The Effect of Conventional and Conservative Tillage Systems on Microbial Community Composition and Physiological Activity in Soils from Bărăgan Plain

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ABSTRACT

The paper aimed to present the results of research carried out on size, taxonomic composition and physiological activity of soil microbiota for assessing the effect of classic (conventional) and conservative (minimum tillage) agriculture systems applied in a zone affected by aridification from Bărăgan Plain. Significant differences concerning the quantitative parameters characterizing the bacterial and fungal communities from the two soil systems of tillage have been evidenced. Total counts of bacteria doubled and total counts of fungi was with one order of magnitude higher in soil minimum-tilled than in soil under conventional tillage system. Soil respiration values registered for both conservative and conventional systems are considered to characterize high levels of microbial physiological activities, with slightly higher values for minimum tillage system application than for conventional system. The beneficial effect of conservative system was evidenced by higher values of diversity indices registered for both bacterial and, especially fungal communities, as compared with those characterizing the communities from soil under conventional tillage system. The minimum tillage system favoured the increasing of abundance and diversity of actinomycetes, the dominance of Pseudomonas and Bacillus bacterial species and fungal species belonging to genera Aspergillus, Trichoderma, Mortierella and Paecilomyces in composition of soil microbiota, with multiple roles in main soil processes: decomposition of vegetal residues, synthesis of humus precursors, carbon sequestration, alleviation of various abiotic stress (drought, salinity), increasing accessibility of nutrients for plants, yields, biocontrol of plant pathogens.

Keywords: minimum tillage, conservative agriculture system, microbial communities, biodiversity, soil respiration.

INTRODUCTION

The quality of soil, as a system of complex habitats, is mainly influenced by its structure, productivity and human activity (Janusauskaite et al., 2013; Bartha et al., 2021). Bulk density, water holding capacity, good infiltration rates, soil porosity, but also high levels of organic matter and beneficial soil microorganisms are taken into account as indicators of soil quality (Wiesmeier et al., 2019).

Tillage as a management practice affects the physical-chemical and biological parameters of the soil (Burtan et al., 2023). Despite the multiple economic and environmental benefits of minimum tillage

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(MT), adoption of the system is still low due to lower crop yields than conventional tillage (CT) due to soil compaction, germination problems, residue management, increased incidence of weeds and pathogens.

Despite all these drawbacks, application of non-tillage (NT) and medium tillage (MT) systems causes increases in the organic carbon (C) content, positively influencing both the soil structure and the activity of the soil microbiota. The major role of soil microorganisms in edaphic processes, but also the effect of processing systems on soil organic matter (OM) appears more evident after a period of several years after their consistent application. In general, the studies on the behaviour of the bacterial and fungal microflora, revealed a more abundant development under MT and NT treatments than in the conventional one (CT) (Xia et al., 2019).

Understanding the effects of tillage on soil microbial communities is important for establishing their functions in order to improve or maintain stability in agroecosystems (Fu et al., 2000; Guttières et al., 2021; Trivedi et al., 2021).

Microbial activity, compared to other parameters, responds more quickly to various disturbances. As a result, a number of microbiological properties have been suggested as potential indicators of soil quality due to their increased sensitivity and rapid response to soil management changes (Hermans et al., 2017; Fernanda et al., 2021). The influence of tillage on microbial communities has been the subject of many scientific works in which comparative studies have been carried out on quantitative changes of the number of microorganisms, soil microbial community composition, microbial biomass, potential level of respiration and enzymatic activities (Feng et al., 2003; Li et al., 2015; Souza et al., 2018; Sainju et al., 2021).

The main difficulties in the use of microbial indicators are the absence of data on the relationships between the characteristics of soil microorganisms, soil management, the reference value and, respectively, the limits of the indicators used. For soil management, it is essential to study the effects of soil conservative works on the microbial characteristics (Wagg et al., 2019).

Tillage contributes negatively to soil quality because it causes soil fracturing, disruption of soil structure, acceleration of surface runoff, increased soil erosion, and reduced crop residues (Çelik et al., 2021). In addition to its major impact on soil quality, the tillage system also influence the quality of the water in the upper layer, the wear and tear of the machines and the work requirements, so that before the initiation of soil processing, the impact of the frequency of their application on the above mentioned quality characteristics must be taken into account. Sediments from increased soil erosion are also a major factor for altering water quality because nutrients transported from the field by surface water led to its eutrophication.

Frequent soil works, carried out over several seasons, cause the appearance of serious problems due to the partial/total destruction of the soil structure. Microorganisms can be affected being registered a lower microbial activity, the reduction of microbial network complexity and of the abundance of keystone taxa (Banerjee et al., 2019) caused by the appearance of closed pores that alter infiltration, increased runoff, decreased productivity, and moderately increased erosion. Over time, the yield decreases, due to the loss of nutrients and organic matter, as well as the deterioration of edaphic properties. Continuing in such a direction will generate a total destruction of the soil structure and its general qualities, with the development of hardpan, with the reduction and blocking of root elongation, with the determination of major effects on the growth and development of the crop (Van Den Putte et al., 2010). At this evolutionary moment high rates of erosion occur, with loss of fertility levels and advanced soil degradation due to loss of organic matter.

If the unfavourable conditions are accentuated by the presence of coarse sand, gravel, high soil density or limited rooting depth, the possibilities of recovery of production losses are reduced.

Soil degradation observed in cultivated land is mainly due to conventional practices (CT) applied for the purpose of agricultural soil processing. In such conditions, it appears vital to apply a sustainable management, by adopting methods to conserve the soil and reduce its erosion (Diaz de Otalora et al., 2021; Fenster et al., 2021).

Studies in the field have highlighted the advantages of applying minimal tillage systems, namely the reduction of erosion, better infiltration and retention of water in the soil, increase in the content of organic matter, microbial diversity and activity, reduced costs and working time, increases in yields (Chețan et al., 2022; Francaviglia, et al., 2023). The research aimed to assess the effect of classic (conventional) and conservative (minimum tillage) agriculture systems applied in South region of Bărăgan Plain on size, taxonomic composition and physiological activity of soil microbiota.

MATERIAL AND METHODS

Research has been carried out in T.A.U. Gura Ialomitei, Ialomita County which is located in a zone affected by aridification from Bărăgan. Due to insufficient precipitations that are not able to assure the necessary water in soil, and to the permanent presence of wind causing soil compaction, erosion and drying phenomena, desertification is the main natural risk factor. Samples (0-10 cm depth) have been taken from two soils cultivated with maize (Zea mays L.) under application of conventional (plowing at 25 cm with plough, discing with disc harrow, sowing and harvesting) and conservative (minimum tillage: shallow cultivation with Vogel noot cultivator, sowing with Monosem seed drills and harvesting with Claas Dominator combine) systems, in August 2023.

Mollic Gleysols (WRB, 2014) from conventional system presented the following characteristics: pH low alkaline (8.17); low humus content (2.49%); moderate total N content (0.171%); moderate available phosphorus content (P_{AL} 30 mg x kg⁻¹); high available potassium content (K_{AL} 222 mg x kg⁻¹); degree of base saturation (V100%) is moderate eubasic; texture - medium loam; total soluble salts content 150 mg x 100 g⁻¹ soil (not salinized).

Mollic Salic Gleysols (WRB, 2014) from conservative system presented the following characteristics: pH low alkaline (7.98); low humus content (2.55%); moderate total N content (0.190%); moderate mobile phosphorus content (P_{AL} 26 mg x kg⁻¹); high mobile potassium content (K_{AL} 253 mg x kg⁻¹); degree of base saturation V100% (eubasic); texture - loamy clay; total soluble salts content 245 mg x 100 g⁻¹ soil (low salinized). Soil samples have been analysed according to the specific methodology described in the manual utilized in soil monitoring system for chemical and microbiological analysis (Dumitru and Manea, 2011).

Microbiological parameters were assessed by plating soil serial dilution on solid agar culture media: Nutrient agar (NA, Difco) for Total Number of Bacteria-TNB and potato-dextrose agar (PDA, Merk) for Total Number of Fungi-TNF. Taxonomic composition of microbial communities was identified by morphologic criteria (under a MC5.A optic microscope) and specific manuals for heterotrophic aerobic bacteria (Bergey and Holt, 1994) and for fungi (Baron, 1968; Domsch and Gams, 1970; Watanabe, 2002).

The global physiological activity of microbiota as an indicator expressing the quantity of CO_2 released by soil microbial communities was assessed by substrate induced respiration (SIR) method. Species richness or total number of species (S), in microbial communities from soil was determined and microbial diversity assessed by calculating Simpson diversity index (D) (Mohan and Ardelean, 1993).

RESULTS AND DISCUSSION

Analysis of results presented in Table 1 reflects significant differences concerning the quantitative parameters characterizing the bacterial and fungal communities from the two soil systems of tillage, with total counts of bacteria doubled and with one order of magnitude higher for total counts of fungi in soil minimum-tilled than in soil under conventional tillage system. Though, the influence on global physiological activities was less, with values of soil respiration slightly higher in the minimum tillage system application (89.983 mg CO₂ x 100 g⁻¹ soil) than in conventional system (88.043 mg CO₂ x 100 g⁻¹ soil).

Generally, respiration soil values registered for both conservative and conventional systems are considered to characterize high levels of microbial physiological activities.

Conservative system favoured the development of high numeric effectives of bacteria and fungi as compared with classical

one, where both groups of microorganisms developed less numerous effectives, considered as being of moderate level.

Table 1. The total counts of bacteria, fungi and soil respiration from conservative and classic systems of tillage

Tillage system	Soil respiration (mg $CO_2 \times 100 \text{ g}^{-1}$ soil)	TNB $(x \ 10^6 \text{ viable cells } x \ g^{-1} \text{ d.s.})$	$\frac{\text{TNF}}{(\text{x } 10^3 \text{ cfus x } \text{g}^{-1} \text{ d.s.})}$
Minimum tillage	89.983	24.888	139.500
Conventional tillage	88.043	11.957	49.964

The high level of microbial counts from conservative system is explained by agrochemical features revealing a higher content of available major elements in the surface soil layer (0-20 cm), even though it is weakly salinized as compared with soil worked in conventional tillage system.

The results are concordant with literature (Wang et al., 2017). Similarly, results of Sharma et al. (2011) revealed the beneficial effect of conservative tillage, optimal water and organic nutrient supply manifested by enhanced soil microbial activities during wheat (*Triticum aestivum* L.) cultivation. Roldan et al. (2005) reported increased soil enzyme activities as effect of conservation tillage practices in sorghum cultivation under subtropical conditions.

Microbial biomass C and soil respiration, [as an energy-producing process, evaluating the amount of carbon dioxide (CO_2) released following the decomposition of soil organic matter (SOM), through soil microbiota, plant roots, soil micro- and meso-fauna] are important indicators of soil microbial characteristics. Soil respiration is also one of the biological indicators of soil health (Bagnall et al., 2023), of the activities of living microorganisms, which reflects the presence of carbon (C), the cycle of nutrients in the soil, as well as the essential elements available for plants (Sciarappa et al., 2016).

A wide range of factors (e.g., moisture, temperature, porosity, soil type, spatiotemporal variations, C supply, microbial biomass and enzyme activities) intervene in affecting the amount and rate of soil respiration (Qu et al., 2023), as well as: tillage, crop type, crop residue amount, C:N ratio, N fertilization and soil management practices affecting SOM, soil moisture, aggregation and pH (Gelybó et al., 2022).

The relationships between the potential level of soil respiration and soil properties are complex and identifying the determinants of soil respiration is important for the provision of ecosystem services, food security, agricultural sustainability, climate change mitigation and agricultural management (Wu et al., 2018; Adhikari et al., 2022; Ciornei et al., 2023). Minimum tillage (MT) has become a soil conservation management practice with known advantages and disadvantages for agriculture, but the short- and long-term effects of MT on the soil microbiome are not well established.

Thus, in some studies, conventional practices (CT) were compared with minimal practices (MT), over a longer period of time (3 years). Edaphic properties were assessed as well as soil microbial community structure to analyse tillage effects (Kraut-Cohen et al., 2019). The results revealed significant changes in the physical-chemical properties of the soil, but also a significant increase in the level of hydrolytic and redox microbial activities.

The structure of microbial communities in MT significantly diversified compared to that in CT. Application of repetitive soil work caused significant changes in the relative abundance of microorganisms at the taxonomic level.

However, no significant differences were found between treatments regarding alpha diversity of microbial communities, and higher levels of pests were identified in MT. Thus, tillage had an important role in shaping the structure of microbial communities but also environmental, ecological and agricultural parameters. In general, conventional tillage (CT) causes disturbances in the upper soil horizon, generating relatively uniform physical and nutrient distribution characteristics, practically a homogeneous layer.

This type of work also affects the chemical properties of the soil, causes the quantitative decrease of organic matter, changes the composition of bacterial and fungal communities, reduces the level of edaphic biodiversity and increases the total counts of aerobic microorganisms (Schmidt et al., 2018; Sun et al., 2018; Xin et al., 2018).

In contrast, when cultivating MT, no major disturbances occur in the soil, it is enriched with nutrients and organic matter, erosion is reduced, water availability is increased, and moisture and temperature are stabilized (Guo et al., 2016). Thus, MT stabilizes stratifies and the edaphic environment for soil microorganisms, micro- and meso-fauna (Tsiafouli et al., 2015). Also, compared to CT soils, soils under a NT or MT practice show significant increases for substrate-induced respiration, microbial biomass, various enzyme activities, organic carbon level, nitrogen mineralization, total nitrogen and potential nitrification (Mathew et al., 2012; Wang et al., 2017, 2018; Wagg et al., 2018).

Other studies highlight the fact that, following NT or MT practices, organic carbon can be distributed differently throughout the soil profile, vs. CT.

CT significantly influences the composition of the community and the level of microbial activities, thus in a short time, the soil properties differ from those determined in MT and NT soils, by reducing the activities in CT soils compared to MT, a trend that increases over time.

In addition, a correlation of potential microbial activity measurements with MT and NT communities appears. It can be considered that conservative practices were beneficial for soil quality, maintaining soil microbial activities at high levels.

The findings of high levels of microbial activities in MT soil are also consistent with experimental studies that showed that microbial activity was lower in CT soils compared to reduced cultivation (MT, NT) systems (Souza et al., 2018).

Taxonomic composition of bacterial community from soil under minimum tillage (Figure 1 and Figure 2) consisted from 12 species, the most abundant being Pseudomonas fluorescens and **Bacillus** circulans (A=16% each), followed by Pseudomonas aurantiaca and Micrococcus roseus (A=12% each).



Figure 1. Composition and species relative abundance of bacteria in soil under minimum-tillage system

Actinomycetes were present as a group belonging to 4 series, with a higher abundance cumulated in community composition than in bacterial community from conventional system.



Figure 2. Bacteria from minimum-tillage system

Bacterial community from conventional system (Figure 3 and Figure 4) included 8 species, half of them with equal abundances of 17%, represented by *Pseudomonas fluorescens, Bacillus circulans, Bacillus* *cereus* var. *mycoides* and actinomycetes from Series Albus, accompanied by other species of the genus *Pseudomonas, Bacillus* and *Arthrobacter* (with A=8% each).



Figure 3. Composition and species relative abundance of bacteria in soil under conventional tillage system

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Figure 4. Bacteria from conventional tillage system

Differences induced in taxonomic composition of bacterial communities by the influence of tillage system applied were confirmed by the value of similarity Index (SI%) calculated, evidencing the percent of 40% species shared between the compared communities, represented by 4 taxa (Pseudomonas fluorescens and *Bacillus* circulans, Pseudomonas pseudoglevi and actinomycetes from Series Albus).

Differential species identified were represented by 4 species, characteristic only for soil under conventional system and by 8 species for conservative system. Differences in taxonomic composition and species abundance registered for fungal communities were even more pronounced.

Taxonomic composition of fungal community from soil under minimum tillage (Figure 5 and Figure 6) consisted from 11 species, characterized by co-dominance of 5 species (*Trichoderma viride, Aspergillus clavatus, Aspergillus terreus, Mortierella* sp. and *Paecilomyces marquandii*) with similar abundance A=13%, and other 6 species, less abundant but with high cellulolytic capacities, too.



Figure 5. Composition and species relative abundance of fungi in soil under minimum-tillage system

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Figure 6. Fungi from minimum-tillage system

Fungal community from conventional system (Figure 7 and Figure 8) included 6 species, dominated by association of 2 species of *Aspergillus (A. clavatus* and *A. terreus)*, each with A=29%, accompanied by *Penicillium corylophillum, Paecilomyces elegans* (with equal abundances A=14%) and

2 less abundant species (A=7%), represented by *A. candidus* and *Fusarium verticillioides*.

Higher differences in community composition were found by calculation of Similarity Index, with value of SI=23.52% lower than in the case of bacterial communities.



Figure 7. Composition and species relative abundance of fungi in soil under conventional tillage system



Figure 8. Fungi from conventional tillage system

Only *Aspergillus clavatus* and *Aspergillus terreus* were identified in both fungal communities. Differential species were represented by 4 species identified only for soil under conventional system and by 9 species identified under conservative system.

Generally, climatic conditions from Bărăgan Plain selected a microbial composition with dominance of species belonging to groups characterized by features revealing a high adaptability to high temperatures and drought stress conditions: bacteria from genus Bacillus capable to form spores with thick membranes, actinomycetes, many species from genus Aspergillus, more thermophilic than those from genus Penicillium usually dominant in soils from temperate regions. Other research evidenced the changes of soil microbiota communities as response to various abiotic stresses, too (Abdul Rahman et al., 2021). Helgason et al. (2009) reported differences between fungal and bacterial abundance in long-term no-till and intensive-till soils.

The higher number of cellulolytic fungi

and exopolysaccharide-producing bacteria in microbiota from MT system compared to soil from CT system reveals beneficial effect on C sequestration and enhancing C stabilisation by facilitating soil aggregation as confirm by numerous studies (Matei et al., 2016; Angst et al., 2018; Totsche et al., 2018; Hartmann and Six, 2022; Zang et al., 2023).

The important role played by a diverse and active soil microbiota in the main processes from carbon cycle was also confirmed by literature data (Liang et al., 2017; 2019; Bahram et al., 2018; Wang et al., 2020; Tao et al., 2023).

The microbial communities from minimum tillage system were richer in both bacterial and fungal species than the microbiota under conventional tillage system. A positive effect was evidenced by higher values of diversity indices registered for bacterial and fungal communities from soil under minimum tillage as compared with those characterizing the communities under conventional soil tillage (Table 2).

Tillage system	Bacterial Diversity	Fungal Diversity
Conventional tillage	S=8 Simpson D=0.840 Shannon H'=2.023bit E(ε)=0.762	S=6 Simpson D=0.786 Shannon H'=1.649bit E(ε)=0.688
Minimum tillage	S=12 Simpson D=0.893 Shannon H'=2.345bit E(ε)=0.759	S=11 Simpson D=0.898 Shannon H'=2.339bit E(ε)=0.786

Table 2. Bacterial and fungal biodiversity in soil under conventional and minimum tillage systems

Bacterial community from soil under conservative tillage presented a higher heterogeneity, with lower values of evenness $E(\varepsilon)=0.759$ than in soil under conventional tillage $E(\varepsilon)=0.762$.

Fungal homogeneity was higher in community from soil under conservative tillage, with $E(\varepsilon)=0.786$, reflecting a more homogenous distribution of "individuals" on species, as compared with lower values of $E(\varepsilon)=0.688$, reflecting the more heterogeneous distribution in soil community under conventional tillage.

These data are in concordance with results showing that tillage not only drastically reduces soil microbial activity, but also alters the structure of the soil microbial community, relative to MT and NT tillage.

Different studies have presented the effect of tillage on the composition of microbial communities (Hartman et al., 2018), in the context of insufficient temporal information on the CT effect.

Over time, the temporal monitoring of microbiomes in soils, for longer periods of time (3 years), revealed the complex effect of the soil processing method, under the influence of various changes (seasonal, environmental, meteorological).

Microbial communities in soils can be grouped according to the types of agricultural tillage carried out over a period of time. Similarly, in the case of co-occurrence/ co-exclusion interaction networks, the microbial taxa that form the specific nodes of the network interact according to the type/intensity of processing.

Studies have reported increased diversities in MT, NT vs. CT based on microbial community fingerprinting methods. The analysed data confirmed the impact of CT processing on the structure and functions of soil microbial communities (Xia et al., 2019). The long-term roles of the microbiota in ecosystems shaped by tillage practices, as well as the patterns of microbial cooccurrence in soil, are relatively little known.

on practice Studies NT revealed significant increases in soil moisture (SMC), bulk density (BD), soil organic carbon (SOC) stocks, total nitrogen (TN) and microbial biomass carbon and nitrogen (MBC and MBN). High levels of bacterial alpha diversity were observed in NT compared to CT, but no significant differences between treatments for fungal diversity. Significant changes occurred in the composition of microbial groups for the bacterial and fungal community. Thus, NT determined significant abundances for the phyla Proteobacteria and phyla Glomeromycota. Redundancy the analysis revealed that the factors most closely correlated with bacterial and fungal composition were SMC, TN and SOC, respectively. Under NT the soil improved both its microbial composition and C storage (Six et al., 2006), and it can be considered that NT offers a chance to improve soil health (Dong et al., 2017; Frac et al., 2018).

The NT and MT work had different effects on the biodiversity of the bacterial and fungal microflora communities, causing an increase in soil bacterial diversity without a significant change in fungal diversity. Also, a medium level of nitrogen (100-200 kg x ha⁻¹) applied altered soil microbial diversity under NT conditions, compared to excessive or low levels with no significant effect. The NT work determined a significant increase in the relative abundance of Acidobacteria, a decrease in Actinobacteria and little effect on Proteobacteria.

Under processing conditions NT had the most significant effect on soil microbial diversity, by changing the content of soil organic carbon and total nitrogen (Yüze et al., 2020).

Bailey et al. (2002) associated an increased fungal activity with increased soil organic C accumulation by increased synthesis of microbial biomass and by-products.

The presence of antagonistic species from bacterial genus *Pseudomonas* with fluorescent representatives and ubiquitous fungus *Trichoderma viride* as dominant species in microbiota from soil under minimum tillage system conferred an increased plants tolerance to drought and salinity stress and a higher resilience of the agroecosystem.

Other research reported the important role of these microorganisms for crop production and described the multiple and complex interconnections microorganisms-plants-soil (Zhang et al., 2017).

Pseudomonas sp. improved antioxidant enzymes activity and increased tomato biomass accumulation in drought conditions (Brilli et al., 2019). Other research results confirmed that fluorescent and nonfluorescent *Pseudomonas* strains and *Bacillus* spp. were able to induce plant disease suppression and had growth promotion capacity (Boruah and Kumar, 2002; Santoyo et al., 2012; Calderón et al., 2014; Veliz et al., 2017).

Soil actinomycetes from conventional tillage system were present only by representatives of Series Albus with A=17%, lower value than the group from conservative system formed by representatives of 4 Series (Fuscus, Albus, Ruber and Luteus) achieving together a relative abundance of 20% in community. These results are in concordance with literature data (Louime et al., 2006) showing that decreased relative abundance of complex polysaccharide decomposers belonging to actinomycetes and cellulolytic bacteria *Cytophaga* sp. from soil reflects decrease of its capacity for organic matter decomposition even after a single soil till.

Penicillium increased plants spp. resistance to various abiotic stresses (Chaudhary et al., 2018), drought tolerant isolates of Trichoderma harzianum promoted growth and drought tolerance in wheat Triticum aestivum (Shukla et al., 2015). Trichoderma sp. enhanced growth and tolerance to water deficit stress in tomato plants through increased N and P uptake, increased shoot dry weight and stomatal conductance (Khoshmanzar et al., 2020). Our results are similar to literature results reporting the plant growth promoting and antimicrobial effect of various Trichoderma isolates (Yan and Khan, 2021; Yan et al., 2021; Al-Surhanee, 2022; Joo and Hussein, 2022; Mukerjee et al., 2022; Yao et al., 2023).

Many *Trichoderma* strains were selected for their plant-promoting or antimicrobial effect and used as bio-fertilizers and biocontrol agents (Thenmozhi et al., 2010; Petcu et al., 2023).

CONCLUSIONS

Research has been carried out on size, taxonomic composition and physiological activity of soil microbiota for assessing the effect of classic (conventional) and conservative (minimum tillage) agriculture systems applied in South region of Bărăgan Plain.

Results reflected significant differences concerning the quantitative parameters characterizing the bacterial and fungal communities from the two soil systems of tillage, with total counts of bacteria doubled and with one order of magnitude higher for total counts of fungi in soil minimum-tilled than in soil under conventional tillage system.

The minimum tillage system favoured the increasing of abundance and diversity of actinomycetes in composition of soil microbiota than in soil under classical tillage system.

Soil respiration values registered for both conservative and conventional systems are considered to characterize high levels of microbial physiological activities, with slightly higher values for minimum tillage system application than for conventional system.

The beneficial effect of conservative system was evidenced by higher values of diversity indices registered for both bacterial and, especially fungal communities, as compared with those characterizing the communities from soil under conventional tillage system.

The higher number of cellulolytic fungi and exopolysaccharide-producing bacteria in microbiota from MT system compared to soil from CT system reveals their beneficial effect on C sequestration and enhancing C stabilisation by facilitating soil aggregation.

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