 2007; Jacoby et al., 2017). Some soil microorganisms are involved in nitrogen fixation, a process by which atmospheric nitrogen is converted into a form that plants can use. This is important because plants need nitrogen to grow and develop (Mus et al., 2016; Soumare et al., 2020). In addition to the role they play in fixing nitrogen and bringing it into forms easily accessible to plants, microorganisms also play an important role in the solubilisation of phosphorus (Alori et al., 2017; Ingle et al., 2017; Rawat et al., 2021) and potassium (Sharma et al., 2016; Bahadur et al., 2016; Ahmad et al., 2016). Also, soil microorganisms are essential to the environment due to their role in promoting plant growth and various biophysical processes (Prasad et al., 2015; Basu et al., 2021). Soil microbiome exhibit natural seasonal dynamics and their biodiversity, abundance, and functions are influenced by various factors including crops, climatic conditions, and agricultural management practices, i.e. tillage systems, fertilizers, pesticides and irrigation regime (Entry et al., 2008; Geisseler et al., 2014; Gafencu et al., 2021).

The objective of this paper is to test the hypothesis that agricultural management practices (i.e. use of irrigation water) lead to changes in the composition and abundance of the soil microbial community.

MATERIALS AND METHODS

The field experiment was conducted at Agralmixt S.A. farm, in North-Eastern Romania, Iasi county, Andrieseni village ($47^0$34'9" N, $27^0$20'38" E, 60 m above sea level). Prior to the experiment establishment, the tillage was carried out by using a scarificator at ~30 cm depth, then was followed by the preparation of the germinal

bed by passes with the seed bed combination system. Soybean (*Glycine max* L.) and corn (*Zea mays* L.) were the crops taken for investigation. Cultivation technology was represented by conventional technology, chemical fertilizers were used and, applied before soil tillage. During the vegetation period, plant protection products were also applied.

During corn and soybean vegetation period a quantity of 200 l/m^2 water was applied to cover the needs of the crops.

The regional climate is a typical temperate continental climate. The average annual temperature is ~9.5^{0}C, with extremes ranging from 40.0^{0}C to -35.0^{0}C (Gafencu, 2019). The annual precipitation is ~520 mm. Significant deviations from the long-term average precipitation and temperature have been observed in the last 10 years. The soil texture is primary clay-loam and the natural vegetation of the site is silvo-steppe.

The soil samples were taken from two agricultural plots cultivated with maize (*Zea mays* L.) and soybean (*Glycine max* L.).

From each plot, 10 points were randomly selected from where soil samples were taken, the entire area of the plots being covered.

Soil samples were taken from three different depths: 7-10 cm, 10-20 cm, and 20-30 cm, using sterile sampling tools. The soil samples were taken six times during the vegetation period of the maize crop, between May and October 2022. Soil samples were transported to the microbiology laboratory, stored overnight at 4^{0}C, dried at room temperature and sieved (2-mm mesh) prior to further use in the experiment.

The total number of bacterial colony forming units (CFUs) was determined by serial dilution method and plating into nutritive media on PDA (Potato Dextrose Agar medium) in different compositions: classic and with streptomycin. Streptomycin (35 mg·L^{-1}) is an antibiotic that has been used to inhibit the growth of Gram negative bacteria.

From the collected samples, successive dilutions were made in sterile water, using a dilution coefficient in the rate of 10 (dilutions 10^{-1}, 10^{-2}, … , 10^{-6}). By this technique a series of dilutions are obtained in which the number of germs decreases in arithmetic regression. To prepare these dilutions, 9 ml of double-distilled water sterilized at 120°C for 30 minutes was distributed in sterile tubes of 15 ml capacity. One g of soil was weighed onto a sterile watch glass and placed in the first dilution tube. After vigorous stirring for five minutes a 10^{-1} (1/10) dilution was obtained. From this dilution, 1 ml of suspension was transferred to another test tube with 9 ml of sterile water, obtaining the dilution 1/100 (10^{-2}). The same way the other dilutions were obtained. 1 ml of suspension from each dilution was introduced into a Petri dish (Gafencu et al., 2022). After 24 h at 28^{0}C, the colonies were counted. Using Scan 1200 colony counter, the bacterial colonies that formed on the medium were counted. To determine the number of bacteria in one gram of soil, the number of colonies that developed in Petri dish was multiplied by the inverse value of the dilution. The count result was related to the dilution used and the final result was expressed in colony forming units (CFUs) per 1 g of soil.

RESULTS AND DISCUSSIONS

Some recent studies on the impact of irrigation water on soil microbiota have shown that water has a positive effect on the structure, abundance and activities of soil microbial communities (Entry et al., 2008).

Following the changes in the abundance and structure of soil microbial communities during the growing season of maize (Figure 1) and soybean (Figure 2) it is observed that the dynamics of bacterial communities follows an increasing trend from May to October. Analysing the results, it can be seen that from the time of sowing until May, the numerical density of bacteria decreased in the case of both crops. This was due to the fact that in the first part of the vegetation period the microbial community was influenced by the phytosanitary treatments applied to the crops.

After the sampling carried out in May, the crops were irrigated. Starting from this moment, in the case of maize crop, the bacterial abundance increased until September, the month in which the last irrigation was applied. In October, there was a slight reduction in the number of bacteria in the soil. In addition to the evolution of the abundance of bacteria in the soil, the changes that take place at different depths were also analysed.

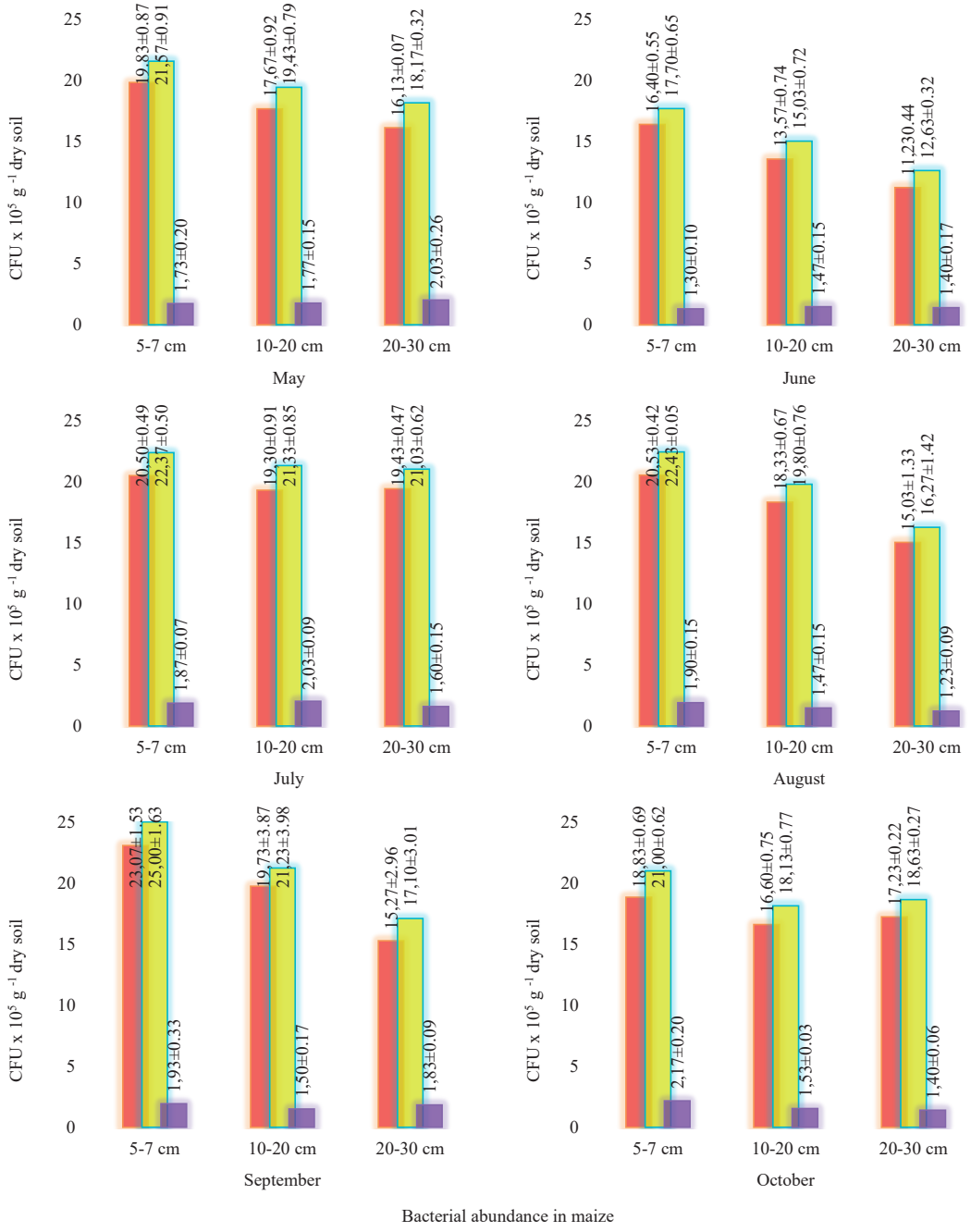


Figure 1. Changes of soil bacterial counts and incidence during the maize growing season

Under this aspect, it can be observed that at 20-30 cm depth, in May there were 18.17 ± 0.32 CFU x 10^5 g^{-1} dry soil. In June, the number of bacteria decreased, and starting from July, when the peak of the increase in the abundance of total number of bacteria was observed, and until

October, the number of bacteria followed an increasing trend. In the case of the soybean crop, the total number of soil bacteria fluctuated during the growing season.

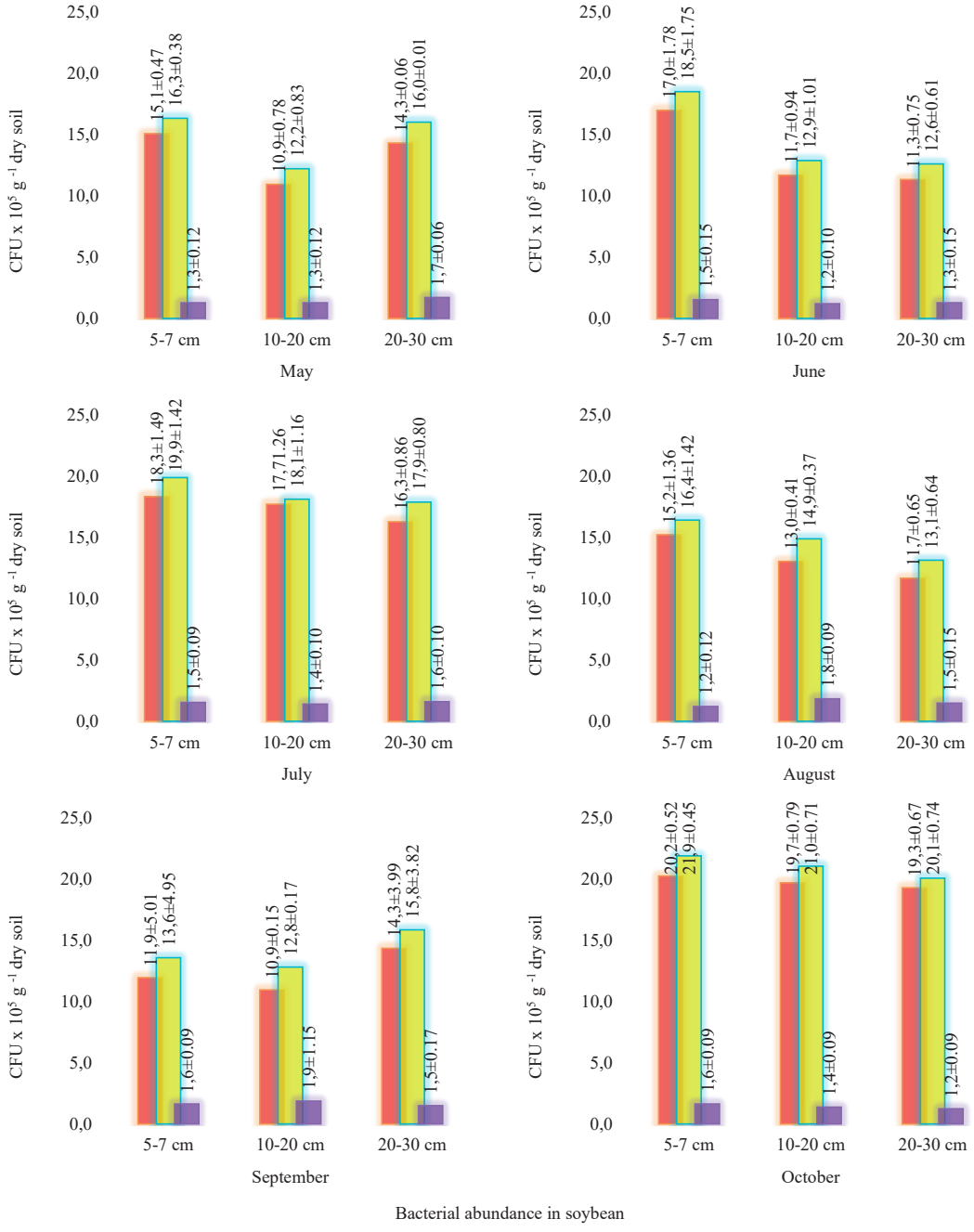
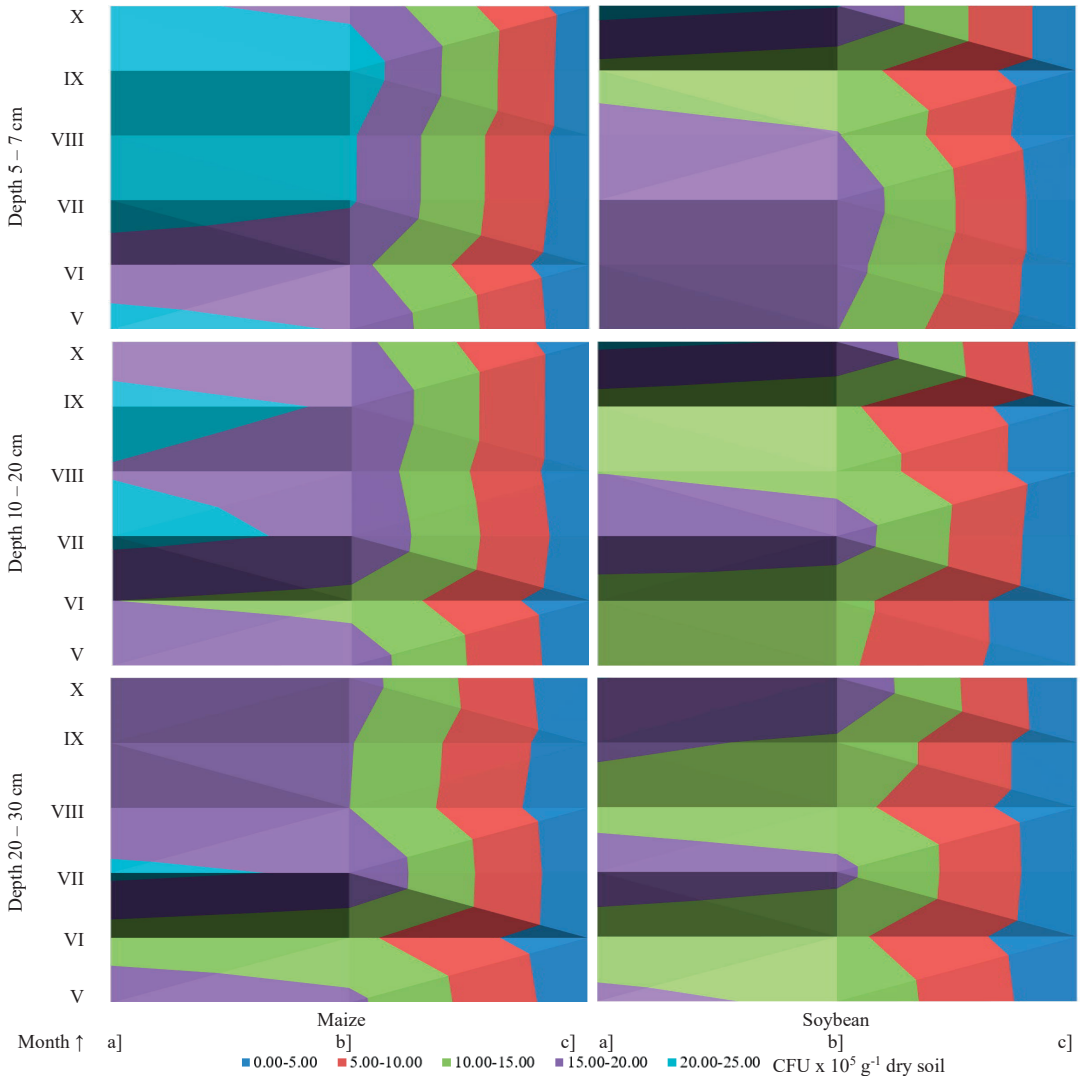


Figure 2. Changes of soil bacterial counts and incidence during the soybean growing season

After the sampling carried out in May, the soybean crop was irrigated and the numerical density of the bacteria increased until July. In August, the total number of bacteria decreased, then increased in September and October, when the highest value was recorded, i.e. 21.90±0.45 CFU x 10^5 g^{-1} dry soil. Both in maize and soybean crops the total number of bacteria increased till the end of the vegetation period at 10-20 cm depth, respectively 20-30 cm. Analysing the effect of seasonal variation on soil bacterial communities, it was observed that Gram-negative bacteria dominated soil bacterial communities (Figure 3).



a] Total number of bacteria (CFU x 10^5 g^{-1} dry soil); b] Gram-negative bacteria (CFU x 10^5 g^{-1} dry soil); c] Gram-positive bacteria (CFU x 10^5 g^{-1} dry soil)

Figure 3. Differences between the abundance of soil bacterial communities during the vegetation period in maize and soybean crops

Analysing the evolution of the numerical density of bacteria, it was observed that in the case of maize crop, the abundance recorded higher values compared to the soybean crop. Regarding the ratio between Gram-negative bacteria and Gram-positive bacteria, it was observed that this ratio remained unchanged throughout the vegetation period, a situation encountered in the case of both crops.

CONCLUSIONS

Following the study, changes were observed in the abundance and structure of soil microbial communities. In the 5-7 cm soil layer, during the entire vegetation period, the highest values of the numerical density of the bacterial communities were recorded. This trend is typical, representing the normal evolution of bacterial communities in the soil, from the time of sowing to the time of crop flowering, the growth being relatively constant. An important aspect is represented by the fact that the microbial communities underwent changes in the 10-20 cm and 20-30 cm depth ranges. This is important because increasing the density of microbial communities at greater depths can have a positive effect on soil and soil processes, as well as plant health and development.
These results represent an important starting point for future research on the influence of irrigation water on soil microbiota.

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