Artícle

Effect of agricultural production system on soil microbial populations

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Abstract: The physicochemical properties of soil and microbial populations are important factors that influence soil quality, nutrient cycling, and ecosystem functioning. These properties play a crucial role in regulating microbial activity and interactions, as well as the biogeochemical processes in soil. This document presents the partial results of the physicochemical and microbiological characterization of the soil from samples taken at 15 and 45 cm depth prior to the establishment of the different tillage and fertilizer treatments. Concerning the values observed in the physical and chemical parameters, no statistically significant differences ($p > 0.05$) were observed between samples from both depths. The microbiological analysis was conducted with soil samples taken at 15 cm depth from three tillage systems, considering the control treatment and the treatment with organic fertilization with poultry manure. Aerobic bacteria and actinomycetes counts did not show statistically significant differences ($p > 0.05$). Anaerobic, coliform, and fungal counts were statistically different ($p > 0.05$) between treatments due to the presence of organic fertilizer. However, no statistically significant difference ($p > 0.05$) was observed between the three tillage systems. In a second culture cycle, the effect of different concentrations of organic matter was evaluated, where T1(N: 60, P: 65.5, K: 74.4) showed the higher CFU g^{-1} (Log) of aerobic and anaerobic bacteria, actinomycetes, and fungi, while T3 had the highest CFU of coliforms. These results are important to understand soil dynamics better and inform agricultural and soil management practices. In addition, they highlight the importance of proper use of organic fertilizers and the need for further research to determine how they affect long-term soil health and quality.

Keywords: Agricultural machinery; fertilizer; microbiological; physicochemical; tillage.

Efecto del sistema de producción agrícola en las poblaciones microbianas del suelo

Resumen: Las propiedades fisicoquímicas del suelo y las poblaciones microbianas son factores importantes que influyen en la calidad del suelo, el ciclo de los nutrientes y el funcionamiento de los ecosistemas. Estas propiedades desempeñan un papel crucial en la regulación de la actividad y las interacciones microbianas, así como en los procesos biogeoquímicos del suelo. En este documento se presentan los resultados parciales de la carac-terización fisicoquímica y microbiológica del suelo a partir de muestras tomadas a 15 y 45 cm de profundidad antes del establecimiento de los diferentes tratamientos de laboreo y fertilización. En cuanto a los valores observados en los parámetros físico-químicos, no se observaron diferencias estadísticamente significativas ($p > 0,05$) entre las muestras de ambas profundidades. El análisis microbiológico se realizó con muestras de suelo tomadas a 15 cm de profundidad de tres sistemas de labranza, considerando el tratamiento control y el tratamiento con fertilización orgánica con gallinaza. Los recuentos de bacterias aerobias y actinomicetos no mostraron diferencias estadísticamente significativas ($p > 0,05$). Los recuentos de bacterias anaerobias, coliformes y hongos fueron estadísticamente diferentes ($p > 0,05$) entre los tratamientos debido a la presencia de abono orgánico. Sin embargo, no se observaron diferencias estadísticamente significativas ($p > 0,05$) entre los tres sistemas de laboreo. En un segundo ciclo de cultivo, se evaluó el efecto de diferentes concentraciones de materia orgánica, donde T1(N: 60, P: 65,5, K: 74,4) mostró la mayor UFC g-1 (Log) de bacterias aerobias y anaerobias, actinomicetos y hongos, mientras que T3 tuvo la mayor UFC de coliformes. Estos resultados son importantes para comprender mejor la dinámica del suelo e informar sobre las prácticas agrícolas y de gestión del suelo. Además, ponen de relieve la importancia del uso adecuado de fertilizantes orgánicos y la necesidad de seguir investigando para determinar cómo afectan a la salud y la calidad del suelo a largo plazo.

Palabras clave: Maquinaria agrícola; fertilizante; microbiológico; fisicoquímico; labranza.

1. Introduction

Microorganisms in soil play a crucial role in nutrient cycling, soil health, and crop productivity (Nabi et al.,2023). They are involved in various activities such as nutrient mobility and absorption, plant growth stimulation, and disease management (Beigmohammadi et al., 2023). They contribute to nutrient cycling, stimulate plant growth, and reduce diseases. Microbes such as mycorrhizal fungi and plant growth-promoting bacteria enhance nutrient mobility and absorption, hormone regulation, and disease management. Beneficial soil microorganisms improve plant health, nutritional status, and soil quality, making them essential for sustainable agriculture. The microbial population in the rhizosphere interacts with plants and influences bacterial activities, which can lead to better plant development. Microorganisms also play a significant role in the decomposition of agricultural waste, aiding in the production of organic compounds and minerals that are beneficial for crop growth (Prisa, 2023; Kaur & Rani, 2022). However, agricultural practices have a significant impact on soil health and soil quality, as conventional systems (such as the use of chemical fertilizers and mechanized tillage) can lead to soil erosion, loss of biodiversity, and declines in soil structure and organic matter (Aseeva et al., 2021). In this context, irregular and irresponsible practices, such as excessive tillage and inadequate fertilization, can lead to the loss of soil carbon and an increase in carbon dioxide emissions (Alori et al., 2020). It is worth mentioning that long-term agricultural use of soil can negatively affect the availability of chemical elements for plants and the number of microorganisms in the soil (Galic et al., 2019), causing a significant loss of biodiversity (Barros-Rodríguez et al., 2021). However, strategies can be implemented to increase crop production without endangering soil health, such as the use of organic fertilizers and conservation tillage techniques (Burcea, 2018). In the case of organic fertilization, fermentation processes have been found to impact soil microbial populations. For example, the use of forest wastes can increase the presence of bacteria and decrease the fungal population (Marois et al., 2022). On the other hand, bacterial communities in soils treated with spent microbial biomass from industrial fermentation processes have been compared with conventional agricultural systems, where a statistically significant increase in the diversity of the microbial population was observed, mainly in the populations of Proteobacteria and Actinobacteria (Halter et al., 2020). In addition, long-term application of soil conditioners derived from fast fermentation altered the distribution of the main functional bacterial communities in the soil, with *Proteobacteria*, *Actinobacteria*, *Acidobacteria* and *Firmicutes* becoming the dominant phyla (Jain and Saxena, 2019).

Regarding the influence of the tillage system on microbial populations, conventional methods can damage soil structure, whereas no-tillage can improve soil quality by maintaining structure and increasing microbial biodiversity (Angon et al., 2023). In turn, crop rotation and tillage also influence the soil environment by altering key soil properties such as pH and organic matter (Behnke et al., 2021). The use of alternative agricultural methods, such as reduced tillage, conservation tillage, no-tillage and organic farming can help preserve the richness and diversity of soil bacterial communities (Khmelevtsova et al., 2022). In addition, different tillage management and crop residue incorporation have been shown to affect soil bacterial community structure, and certain treatments lead to higher levels of specific fatty acids and bacterial populations (Tang et al., 2022). In general, the choice of tillage and fertilization system can have important implications for agricultural soil microbial populations. Therefore, the present research aims to evaluate the effect of nine agricultural production systems on soil microbial populations.

2. Materiales y Métodos

Experiment Location

The experiment was established in the spring-summer 2018 cycle, in the Marín experimental field of the Faculty of Agronomy belonging to the UANL, located in Marín Nuevo León, with geographical location 25° 52' 13.5'' north latitude and 100° 02' 22.56'' west longitude, at an altitude of 355 masl. The climate corresponds to a BSI (h) w (e), described as a dry warm steppe climate with rainfall in summer, an average annual precipitation of 595 mm and an average annual temperature of 22 °C. The predominant soil type is calcareous-clay with a pH between 7.5 and 8.5 and low organic matter content.

Genetic material

Sweet sorghum [Sorghum bicolor (L.) Moench] of the Roger genotype variety from the Sorghum Program of the Agronomy Faculty of the Universidad Autónoma de Nuevo León was used.

Life Cycle Assessment (LCA)

This method of analysis was performed according to Wanga et al. (2014) where he states that a product system is a collection of unit processes connected by intermediate product flows that perform one or more defined functions.

Experimental design

The research comprises a data collection period of two crop cycles comprising the fall-winter cycle of 2017-2018 and 2018-2019. The experiment was comprised of nine 40x24 m experimental plots, with a total area of 9 000 m². Three soil tillage systems in combination with two fertilization and no fertilization systems were evaluated. A split-plot design was used for data collection and its model is as follows:

$$Y_{ijk} = \mu + \beta_i + F_j + e_{ij} + e_{ij}(a) + V_k + (FV)_{jk} + e_{ijk}(b)$$

$$i = 1,2,..., r \quad j = 1,2,...,a \quad k = 1,2,...,b$$

Y_{ijk} is the observation at tillage j, at moisture content k, in block i.

μ is the overall true mean.

β_i is the effect of block i.

F_j is the effect of date level j.

$e_{ij}(a)$ is the experimental error for the i j-th large plot for dates.

V_k is the effect of the level k of varieties.

FV_{jk} is theeffect of the interaction of tillage j and moisture k.

$e_{ijk}(b)$ is the experimental error of the i j k-th subplot.

Soil tillage systems:

- Tillage system 1 consists of clearing and harrowing labors and sowing.

- Tillage system 2 is composed of clearing, plowing, and harrowing labors and sowing.

- Tillage system 3 is composed of clearing, subsoil, plowing, and harrowing labors, and sowing; in this technology, subsoiling and plowing are done in November and when the sowing date approaches, harrowing is done a day or two days before planting.

Fertilization systems:

- Organic fertilization, as a base source poultry manure.

- Inorganic fertilization, commercial chemicals (100, 50, 0).

- Without fertilization.

Table 1 shows the systems.

Table 1. Treatment specifications.

Treatment	Description
T1	L 1 + F1
T2	L1 + F2
T3	L 1 + F3
T4	L 2 + F1
T5	L 2 + F2
T6	L 2 + F3
T7	L 3 + F1
T8	L 3 + F2
T9	L 3 + F3

L1: Minimum tillage (clearing and harrowing); L2: Traditional tillage (clearing, plowing, and harrowing); L3: Traditional tillage with breaking of the plow layer (clearing, subsoil, plowing, and harrowing); F1: Organic fertilizers; F2: Inorganic fertilizers; F3: No fertilizers.

A second crop cycle was established with traditional tillage with breaking of the plow layer and three concentrations of organic fertilizer (poultry manure): Summer-Winter Cycle 2019

Treatments

- T1= Organic fertilization N: 60, P: 65.5, K: 74.4
- T2= Organic fertilization N: 90, P: 98, K: 112
- T3= Organic fertilization N: 120, P: 131, K: 149.4

Soil preparation

Data collection for the determination of the physicochemical properties of the soil were carried out according to the methodology described by the Mexican Official Standard NOM-021-RECNAT-(2000), which establishes the specifications for fertility, salinity, and soil classification.

Physical and chemical properties

Soil sampling and determination of soil physical-chemical properties were carried out according to the methodology described in the Mexican Official Standard NOM-021-RECNAT-(2000), which establishes the specifications for soil fertility, salinity, and classification. Samples were taken at 0.15 m and 0.45 m depth to compare the initial soil conditions with the changes derived from the establishment of tillage and fertilization treatments.

Partial microbiological characterization of the soil.

Soil samples were diluted 1:10 and homogenized in 0.1% sterile peptone water. The dilutions were sown on a plate, taking 1 ml of each one and adding approximately 15 ml of the corresponding medium. Mesophilic and anaerobic counts were performed on standard count agar, varying the presence of O_2 and CO_2, respectively. Bile and red violet agar (RVBA) were used for coliform quantification. Fungal counts were carried out on potato dextrose agar (PDA)

medium, modified with 10% tartaric acid. Quantification of actinomycetes was performed on selective medium for isolation. All the plates were incubated at 37 °C for 24 h. All assays were performed in triplicate per treatment. The culture media were purchased from Laboratorios CONDA (Spain).

Statistical analysis

The data obtained from the variables evaluated were analyzed with the SPSS Statistics computer statistical package. Analysis of variance and correlation between variables were applied. Mean differences were determined by the Tukey method for a significance level of 95 % ($p \leq 0.05$).

3. Results and discussion

The composition of microbial communities in agricultural production systems is influenced by several factors, including the tillage and fertilization system. It is worth mentioning that the source of water used to produce agricultural products is also a factor that influences populations, as it can introduce foodborne pathogens. In general, agricultural practices, fertilizer applications, water sources and soil management practices play a role in shaping the composition of microbial communities in agricultural production systems.

Soil physicochemical characterization

The chemical characterization of the soil was carried out prior to soil preparation with the different production systems. This included quantification of soil organic matter (OM), nitrogen, phosphorus, potassium, zinc, and copper content (Table 2). In the initial soil condition, the organic matter content at 15 and 45 cm showed statistically significant differences ($p \leq 0.05$). The contents of N, P, K, Cu and Zn showed no difference ($p > 0.05$) at both depths. With respect to the nutrient contents observed, they were similar to those reported for other saline soils (Corwin et al., 2003).

The pH results at two depths in the initial soil condition prior to treatment and crop establishment showed no statistically significant difference ($p \leq 0.05$) at 0.15 and 0.45 cm depth. Electrical conductivity values observed at 0.15 and 0.45 m (5.40 ± 0.666 and 2.65 ± 0.667 mS/cm at 25 °C, respectively) had statistically significant difference ($p \leq 0.05$). All these results are like those reported by previous works such as Escoto (2014) for soils from the Marin Experimental Campus and similar to those reported for other saline soils (Corwin et al., 2003).

Table 2. Chemical characterization of the soil.

Parameter	Initial condition		Sig.
	15 cm	45 cm	
M.O (%)	2.19 ± 0.122	1.84 ± 0.164	0.000
N (ppm)	8.073 ± 0.205	8.096 ± 0.224	0.947
P (ppm)	40.415 ± 6.682	46.647 ± 6.074	0.184
K (ppm)	2.086 ± 0.565	1.694 ± 0.338	0.129
Zn (ppm)	0.227 ± 0.048	0.231 ± 0.332	0.537
Cu (ppm)	0.114 ± 0.026	0.112 ± 0.022	0.460

Identification of Microbial Populations

Aerobic bacteria and actinomycetes counts did not show statistically significant differences ($p \leq 0.05$) (Table 3). Anaerobic, coliform, and fungal counts were statistically different ($p \leq 0.05$) between treatments.

Table 3. Microbiological analysis completed for the Fall-Winter 2018 Cycle

Tt	Aer	Anr	Col	Acn	Fun
	CFU g^{-1} (Log)				
T1	8.69 ±0.93 [a]	8.82 ±0.08 [ab]	8.76 ±0.04 [b]	8.94 ±0.08 [a]	4.00 ±0.00 [a]
T2	9.28 ±0.27 [a]	9.09 ±0.12 [ab]	8.88 ±0.02 [ab]	9.18 ±0.16 [a]	4.08 ±0.15 [c]
T3	9.30 ±0.30 [a]	9.07 ±0.41 [a]	8.83 ±0.05 [b]	7.41 ±3.52 [a]	4.46 ±0.53 [c]
T4	9.46 ±0.06 [a]	9.29 ±0.10 [ab]	8.87 ±0.03 [a]	9.05 ±0.07 [a]	4.12 ±0.24 [c]
T5	9.14 ±0.26 [a]	9.20 ±0.13 [b]	9.02 ±0.23 [ab]	9.09 ±0.01 [a]	4.00 ±0.00 [c]
T6	9.24 ±0.24 [a]	9.12 ±0.03 [a]	8.90 ±0.02 [b]	9.12 ±0.02 [a]	4.00 ±0.00 [c]
T7	9.18 ±0.25 [a]	9.27 ±0.09 [ab]	8.98 ±0.07 [ab]	9.00 ±0.09 [a]	4.81 ±0.13 [c]
T8	8.93 ±0.63 [a]	9.09 ±0.08 [a]	8.88 ±0.10 [ab]	9.17 ±0.04 [a]	4.07 ±0.15 [b]
T9	9.37 ±0.17 [a]	9.15 ±0.03 [ab]	8.92 ±0.09 [ab]	9.17 ±0.17 [a]	4.07 ±0.15 [c]
Sig.	0.314	0.020	0.034	0.515	0.000

Tt=treatment; Aer=aerobes; Anae=anaerobes; Colif=coliforms; Act=actinomycetes; Fun=fungi. [a-c]Different literals in the same column denote statistically significant difference (Tukey, $p \leq 0.05$).

Differences ($p \leq 0.05$) in anaerobic, coliform, and fungal counts were also observed among the poultry manure treatments (Table 4), which could be explained by the different tillage systems. However, no statistically significant difference ($p > 0.05$) was observed among the control treatments of three tillage systems (Table 5). This suggests that the presence of poultry manure and tillage systems influence the microbial populations present.

Table 4. Microbiological analysis of treatments with organic fertilization

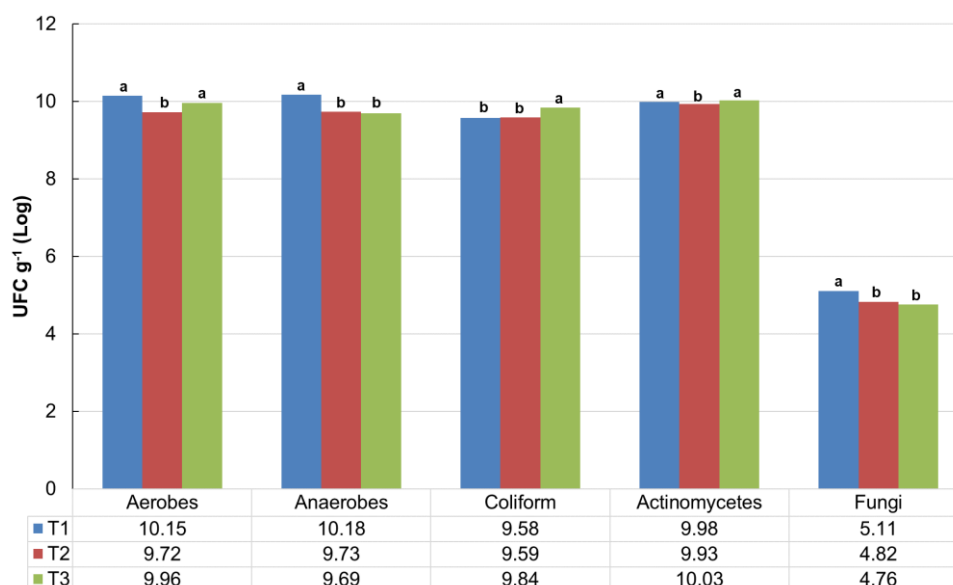| Tt	Aer	Anr	Col	Acn	Fun
	UFC (Log)				
T1	8.68 ±0.93 [a]	8.8 2 ±0.08 [b]	8.76 ±0.04 [c]	8.94 ±0.07 [a]	4.00 ±0.02 [b]
T4	9.460 ±0.06 [a]	9.28 ±0.09 [a]	8.87 ±0.03 [b]	9.05 ±0.07 [a]	4.12 ±0.24 [b]
T7	9.18 ±0.26 [a]	9.27 ±0.09 [a]	8.98 ±0.07 [a]	9.00 ±0.09 [a]	4.81 ±0.13 [a]
Sig.	0.187	0.000	0.000	0.204	0.000

Tt=treatment; Aer=aerobes; Anae=anaerobes; Colif=Coliforms; Act=actinomycetes; Fun=fungi. a-cDifferent literals in the same column denote statistically significant difference (Tukey, p ≤ 0.05).

Table 5. Microbiological analysis by tillage systems

Tt	Aer	Anr	Col	Acn	Fun
	CFU g^{-1} (Log)				
T3	9.30 ±0.30 [a]	9.07 ±0.41 [a]	8.87 ±0.05 [a]	9.11 ±3.52 [a]	4.16 ±0.53 [a]
T6	9.24 ±0.24 [a]	9.12 ±0.03 [a]	8.90 ±0.02 [a]	9.12 ±0.02 [a]	4.00 ±0.00 [a]
T9	9.37 ±0.17 [a]	9.15 ±0.03 [a]	8.92 ±0.09 [a]	9.17 ±0.17 [a]	4.07 ±0.15 [a]
Sig.	0.767	0.833	0.144	0.177	0.146

Tt=treatment; Aer=aerobes; Anae=anaerobes; Colif=coliforms; Act=actinomycetes; Fun= fungi. [a] Different literal in the same column denote statistically significant difference (Tukey, $p \leq 0.05$).

On the other hand, the overall results of CFU g^{-1} fungi were similar to those reported by Escoto-González (2014), but the number of CFU g^{-1} of aerobic bacteria reported in the present paper is higher than those mentioned by the same author for the nursery area of the Campo Agrícola Experimental Marín. These differences can be explained as a function

of microclimate variants. This would also explain the differences observed in the poultry manure treatments in the different tillage systems.

Likewise, the results reported here are higher than those reported for saline soils of intensive vegetable production (Crecchio et al., 2004). In comparison with acid soils, a lower number of bacteria has been reported (Álvarez et al., 2004) and similar counts of actinomycetes and fungi to those shown in the present work.

On the other hand, at the end of the second crop cycle, the analysis of the microbial populations of the soil fertilized with different doses of organic matter showed statistically significant differences ($p \leq 0.05$) in the groups of bacteria analyzed (Figure 1). T1(N: 60, P: 65.5, K: 74.4) showed the higher CFU g^{-1} (Log) of aerobic and anaerobic bacteria, actinomycetes, and fungi, while T3 had the highest CFU of coliforms. Population counts increased after the second cycle, which can be explained by incorporating organic matter through chicken manure fertilization (Zou et al., 2022). Although it is known that the efficiency of organic fertilization and the dynamics of soil microbial populations can be affected by salinity, negatively impacting soil health and crop quality (da Costa et al., 2023). It is worth highlighting the importance of actinomycetes in the growth and development of plants as biocontrol agents against phytopathogens, solubilizing phosphate, fixing nitrogen, producing phytohormones, antibiotics, and high-value enzymes, in addition to contributing to the recovery of saline soils (AbdElgawad et al., 2020). Therefore, the results obtained by the different doses of organic matter can counteract, to a certain extent, the negative effects of salinity, explaining the increase in microbial populations from one cycle to another.

	Aerobes	Anaerobes	Coliform	Actinomycetes	Fungi
■ T1	10.15	10.18	9.58	9.98	5.11
■ T2	9.72	9.73	9.59	9.93	4.82
■ T3	9.96	9.69	9.84	10.03	4.76

Figure 1. Initial microbiological analysis Fall-Winter 2019 Cycle. T1 = Fertilización orgánica N: 60, P: 65.5, K: 74.4; T2 = Fertilización orgánica N: 90, P: 98, K: 112; T3 = Fertilización orgánica N: 120, P: 131, K: 149.4.

The CFU contents of aerobic and anaerobic bacteria in agricultural soils may vary depending on the type of fertilization used. In general, it is considered that organic fertilization can contribute to increasing the levels of aerobic and anaerobic bacteria in soils, while inorganic fertilization can contribute to reducing them. In organically fertilized soils, it has been observed that the microbial community composition shifted from aerobic to anaerobic degradation of soil organic carbon, leading to increased carbon accumulation (Li et al., 2021). In contrast, inorganically fertilized soils showed an increase in the relative abundance of Proteobacteria and Firmicutes, which are associated with organic carbon accumulation (Zhang et al., 2014). However, under the conditions of the present study, similar values of aerobic and anaerobic bacteria were observed, which could be due to soil salinity. It is known that the ratio of these bacteria populations can vary in saline agricultural soils fertilized organically or inorganically, depending on the type and origin of the fertilizer used, as well as environmental conditions (Dong et al., 2022).

Concerning the presence of coliform, it is worth mentioning that the isolated colonies did not present the typical dark red color, generally surrounded by a halo of light red or pink precipitation due to bile salts. The above suggests that the total coliform obtained in the count could be from the water, although it should be noted that they are a relatively harmless set of microorganisms (Vahith & Sirajudeen, 2016).

Similar values were observed in all production systems for the actinomycetes count, so the biological implication of this group of bacteria in promoting plant growth and soil fertility is noteworthy (Shivlata & Satyanarayana, 2017).

Finally, concerning the effect of tillage, conservation tillage systems, such as no-till and strip tillage, can positively affect soil microbial diversity and its function in agricultural soils (West et al., 2023). These practices may maintain soil microbial health better than conventional tillage, which alters microbial communities and processes (Mackay et al., 2023), although no statistically significant differences were observed between the populations evaluated and the tillage treatments used. Therefore, to know the populations and their dynamics according to the different production systems, studies at the metagenomic level are required.

4. Conclusions

The results show no statistically significant differences in the physical and chemical parameters between the different depths of the soil. Furthermore, the counts of aerobic bacteria and actinomycetes did not show significant differences. However, statistically significant differences were observed in the counts of anaerobic bacteria, coliforms, and fungi, which are attributable to using organic fertilizers. Likewise, no significant differences were found between the three tillage systems studied. These findings suggest that, although the type of fertilizer can influence the microbiological composition of the soil, the different tillage methods do not significantly impact the parameters evaluated in this study. Regarding the effect of incorporating organic matter, treatment T1 (N: 60, P: 65.5, K: 74.4) showed the higher CFU values of the studied populations, except for the coliform count. These results are important to understand soil dynamics better and inform agricultural and soil management practices. In addition, they highlight the importance of proper use of organic fertilizers and the need for further research to determine how they affect long-term soil health and quality.

5. Acknowledgments

6. Conflicts of Interest

The authors declare no conflict of interest.

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