







Article

Effect of Organic and Conventional Systems Used to Grow Pecan Trees on Diversity of Soil Microbiota

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Abstract: Agronomic management modifies the soil bacterial communities and may alter the carbon fractions. Here, we identify differences in several chemical and biological soil variables, as well as bacterial composition between organic (Org) and conventional (Conv) agronomic management in pecan (*Carya illinoensis*) orchards located in Coahuila, Mexico. The analyzed variables were pH, N, P, K, soil organic matter, organic matter quality, soil organic carbon, C/N ratio, carbon fractions, microbial biomass carbon, easily extractable Glomalin, colony-forming units, CO₂ emissions, and the enzyme activity. The DNA of soil bacteria was extracted, amplified (V3-V4 16S rRNA), and sequenced using Illumina. To compare variables between agronomic managements, *t* tests were used. Sequences were analyzed in QIIME (Quantitative Insights Into Microbial Ecology). A canonical correspondence analysis (CCA) was used to observe associations between the ten most abundant phyla and soil variables in both types of agronomic managements. In Org management, variables related to the capture of recalcitrant carbon compounds were significant, and there was a greater diversity of bacterial communities capable of promoting organic carbon sequestration. In Conv management, variables related to the increase in carbon mineralization, as well as the enzymatic activity related to the metabolism of labile compounds, were significant. The CCA suggested a separation between phyla associated with some variables. Agronomic management impacted soil chemical and biological parameters related to carbon dynamics, including bacterial communities associated with carbon sequestration. Further research is still necessary to understand the plasticity of some bacterial communities, as well as the soil–plant dynamics.

Keywords: organic agriculture; soil organic carbon; 16S rRNA; sequencing; structure of the soil bacterial community

1. Introduction

Microorganisms that live in the soil are among the most abundant and diverse organisms on earth [1]. The structure and metabolism of the soil bacterial communities are influenced by elements of the ecosystem such as climate, type of soil, and plant composition; however, one factor that greatly affects their composition and functioning is agronomic management [2–5]. Thus, conventional agronomic management (CAM) alters the distribution of organic material and affects the rate of mineralization of micro and macro elements in the soil [3], negatively impacting the long-range productivity of the soil due to the loss of organic matter and erosion [6]. In CAM, inorganic supplies, such as synthetic fertilizers and pesticides, are used [7]. These supplies affect the availability of nutrients in the soil, contaminating the surface and underground water, thus affecting the native biotic community [8]. Conversely, in organic management, the traditional cultivation methods (conservationist) are combined with modern techniques, excluding conventional supplies [9]. In these systems, crop rotation is practiced and residues from animals and organic vegetables are used to increase soil fertility and productivity [7–10]. Likewise, it has been reported that these practices also affect the long-term structure of the microbial community through the accumulation and chemistry changes of soil organic matter (SOM) [2].

Regarding the above, greater attention should be given to organic agricultural systems in perennial woody crops with commercial interest, such as pecan trees (*Carya illinoensis*). These systems have the potential to improve soil fertility through microbial activity and carbon accumulation in the soil [10–13]. For pecan tree orchards, the essential practices to promote soil fertility involve using leguminous plants or wild herbs as ground cover, as well as using organic fertilizers [14]. The pecan tree is a perennial woody crop which produces the pecan nut, which is a highly nutritious food [15]. The world's leading producers of pecan nuts are China, United States, Iran, Turkey, and Mexico [16]. Furthermore, in Mexico, the states with a greater volume of pecan production are Chihuahua, Sonora, and Coahuila. These pecan nuts are exported mainly to the United States, China, and Vietnam, at an annual amount in 2018 worth USD 751 million [17]. Considering the cultivation of organic pecan trees in Mexico, in 2011 there were 1000 hectares certified as organic [14].

Given the importance of preserving and increasing soil fertility in pecan tree cultivation, several research studies have been developed to determine soil organic carbon (SOC), SOM, carbon–nitrogen relation, the mineralization of carbon and nitrogen, microbial biomass carbon, enzyme activities in diverse management systems, age of the crops, and association with leguminous plants and grasses [11,12,18]. Other research has focused on the qualities of the essential oils in nuts and on the nutritional deficiencies of the foliage, as well as on pests and diseases [15,19,20]. However, although the role of microbial communities in carbon sequestration is relevant, there are not enough research studies related to the structure and functioning of bacterial communities in the soil wherein pecan trees are grown under different agronomic management. Therefore, the objectives of this study were to identify the soil variables that respond to agronomic management related to carbon dynamics, and to determine the structure and composition of the bacterial communities in the soil wherein pecan trees are grown under organic and conventional management. We hypothesize that the organic management of pecan tree cultivation will generate greater soil bacterial diversity, capable of promoting greater efficiency in carbon sequestration than conventional management.

2. Materials and Methods

2.1. Study Area

Soil samples were collected from pecan orchards (*Carya illinoensis* (Wangenh.) K. Koch) containing Cheyenne, Wichita, and Western varieties under organic (Org) and conventional (Conv) managements, located in the municipality of Allende, Coahuila, Mexico (Org: N 28°20'05.72" W –100°49'24.73"; Conv: N 28°21'57.30" and W –100°46'06.02") (Figure 1). Both orchards are located in the same geographical region, where the type of soil corresponds to haplic xerosol and the texture is clay [21].

The prevalent climate is dry and semi-warm, where annual mean temperature ranges between 20 and 24 °C, and the annual mean rainfall is about 461 mm [22]. The orchard under organic management (100 ha) is 20 years old, and the commonly applied practices to the soil are the use of plant covers and the placing of organic matter (pecan tree residues). On the other hand, the orchard under conventional management (35 ha) is 30 years old, and chemical fertilizers and pesticides are applied in accordance with the technical guide for pecan tree management proposed by INIFAP (Instituto Nacional de Investigaciones Forestales Agrícolas y Pecuarias) [23].

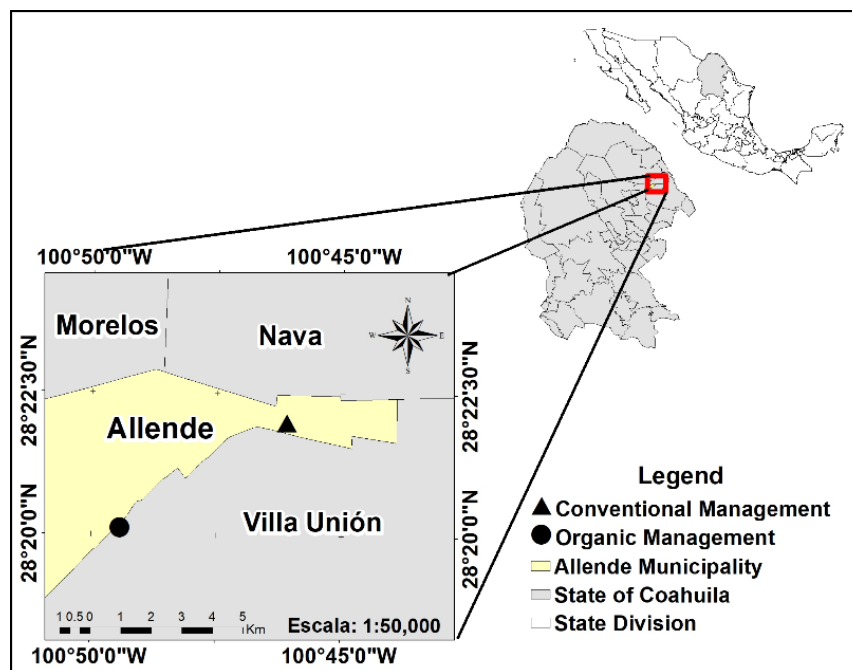


Figure 1. Geographical location of pecan tree (*Carya illinoensis*) orchards in Coahuila, Mexico.

2.2. Soil Sampling and Analysis of Chemical and Biological Variables

Four pecan trees were systematically selected from each orchard. From each tree, four sub-samples were taken (one from each cardinal point) at a depth of 20 cm. Respective sub-samples were mixed obtaining composite samples (approximately 1 kg each). The samples were air-dried and sieved using a 2 mm mesh before analytical determinations. The pH was determined with a soil/water ratio of 1:2 [24]. The essential nutrients, nitrogen (N) [25], phosphorous (P) [26] and potassium (K) [27], were quantified. Likewise, the SOM [28] and the organic matter quality (humic acids (HA), fulvic acids (FA), and humins (HS) [29,30]) were obtained. The SOC was obtained using a total organic carbon analyzer (TOC), and later the C/N ratio was estimated. Furthermore, the carbon fractions very labile (F1), labile (F2), less labile (F3) and recalcitrant (F4) were analyzed by digestion with H₂SO₄ at concentrations of 12, 18, and 24 N [31]. The microbial biomass carbon (MBC) was analyzed using the extraction fumigation method [32]. Furthermore, the easily extractable Glomalin (EEG) was determined [33], as well as the colony-forming units (CFU) by plate count (trypticase soy agar (total aerobic bacteria) and potato dextrose agar (PDA) (filamentous fungi and yeasts). Additionally, the CO₂ emissions from the soil were measured over 42 days under controlled conditions of humidity and temperature [34,35]. Furthermore, the enzyme activity of the soil was evaluated for lacasse (LAC), peroxidase (PER), polyphenol oxidase (PPO) [36,37], B-glucosidase (B-glu), and B-galactosidase (B-gal) [38].

2.3. DNA Extraction, Amplification and Sequencing

Three trees from each pecan orchard were randomly selected to collect 0.25 g of soil from the rhizosphere zone, at a depth of 10 cm. Each sample was placed in a BashingBead™ (Zymo Research

Corp., Irvine, CA, USA) cell lysis tube, containing 750 µL of lysing/stabilizing solution. Each tube was processed in a cellular disruptor (TerraLyzer™) for 30 s; samples were kept at ambient temperature. DNA was extracted using a Zymo BIOMICS™ (Zymo Research Corp., Irvine, CA, USA) kit. The amount of DNA obtained was measured in a Qubit fluorometer (Invitrogen, Carlsbad, CA, USA). The V3–V4 region of the 16S rRNA gene was amplified using primers suggested by Klindworth et al. [39] (S-D-Bact-0341-b-S-17, 5'-CCTACGGGNGGCWGCAG-3' and S-D-Bact-0785-a-A-21, 5'-GACTACHVGGGTATCTAATCC-3', (~460 pb amplicon)) using the Illumina protocol [40]. The amplicons were purified with Agentcourt® AMPure® XP 0.8% beads (Beckman Coulter Inc., Brea, CA, USA). The Nextera XT Index Kit™ was used to create the library, following the Illumina protocol [41]. The library quantification, normalization (equimolarity) and next-generation massive sequencing (MiSeq; Illumina, San Diego, CA, USA) 2 × 250 paired final readings) were developed following the 16S metagenomic protocol [40]. Sequence data were submitted to The National Center for Biotechnology Information (GenBank), with the following accession numbers: Org samples (SAMN15365245, SAMN15365246, SAMN15365247), Conv samples (SAMN15365249, SAMN15365250, SAMN15365252).

2.4. Statistical Analysis

After verifying normality and homogeneity of variance, Student's *t* test or Welch's *t* test ($p < 0.05$) were used to compare the chemical and biological variables between pecan orchards. The DNA sequences were analyzed using Quantitative Insights Into Microbial Ecology (QIIME) [42] as suggested by García-De la Peña et al. [43]. The absolute abundance of OTUs at genus level was used to visualize the number of sequences vs. the number of OTUs to observe depth cover (asymptote curves); this graph was made in PAST ver 3.15 (44). A simple random rarefaction process was made to standardize all samples. Using the standardized file, relative abundances for the phylum level were obtained and represented as bar charts using Excel. Taxa at the genera level with a relative abundance greater than 1% were listed. Finally, a canonical correspondence analysis (CCA) was used to observe associations between the ten most abundant phyla and soil variables in both types of agronomic managements. The CCA was made in PAST [44].

3. Results

3.1. Chemical and Biological Variables of the Soil

Some chemical and biological variables of the soil showed significant differences between both orchards. The significantly higher variables in soil under Org management were N, P, SOC, MBC, and HS. For Conv management, the soil variables that showed significantly higher values were F2, CO₂ emission, EEG, HA, FA, LAC, B-glu, and B-gal (Table 1).

3.2. Abundance of Bacterial Taxa

The average number of sequences assembled for Org was 230,680, and for Conv it was 267,539. After taxonomic designation, averages of 28,062 bacterial sequences for Org, and 48,775 for Conv, were obtained. The average number of OTUs was 5995 for Org, and 7937 for Conv (Table 2). Simple random rarefaction was made at 20,000 sequences, since at this point the number of OTUs reached asymptotes (Figure 2).

Table 1. Chemical and biological characteristics of soil in pecan tree (*Carya illinoensis*) orchards under organic and conventional management in Coahuila, Mexico. Mean values and standard deviation (\pm) are shown. An asterisk indicates when a Welch's *t* test was used; df = degrees of freedom; bold numbers indicate significant differences between managements ($p < 0.05$).

Variable	Organic	Conventional	<i>t</i>	df	<i>p</i>
pH	8.1 \pm 0.09	8.1 \pm 0.05	1	3	0.391
Nitrogen%	0.050 \pm 0.004	0.043 \pm 0.003	3.13	6	0.020
Phosphorous mg kg ⁻¹	16.3 \pm 5.80	5.6 \pm 1.00	4.901	6	0.003
Potassium mg L ⁻¹	0.52 \pm 0.31	0.31 \pm 0.19	2.06	3.14	0.127 *
Organic Matter%	2.97 \pm 0.31	3.11 \pm 0.11	-812	6	0.448
Organic Carbon%	1.91 \pm 0.04	1.72 \pm 0.02	7.071	6	0.000
Relation C/N%	38.6 \pm 3.10	40.5 \pm 2.00	-1.116	6	0.307
Very labile fraction C g kg ⁻¹	12.30 \pm 1.35	12.80 \pm 1.59	-0.522	6	0.620
Labile fraction C g kg ⁻¹	7.57 \pm 0.70	10.65 \pm 0.45	-6.392	6	0.001
Less labile fraction C g kg ⁻¹	18.67 \pm 3.17	18.50 \pm 0.91	-0.068	6	0.948
Recalcitrant fraction C g kg ⁻¹	4.94 \pm 3.03	2.43 \pm 0.49	1.822	3.58	0.151 *
Mineralization of C mg CO ₂ g ⁻¹	176.0 \pm 29.30	278.5 \pm 64.80	-2.781	6	0.032
Easily Extractable Glomalin mg g ⁻¹	0.5 \pm 0.00	0.8 \pm 0.00	-9.076	6	0.000
Microbial biomass carbon μ g C g ⁻¹	751.1 \pm 73.70	77.0 \pm 0.00	45.195	3	0.000
Colony forming units g ⁻¹	516,000 \pm 323,777	1,200,777 \pm 701,683	-1.516	6	0.180
Humic acids mg C kg ⁻¹	1657.4 \pm 91.90	2618 \pm 181.80	-10.464	6	0.000
Fulvic acids mg C kg ⁻¹	8671.4 \pm 144.20	9632.2 \pm 144.10	-8.497	6	0.000
Humins mg C kg ⁻¹	14,316.3 \pm 221.80	7350 \pm 166.40	50.229	6	0.000
Peroxidase μ mol g ⁻¹ h ⁻¹	4.34 \pm 0.71	4.50 \pm 0.16	-0.472	6	0.653
Polyphenol oxidase μ mol g ⁻¹ h ⁻¹	6.41 \pm 0.53	7.23 \pm 0.57	-2.021	6	0.090
Lacasse μ mol g ⁻¹ h ⁻¹	0.02 \pm 0.01	0.18 \pm 0.00	-13	6	0.000
B-glucosidase mg PNP g ⁻¹	145.1 \pm 7.20	510.6 \pm 19.5	-42.287	6	0.000
B-galactosidase mg PNP g ⁻¹	24.2 \pm 9.50	54.4 \pm 1.00	-4.608	3.03	0.019 *

Table 2. Soil bacterial sequences of pecan tree (*Carya illinoensis*) orchards under organic (Org) and conventional (Conv) management in Coahuila, Mexico. CD = chimeras discarded, QS = quality sequences after chimeras were discarded, BS = bacterial sequences, OTUs = operational taxonomic units.

Sample	Total	Assembled	Discarded	CD	QS	BS	OTUs
Org 1	278,980	68,366	210,608	568	67,798	27,154	6014
Org 2	225,583	52,984	172,599	486	52,498	22,087	5594
Org 3	187,477	57,859	129,607	610	57,249	34,945	6377
Mean	230,680	59,736	170,938	555	59,182	28,062	5995
Conv 1	212,217	51,586	160,618	523	51,063	33,292	6022
Conv 2	272,201	83,983	188,207	870	83,113	53,264	8653
Conv 3	318,199	94,434	223,744	842	93,592	59,769	9135
Mean	267,539	76,668	190,856	745	75,923	48,775	7937

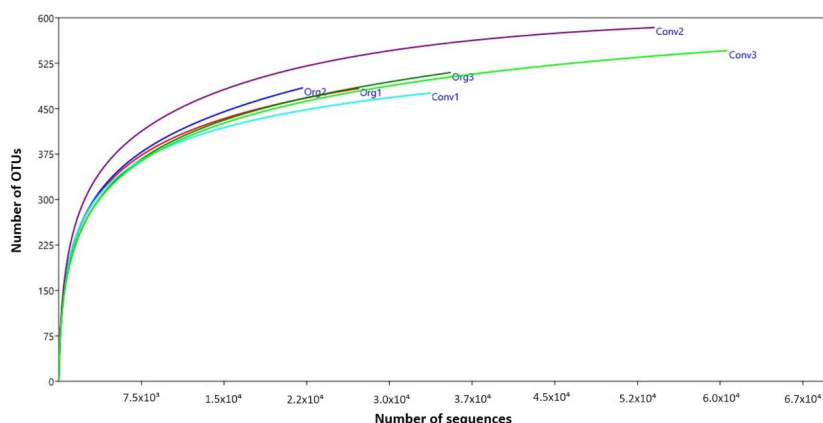


Figure 2. Rarefaction curves for soil bacteria OTUs identified from pecan tree (*Carya illinoensis*) orchards under organic (Org) and conventional (Conv) management in Coahuila, Mexico.

For Org management, the most abundant phyla were Proteobacteria ($\bar{x} = 36\%$), Actinobacteria ($\bar{x} = 24\%$), Planctomycetes ($\bar{x} = 18\%$) and Chloroflexi ($\bar{x} = 13\%$), (Figure 3a). A similar phyla composition was observed for the Conv management: Proteobacteria ($\bar{x} = 32\%$), Actinobacteria ($\bar{x} = 26\%$), Planctomycetes ($\bar{x} = 19\%$) and Chloroflexi ($\bar{x} = 15\%$), (Figure 3b). The remaining phyla were Acidobacteria, Gemmatimonadetes, Verrucomicrobia, Cyanobacteria, and Saccharibacteria.

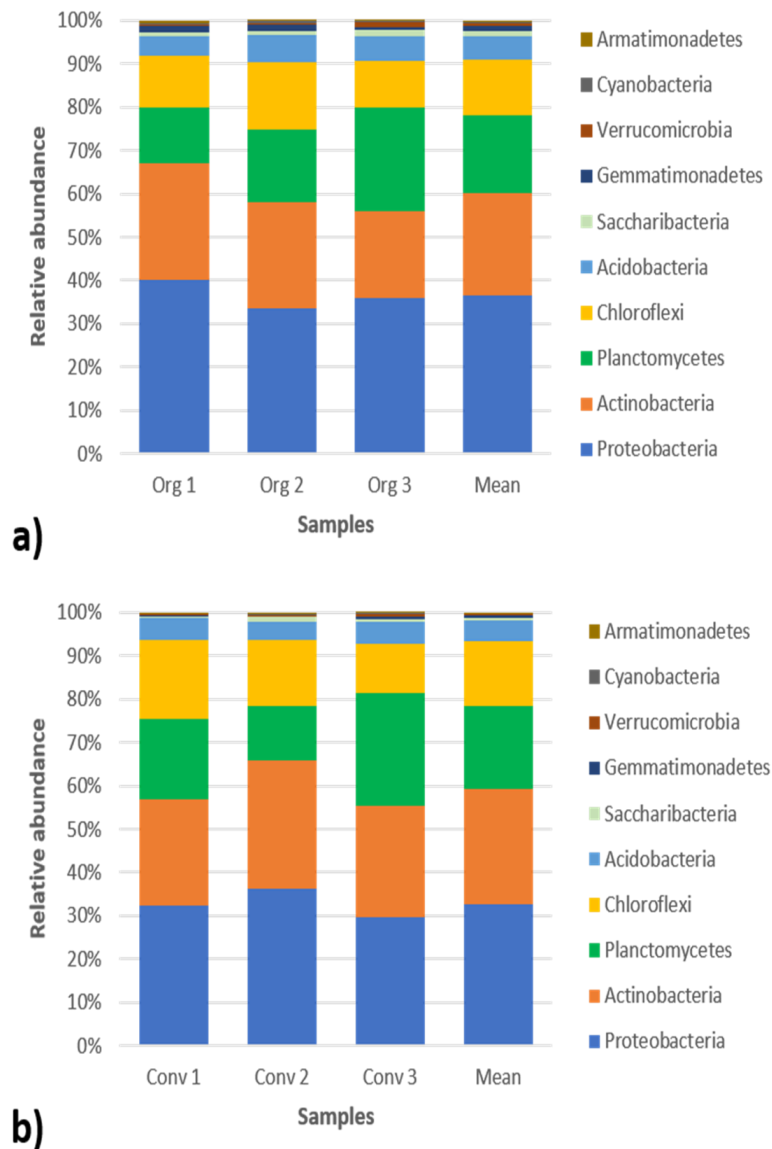


Figure 3. Relative abundance (%) per sample and means of the main bacterial phyla in soil samples of pecan tree (*Carya illinoensis*) orchards under organic (a) and conventional (b) management in Coahuila, Mexico.

A total of 776 bacterial genera was obtained, of which 29 had a relative abundance greater than 1% (20 had a taxonomical name, and 9 had a taxonomical key). The three more abundant cultivated genera were *Tepidisphaera* ($\bar{x} = 7.1\%$), *Sphingomonas* ($\bar{x} = 3.2\%$), and *Gemmata* ($\bar{x} = 4.0\%$). The first two genera were more representative in the Conv management, while the third one was more representative in the Org management. The remaining genera were *Dongia*, *Microvirga*, *Sphingosinicella*, *Streptomyces*, *Rhizomicrobium*, *Stenotrophobacter*, *Pseudolabrys*, *Zavarzinella* and *Catelliglobospora*; all of these were present in both managements (Table 3).

Table 3. Relative abundance of the bacterial genera found in the soil of pecan tree (*Carya illinoensis*) orchards under organic and conventional management in Coahuila, Mexico. Only those genera whose relative abundance was $\geq 1\%$ are shown. Asterisks indicate greater abundance according to the type of management.

Genera	Relative Abundance%	
	Organic	Conventional
<i>Tepidisphaera</i>	3.8	7.1 *
GQ396871	3.9	3.7
<i>Sphingomonas</i>	2.6	3.2 *
<i>Gemmata</i>	4.0 *	3.1
<i>Dongia</i>	3.1 *	2.1
FJ478799	4.2	2.0
<i>Microvirga</i>	0.9	1.9 *
GQ263023	1.4	1.8
<i>Sphingosinicella</i>	0.5	1.7 *
<i>Streptomyces</i>	1.5	1.6 *
<i>Rhizomicrobium</i>	1.1	1.3 *
EU335288	0.9	1.2
AF370880	1.6	1.2
FJ479444	0.7	1.2
<i>Stenotrophobacter</i>	0.9	1.2 *
EF125410	0.3	1.2
EU669599	0.3	1.1
<i>Pseudolabrys</i>	1.2 *	1.1
<i>Zavarzinella</i>	1.7 *	1.1
EU335161	1.1	1.0
<i>Catelliglobospora</i>	1.2 *	1.0

The CCA suggested that in both managements there is a separation between the phyla, which is associated with some chemical and biological characteristics of the soil. However, this separation was visible only in the second axis (Figure 4). Regarding axis 1, the phyla located left of the “y” axis belong to Gemmatimonadetes, Cyanobacteria, Parcubacteria, Chloroflexi, Actinobacteria, Proteobacteria, and Saccharibacteria—the same that are favored by PER (−0.64) and F3 (−0.62). In contrast, on the right side of the “y” axis, the Verrucomicrobia, Planctomycetes and Acidobacteria phyla were located in association with pH (0.66) and C/N (0.94). Above the “x” axis, the Org management samples were found, wherein the phyla belonging to Gemmatimonadetes, Parcubacteria, Proteobacteria, Cyanobacteria, Acidobacteria, and Verrucomicrobia were favored by the presence of HS (0.96). On the other hand, the phyla located below the “x” axis were Chloroflexi, Actinobacteria, Planctomycetes and Saccharibacteria, which were associated with EEG (−0.98), FA (−0.97) and B-glu (−0.97).

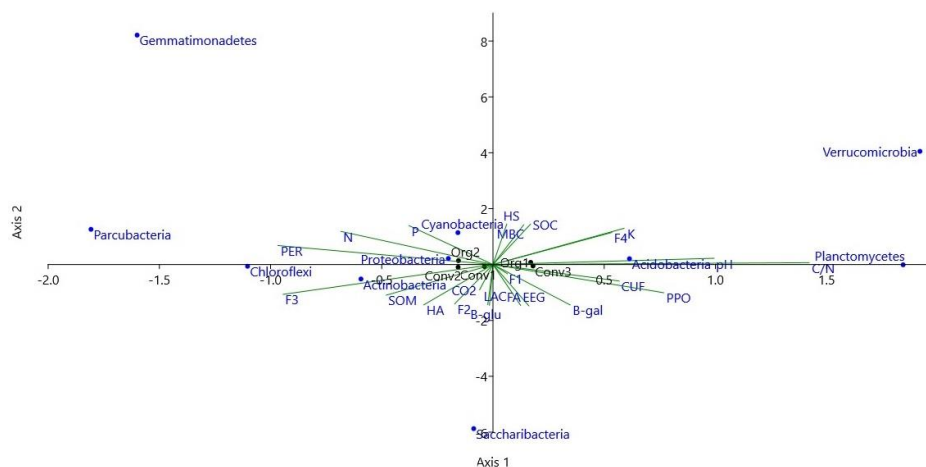


Figure 4. Canonical correspondence analysis of soil from pecan tree (*Carya illinoensis*) orchards under organic and conventional management in Coahuila, Mexico, identifying associations among the main phyla and the evaluated soil variables.

4. Discussion

4.1. Chemical and Biological Variables of the Soil

The management of the soil in agricultural systems affects its physical, chemical and biological characteristics [5]. It has been demonstrated that the concentration of N is higher in soils under Org management, due to the abundance of microorganisms capable of mineralizing N more efficiently [2,45]. Likewise, the addition of organic amendments generates a greater availability of nutrients such as P, which is mainly found in humic substances or in the microbial biomass of the soil [46,47]. In this study, the SOC content was higher than reported by other authors in pecan tree orchards [11,18]. In addition, HS are considered to be the most recalcitrant fraction of the organic soil and, therefore, are able to stay in the soil for longer [48]. It is likely that most of the SOC under Org management will be stabilized in less labile and recalcitrant forms. With respect to MBC, it has been shown that its content increases with the long-term establishment of plant cover, as in this study [49,50], while nitrogen fertilization tends to decrease it [51]. Likewise, it is the main agent of SOM decomposition, transforming nutrients and making them available [52], which may explain the high content of MBC and the low percentages of SOM in pecan orchards under Org management. In contrast, it has been shown that the F2 fraction has a high rate of decomposition and a shorter residence time in the soil [53], thus responding to Conv management by releasing carbon into the atmosphere in the form of CO₂, causing losses of nutrients and soil fertility [54]—contrary to what happens in soil Org management [55,56]. On the other hand, organic materials with a low degree of humification, i.e., labile, increase the HA and FA fractions [57,58]. According to Vásquez et al. [59], there is a positive correlation between CO₂ emissions and carbon labile fractions. Carbon loss in the form of CO₂ is caused by the decomposition of SOM by heterotrophic microorganisms, and occurs mainly when there is an increase in the availability of SOM and when it lacks a biochemical composition enriched with recalcitrant organic compounds, which makes it more difficult for microorganisms to disintegrate [60]. The results herein reported suggest that in the pecan tree orchard under Conv management, in spite of the fact that the content of SOM is greater than under Org management, the SOC is less stable and could easily be lost in the form of CO₂, because the SOM lacks recalcitrant organic compounds [60–62].

Agronomic management is influential in the increase of concentrations of glomalin [63], which agrees with the current study since the amount of glomalin was greater in Conv management. In this regard, the high concentration of CO₂ produces effects in the increase of the glomalin reserves [64], which suggests that glomalin is related to the high respiration rate in soils under Conv management. Furthermore, the oxidative enzyme LAC (EC 1.10.3.2) participates in the degradation and biosynthesis of lignin, and its activity may be increased by substrates that degenerate rapidly, such as cellobiose and glucose, and with an increase in fungi growth [65,66]. The above may suggest that the increase in oxidative enzymatic activity in the soil under Conv management may be due to the presence of substrates that may easily be degraded by fungi, which could also explain the high content of glomalin under this same management. As for β-glu (EC 3.2.1.21), it participates in the hydrolysis of cellobiose to glucose [67], degrading plant cell walls and contributing to the first phases of plant cell tissue decomposition [68]. The increased activity of β-gal (EC 3.2.1.23) may suggest that soil microorganisms are metabolically more active with rapid proliferation, thus increasing the efficiency of enzyme production [69]. Furthermore, as these enzymes degrade labile carbon compounds, their activity shows how the microorganisms present in the soil under Conv management mineralize this carbon fraction to obtain nutrients, but not to promote carbon sequestration [70].

4.2. Abundance of Bacterial Taxa

Proteobacteria phyla abound when there is a high availability of nutrients due to an increase in SOM, and also, they are able to consume labile organic carbon [71–73], which may suggest that the disposition of SOC in soil under Org management is subject to microbial decomposition of the SOM, and the velocity of this decomposition depends on, among other variables, the availability of

nutrients [74]. The Actinobacteria phylum has diverse physiological properties, such as the production of extracellular enzymes for the decomposition of organic matter [75]. It has also been shown that Actinobacteria abundance is associated with the respiration rates of the soil [76,77], which agrees with the current study, since CO₂ emission was greater under Conv management. Regarding bacterial genera that were more abundant in soil under Org management, *Gemmata* is capable of using glucose and galactose as a source of carbon in order to thrive, and therefore it is an important producer in the carbon and N cycles [78,79]. Likewise, it has been shown that *Dongia* and *Pseudolabrys* genera were significantly more abundant in the soils under non-tillage and addition of organic residues [80]. Regarding *Zavarzinella*, in spite of its importance, nowadays its isolation and behavior have been demonstrated in macroalgae [81], while there has been little or no research done in soils. Lastly, the *Catelliglobospora* genera have also been positively correlated with sucrose [82] and have a high potential for the deconstruction of cellulose and chitin [83]. It seems probable that the establishment of vegetation covers and deposits of organic matter in Org management will promote sources of carbon, which increase the abundance of *Gemmata*, *Dongia*, and *Pseudolabrys*. Regarding the more representative genera under Conv management, *Tepidisphaera* hydrolyzes a broad range of carbohydrates, among which are glucose and galactose, essential components in SOM [84]. On the other hand, in agricultural soils, some species of *Sphingomonas* have shown the capacity for degrading chemical compounds of herbicides into CO₂ that is liberated into the atmosphere [85], which may suggest that the abundance of both genera may be related to the SOM content and the mineralization process of carbon under this management.

The *Streptomyces* genera have been described at length for their adaptation to soils, where they are capable of forming hyphae that branch out to attach to and penetrate into insoluble organic residues from plants and other organisms, as well as recalcitrant insoluble inorganic polymers such as chitin and cellulose [86,87]. In this regard, studies show that the production of oxidative enzymes, such as LAC, associated with the population growth of *Streptomyces*, intervene in the degradation of lignocellulosic compounds [88,89]. Regarding *Rhizomicrobium*, a significant abundance has been reported in soils contaminated with fluoride and chloride [90] as well as in soils where organic residues are applied [80]. Finally, it has been shown that the *Stenotrophobacter* genera participate in the carbon and N cycle and respond to agronomic management [91,92]. These results suggest that the application of organic and inorganic compounds to the soil used in the conventional cultivation of pecan trees affects the bacterial abundance and functional diversity, which impacts the functional properties of the soil, particularly those related to carbon forms [6,93,94]. The results obtained from the CCA confirm that the bacterial communities in the soil were influenced by the type of management. Under the Org management, the Acidobacteria phylum was benefited by HS content. As was mentioned before, HS are the most recalcitrant fraction of organic soil due to the stabilization of SOC [31,48,95]. Rawat et al. [96] showed that Acidobacteria communities are essential to the cycle of carbon in the soil, and that its activity and dominion depend on them. Likewise, being classified as oligotrophic organisms, they are related to C sequestration, since it has been demonstrated that they are autotrophic and have the capacity to fix atmospheric CO₂ in the soils of arid and semi-arid ecosystems [97,98], and thus contribute to the generation of organic carbon reservoirs [99,100]. Conversely, under Conv management, the bacterial communities of the Actinobacteria Phylum were influenced by the EEG, FA, and B-glu variables. Thereon, the change in the microbial community of fungi and Actinobacteria is due to the amounts of organic residues that result from the availability of resources [6,72,101]. It has been shown that both microbial communities are fundamental in the degradation process of complex compounds such as cellulose, lignin, and chitin [102], where Actinobacteria, in particular, present diverse physiological properties, such as the production of extracellular and metabolic enzymes related to the decomposition of SOM [75].

5. Conclusions

The use of organic practices in the cultivation of pecan trees seems to influence the concentration of nutrients and various chemical and biological variables in the soil, mainly in the capture of recalcitrant C compounds. Furthermore, this type of management could favor bacterial communities capable of promoting greater efficiency in organic carbon sequestration. On the other hand, conventional management practices influence the increase in carbon mineralization, as well as the enzymatic activity of the soil, particularly that of the enzymes related to the metabolism of labile compounds. The use of genomic technologies has allowed the discovery of the soil microbiome in recent years, however it is still necessary to understand the adaptation and plasticity of some bacterial communities and other soil microorganisms, as well as their functional biodiversity and soil–plant dynamics, which are essential in order to preserve the optimal state of the soil.

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