Short-term evaluation of soil physical, chemical and biochemical properties in an abandoned cropland treated with different soil organic amendments under semiarid conditions

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Abstract

This study evaluate the effects of four organic soil amendments on soil. Physical, chemical and biochemical properties were compared to untreated and natural (not cultivated) soils in a semiarid region (Andalusia, Spain). A large set of physical, chemical biochemical properties and, the composition of bacterial communities; and overall soil quality index (SQI) were evaluated on soils treated with organic soil amendments of animal origin (compost from sheep and cow manure [CS] or chicken manure, [CK], vegetal origin (greenhouse crop residues [CC]), and vermicompost (CV). Immediately after application, the animal origin compost significantly increased pH, electrical conductivity (EC), and total nitrogen (TN) as well as the enzymatic activities associated with the carbon (C) cycle but decreased the richness and evenness of bacterial communities. After 3 months of treatment, all measured properties recovered except for EC, TN and dehydrogenase activity (whose increase was stable over time), as did bacterial richness, which remained lower. The vegetal-originating compost increased EC and pH whereas the other effects were not significant throughout the monitoring period. CV application did not affect soil properties. The SQI was the highest for soils treated with CK compost, both immediately after application and over time. The soil treatments with the other organic amendments did not result in a significantly different SQI over time compared to both untreated and natural sites.

Keywords: Labile organic matter, Soil restoration, Enzymatic activity, Organic amendments, Basal soil respiration.

1. Introduction

The equilibrium between ecosystem protection and crop production is one of the most challenging goals of modern agriculture. In this context, the need to control the effects of the growth of the world population, climate changes and degradation of natural resources on agricultural soils requires the development of suitable agricultural practices (Bouhia et al., 2022b). These effects often lead to the abandonment of agricultural farmlands after their productivity has been fully exploited, which is an important global issue (Yang et al., 2020). According to Li and Li (2017), changing socioeconomic factors were the main driving forces for farmland abandonment, and land marginalization was a result of the drastic increase in the cost of farming opportunities. It is estimated that globally during the twenty-first century, the land abandonment rate reached approximately 8%–10% of cropland area (Zhang et al., 2023). Europe is particularly affected by this problem: it suffers from a noticeable abandonment rate because many cultivation activities are not profitable. For this reason, soils have become unsuitable for production over large areas, presumably exceeding 20 million hectares by 2030 (Perpiña Castillo et al., 2018), and therefore will be exposed to noticeable soil degradation rates. Abandoned ecosystems rarely recover their functionality and improve the provision of those ecosystem services that are closely associated with soil quality (Lal, 2016).

In arid and semiarid regions, abandoned agricultural soils experience even more difficulties in ecosystem provisioning and regulation functions, and undergo more severe loss of biodiversity than other environments (Smiraglia et al., 2016; Stanturf, 2021). Furthermore, the high level of solar radiation and the infrequent but heavy rainfalls that are typical of semiarid regions complicate the processes of natural restoration (Lasanta et al., 2019). Natural recovery or return to a precultivation state in these areas may require a long time and sometimes requires active restoration actions to fully recover their original state (Yang et al., 2020). Rehabilitation of degraded soils is essential to maintaining a balance between degradation processes and the recovery of soil quality and health (Doran and Zeiss, 2000; Lal, 2014).

A viable option to contrast soil degradation and the abandonment of unproductive cropland is the application of organic soil amendments to degraded lands (Gupta et al., 2021; Ortega et al., 2020). Organic amendment provides many direct and indirect benefits to crop productivity, such as

improving soil structure and stability, reducing erosion, and enhancing nutrient availability and water retention capacity (Bouhia et al., 2021a; Rodríguez-Berbel et al., 2021). In particular, organic soil amendments increase organic soil matter (OM), which is considered the main source of nutrients for vegetation growth and development (Risse et al., 2006). An appropriate OM content ensures the efficient biological cycling of nutrients, which contributes to sustainable management of soil and agricultural productivity (Bouhia et al., 2021a). By contrast, OM depletion is one of the critical indicators of soil degradation because it is associated with the decay of most soil parameters and processes, including fertility and overall biological functions (Bouhia et al., 2023). Moreover, the increase in OM following application of organic soil amendments could promote the activity of soil microorganisms, which are related to microbial communities in the soil. This enhanced activity improves soil enzymatic activities and microbial diversity, which in turn play an essential role in stabilization and treatment of organic matrices within biological processes (Bouhia et al., 2023). Soil microorganisms play an essential role in mineralization, decomposition of plant residues, efficiency of nutrient use, and production of root exudates (Daynes et al., 2013), generating positive feedback for soil quality (Urra et al., 2019). It is also worth mentioning that the production of stable organic soil amendments from animal and/or vegetal residues is one of the best approaches to waste management, aligned with the concept of a circular economy, because this practice fully integrates both economic and environmental aspects (Bouhia et al., 2022a). In recent decades, numerous studies on the effects of organic soil amendments on soil restoration in arid and semiarid ecosystems have confirmed that these matrices, especially compost, are effective in accelerating regeneration processes by favoring plants' establishment and development and increasing soil quality and health (Hueso-González et al., 2018; Miralles et al., 2012; Soria et al., 2021). Hueso-González et al. (2018) reviewed the role of organic soil amendments in dryland restoration under different types and application rates, showing the role of the type, dose, stability and maturity of amendments in determining the success or failure of this practice. Soria et al. (2021) demonstrated that organic soil amendments significantly improved all properties of limestone quarry soils compared with untreated sites in the southeastern region of Spain. Donn et al. (2014) showed that soil fertility improvement increases root growth and reinforces surface soil on slopes because of compost application. Miralles et al. (2012) found a general decline in organic soil carbon sequestration and associated enzymatic activities in the semiarid mountain soils of southern Spain because of changes in land use (cultivations, secondary bush, high mountain bush, juniper, evergreen oak and pine stands) and application of organic soil amendments.

However, in spite of these experiences, the effects of the organic soil amendments depend on several factors—soil characteristics, application rates, quality of substrates—and are therefore site-

specific. This means that the effectiveness of this technique in restoring soils in abandoned croplands in arid and semiarid areas needs to be further studied with specific investigations. This effectiveness, resulting from the great diversity of organic residues in composing soil amendments and from the variable effects on the physical, chemical and biological properties of soil to be treated, requires the use of proper indicators of soil quality that are able to provide important information on the pre- and post-treated soils and recovery levels. To the best of our knowledge of the authors, few studies have compared changes in complete datasets of the physical, chemical, biochemical and microbiological properties of soils, resulting from the application of different organic soil conditioners by comparing different materials. This task is essential to evaluating whether and how much a specific organic soil conditioner is able to improve the quality of degraded soils compared to untreated soil and how far the treated soils are from sites with better soil quality, such as the uncultivated soils. This evaluation is important in the short window after the application of organic soil conditioner because a prompt restoration of a degraded agricultural system is essential if farmers are to quickly recover as much as possible of the original soil quality and crop productivity.

The aim of this study to evaluate the changes in soil quality of abandoned agricultural land in a Mediterranean region (southeastern Andalusia, Spain) treated with different organic soil amendments of animal or vegetal origin. To this aim, we compared the short-term effects of 4 different composts on several physical, chemical, biochemical and microbiological properties as well as the overall quality of abandoned and cultivated soils and uncultivated sites. Three research questions support this study: (i) Which are the soil properties that are modified by the application of each organic soil amendment? (ii) Are the effects of the treatments stable in the short term? (iii) And which is the most effective organic soil amendment for restoration of soil quality in the experimental soils? The results of this study may be useful to land planners and agronomists in selecting suitable organic soil amendments to restore degraded croplands under semiarid conditions.

2. Materials and Methods

2.1 Description of the study area

The study was conducted on the natural site of the Sierra Alhamilla province of Almería (Andalusia, SE Spain) (Figure 1). The climate is semiarid Mediterranean, with an average annual temperature of 17.6 °C. August and January are the hottest and coldest months, with an average temperature of 25.4 °C and 11.2 °C, respectively. Rainfall is often torrential (few events, often with

high to very high intensity) and irregularly distributed over time, with an average accumulated depth of 222 mm (mean values between the years 1995–2021) and 240 mm in 2000–2021 (SAIH Hidrosur, 2021). The study site is abandoned farmland (36 ° 5 9’ 23.87’’N, 2° 19’ 05.29’’W) at an altitude of 1255 m.a.s.l. and with a slope of about 7% (Fig. 1). Soils in the study area are mainly eutric Regosols on sandstone and micaesquitos (Peinado and Sierra, 2004).

The study area was subjected to indiscriminate logging, charcoal extraction, and intensive agriculture in the past and was reforested at the end of 1960s. The site selected for the soil amendment experiments was not reforested and was used as a self-subsistence orchard and later for cereal cultivation. The surrounding natural vegetation was not recolonized after its abandonment.

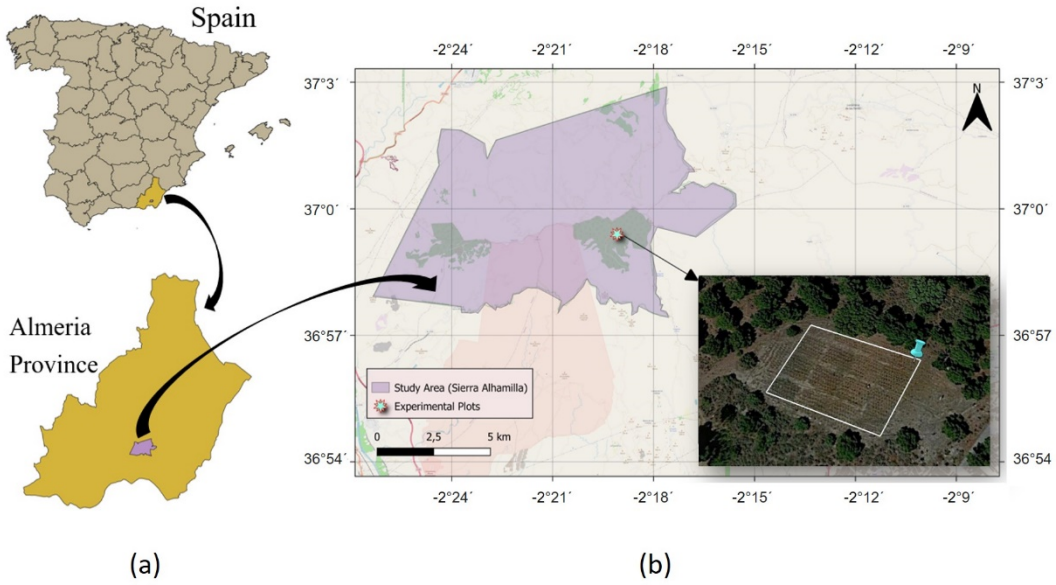

Figure 1: Location of the study site (a) and an orthophotograph of the experimental plots (b, image source: Google Earth, 2022).

2.2. Experimental design

Six soil conditions were analyzed, of which 4 contained treatments with organic soil amendments (described in detail in section 2.3). Furthermore, a fifth soil condition was taken as a control (CON) with 3 plots that were cultivated and then abandoned but not treated with organic amendments. This soil condition allows for a comparison of soil quality with or without a supply of organic soil amendments on both survey dates. Finally, a natural soil (NAT), which was not subjected to any agricultural activities, was also considered as a soil quality reference and selected in

a site close to the agricultural plots. Therefore, the experimental design comprised 6 soil conditions (agricultural abandoned soil treated with the 4 organic amendments, agricultural abandoned and untreated soil, CON, and natural and uncultivated soil, NAT) x 2 survey dates ('t1' and 't2', see Section 2.4) x 3 replications.

2.3. Plot installation

Before starting the experiment, the soil was tilled to reduce compaction, using a farm tractor and ripper. Then, 18 experimental plots, each one covering 35 m² (7 m × 5 m), were installed. The 4 soil treatments with organic soil amendments were applied to the plots on 1April 2021.

The organic substrates used for soil treatment were marketed by local companies and produced by composting the following waste materials: (i) vermicompostimg manure of sheep and cow (CV); (ii) greenhouse crop residues (CC); (iii) manure of poultry raised on ecological farms (CK); and (iv) certified organic compost, produced from a mixture of chicken and sheep manure and vegetable waste (CS). For each organic amendment of the soil, a single dose was used, to increase the initial soil organic matter (SOM) content to 1.5%. Table 1 reports the primary chemical characteristics of the 4 organic soil amendments.

Table 1: Main chemical characteristics of organic soil amendments.

Compost characteristics	**Organic soil amendments**			
	CV	CC	CK	CS
pH	8.01	9.20	7.33	6.24
OM content (%)	35	35	49	59
Total nitrogen content (%)	2.2	1.5	2.9	2.7
Total phosphorus content (%)	1.2	0.8	2.7	2.0

Notes: CV: soil treated with vermicompost; CC: soil treated with compost of greenhouse crop residues; CK: soil treated with manure from chickens; CS: soil treated with organic compost derived from mixture of chicken and sheep manure; CON: untreated soil as control; NAT: natural and uncultivated soil. Data derived from producers.

After installation of the plots, the topsoil was homogenized in the upper range of 20-30 cm. Then, 60 plants (16 *Rosmarinus officinalis* L., 16 *Lavandula stoechas* L., 12 *Thymus mastichina* L., and 16 *Ulex parviflorus* Pourr.) were planted at a spacing of 60 cm × 60 cm.

2.4. Soil sampling

In the experimental plots, the soil samples were collected on 2 dates (16 April and 30 July 2021), that is, 2 weeks (t1) and 3 months (t2) after the application of the organic soil amendments. The 18 samples, each consisting of subsamples collected at 10 randomly chosen points for each plot on the same day, were immediately transported to the laboratory in isothermal bags at 4 °C. A portion of the samples was air-dried, homogenized, and sieved (ø < 2 mm) to determine the physical and chemical properties of the soil, and another portion was kept at 4 °C for immediate enzyme assays. Of the latter portion, a part was immediately used for DNA extraction and next generation sequencing (NGS) analysis.

2.5. Measurements of physical, chemical and biochemical properties of soil

In the soil composite samples, electrical conductivity (EC) and pH were determined in an aqueous suspension (soil/water ratio 1:5 and 1:2.5, respectively) with a digital conductivity meter (CRISON BasiC 20, Barcelona, Spain) and a pHmeter (LAQUA PH1100, ORIBA, Tokyo, Japan), respectively. Total organic carbon (TOC) was determined by colorimetric methods following Mingorance et al. (2007) in a Spectronic Helios Gamma UV–Vis spectrophotometer (Thermo Fisher Scientific, Waltham, Massachusetts, USA). TTotal nitrogen content (TN) was analyzed by total combustion at a temperature of 960 °C and a heating column with thermal conductivity detector (TCD) for the measurement of the separated gases (ELEMENTAR Rapid N; Elementar Analysensysteme GmbH, Hanau, Germany). C:N ratio was calculated from the TOC and TN measures. Available phosphorus (P) was determined following the method described by Olsen and Watanabe (1957). Available water (AW) for plants was estimated by measuring pFs at -1500 and -33 kPa using the Richards (1941) method. Carbohydrate (CH) and polyphenol (PF) contents were determined by cold extraction from an aqueous solution (soil/water 1:10 solution ratio). The CH content was determined by the anthrone-sulfuric acid method proposed by Brink et al. (1960) and measured PF content following the Folin-Ciocalteu method (Ribéreau-Gayon, 1968). Neither soil bulk density because amendment application that was conducted manually did not result in soil compaction;) or available potassium because of the small amount in the used composts) or hazardous microelements such as heavy metals, which were thought to have been supplied to soil, because of the use of only marketable compost) were measured.

2.6. Measurements of basal soil respiration and enzymatic activities

Soil basal respiration (SBR) was measured in hermetically-sealed 100-ml vials containing 10 g of soil with a moisture content of 40%–50 % of its water-holding capacity and incubated for 35 days at 28 °C in the dark. More specifically, the volume of CO_2 released by soil microorganisms was determined every day during the first week and every 3 days thereafter, using an infrared CO_2 sensor (IRGA S151; Qubit Systems Inc., Canada).

Dehydrogenase activity (DHA) was measured from 1 g of soil with a level of 60% of its water holding capacity, following the method of Garcia et al. (1994) with the reduction of 0.2 ml of p-iodonitrotetrazolium chloride to iodonitrotetrazolium formazan. β-glucosidase (BGA) and alkaline phosphatase (PA) enzyme activities were measured on 0.5 g of soil, according to the methods of Eivazi and Tabatabai (1977) and Tabatabai and Bremner (1969), respectively. Urease activity (UA) was measured using 1 g of soil, according to the procedure of Kandeler and Gerber (1998).

2.7. Soil DNA extraction, high-throughput sequencing and identification of bacteria taxa

DNA from soil samples was extracted using the DNeasy PowerSoil Kit (QIAGEN, Hilden, Germany) from 0.3 g of soil and quantified with an ND-2000 Nanodrop spectrophotometer (Thermo Fisher Scientific, USA). To verify the absence of contamination during DNA extraction, a blank control was added using one of the kit tubes. The V4–V5 regions (400–500 bp) of the 16S bacterial rRNA were amplified in vitro by polymerase chain reaction using the primer pair 515FB (5'-GTGYCAGCMGCCGCGGTAA-3') and 926R (5'-CCGYCAATTYMTTTRAGTTT-3') (Walters et al., 2016) at the Centre for Comparative Genomics and Evolutionary Bioinformatics, Dalhousie University, Canada. Paired-end sequencing was performed using the Illumina MiSeq platform (Reagent Kit v3 - 2 × 300 cycles) as described in Comeau et al. (2017). In addition, one negative control per 96-well plate was analyzed. Sequences were processed with Quantitative Insights Into Microbial Ecology software (QIIME2 version 2019.7) following the protocol of Comeau et al. (2017) to identify the soil bacterial community at the phylum and genus levels. Bacterial taxa with relative abundances over 0.5% were selected for the phylum level and over 0.1% for genus or the next available upper taxonomic level in all samples (n = 18). Alpha diversity indices of bacteria were calculated using the QIIME2 software, which determines the number of amplicon sequence variants

(ASV) observed in each sample. Moreover, phylogenetic diversity indices (number of ASVs' richness, Nsp and Pielou index, Pi) were sampled uniformly at 1000 reads per sample. Nsp is an index of species richness and Pi expresses the evenness of individual species.

2.8. Statistical analysis

Statistical differences in the physical, chemical and biological properties, enzyme activities and bacterial abundance (in terms of phylum and diversity indices) were analyzed using a two-way ANOVA. Treatments (CV, CC, CK, CS, CON and NAT) and time (t1 and t2) were considered as independent factors. The differences in the response variables among factors were evaluate using the Tukey's pairwise comparison test (at $p < 0.05$). The equality of variance and normal distribution, which are assumptions of the statistical tests, were evaluated by normality tests or square root-transformation when necessary.

Then an indicator species analysis (ISA) was conducted using the multipatt function with 9999 permutations to identify the bacterial taxa of the genus or next higher taxonomic level that was specifically associated with the different soil conditions (De Cáceres and Legendre, 2009).

Finally, a principal component analysis (PCA) was applied separately at the 2 survey times. The first 3 PCs were chosen, which together explained 70% of the original variance. The PCA was integrated using agglomerative hierarchical cluster analysis (AHCA) to group parameters with similar characteristics. The Euclidean distance was used as a similarity-dissimilarity measure (Chatterjee et al., 2020).

All statistical analysis was conducted using the XLSTAT software (release 2019, Addinsoft, Paris, France) except ISA, which was conducted using the IndicSpecies R package.

2.9. Evaluation of the soil quality index

To have determine the overall soil quality among the conditions, the well-known soil quality index (SQI) proposed by Andrews et al. (2002) was calculated for each soil condition at the 2 survey dates in 3 main steps: (i) choice of appropriate indicators for a minimum data set (MDS); (ii) conversion of the indicators into scores; and (iii) aggregation of the scores into the SQI.

In more detail, a PCA (applied to all physical, chemical and biological properties; enzyme activities were considered in Section 2.8 and used as an MDS method to select the most suitable soil quality indicators. However, in terms of bacterial abundance, only diversity indices were considered

because there are no optimal values for *phyla*. Only highly weighted variables were retained from each PC for the MDS, that is those loadings having absolute values within 10% of the highest factor loading or ≥ 0.40 (Wander and Bollero, 1999). 4 and 3 PCsat the 2 survey dates 't1' and 't2', respectively; and these selected PCs explained 89.3% and 80.5% of the variance in the original variables. At 't1' the following variables were EC, P, PF, DHA, BGA, TOC, C:N, PA, AW, pH and UA. At 't2' the retained variables were EC, TN, P, CH, PF, DHA, Nsp, C:N, BGA, PA and UA.

After selecting the MDS, all indicators were converted into scores for inclusion in the SQI using a linear method. Indicators for plots under each soil condition were ranked in ascending or descending order, depending on whether a higher value was considered 'good' or 'bad' in terms of soil function. For 'more is better' indicators, each observation was divided by the highest observed values, and therefore the highest observed value received a score of one. For 'less is better' indicators (in our case EC and pH), the lowest observed value (in the numerator) was divided by each observation (in the denominator) so that the lowest observed value received a score of one (Andrews et al., 2002). Although pH should be standardized using a midpoint optima, such as the Gaussian function (Andrews et al., 2002), following Liebig et al. (2001), this variable was also scored as 'lower is better' because all values were higher than 6.5. Then the scores of the plots were weighted using the PCA results. The amount (in percentage) of the variation in the total data set explained by each PC, standardized to unity, was considered as the weight for scores under a given PC. Finally, the weighted scores for each plot were tallied and calculated the mean and standard errors for each soil condition. Because the SQI is a linear combination of scores by coefficients, its value can be higher than one.

3. Results

3.1. Changes in physical and chemical properties among soil conditions

According to ANOVA, most of the physical and chemicals properties were significantly different among the 6 soil conditions (4 treatments, cultivated but untreated and uncultivated soils). By contrast, only TN, P, CH, PF and PA were significantly different between the 2 sampling dates (Table 1.SI).

Compared with NAT, plots treated with organic soil amendments showed significantly higher EC and pH and a lower C:N ratio immediately following the compost addition. On the same date, the treatments significantly increased soil EC and TN (except for CV) compared with untreated soils

(CON). The soils treated with CK and CS showed increased EC, PF, CH and nutrient contents; CC treatments increased only EC; and no changes were observed in plots with CV addition (Table 2). Over time (3 months after compost application), only EC was significantly different between the treated and the control soils (except those supplied with CV): TN in CK and CS soils and P, CH and PF in CK soils were higher compared with CON plots.

Table 2**:** Physical and chemical properties of soil (mean ± standard error, n = 3) measured under 6 soil conditions at 2 sampling dates.

Sampling date	Variables	Soil conditions					
		CV	**CC**	**CK**	**CS**	**CON**	**NAT**
t1	EC ($mS\ cm^{-1}$)	0,410 ± 0,03 ab	0,746 ± 0,07 bcd	0,888 ± 0,07 bcd	1,091 ± 0,24 cd	0,043 ± 0,00 a	0,050 ± 0,01 a
	pH	8.046 ± 0.12 cd	8.400 ± 0.06 d	8.216 ± 0.10 d	8.330 ± 0.07 d	7.756 ± 0.11 bc	7.76 ± 0.04 bc
	TOC (%)	2,717 ± 0,19 ab	3,235 ± 0,13 abc	4,088 ± 0,34 bc	3,885 ± 0,16 bc	1,774 ± 0,19 ab	5,338 ± 1,57 c
	AW (%)	11,43 ± 0,26 ab	10,41 ± 0,58 ab	8,853 ± 0,03 ab	12,00 ± 0,84 ab	9,37 ± 1,46 ab	12,39 ± 1,47 b
	TN (%)	0,296 ± 0,01 ab	0,331 ± 0,01 ab	0,435 ± 0,03 bc	0,525 ± 0,01 c	0,203 ± 0,01 a	0,349 ± 0,07 abc
	C:N	9,14 ± 0,44 abc	9,79 ± 0,16 bc	9,59 ± 1,50 abc	7,39 ± 0,07 ab	8,701 ± 0,44 abc	14,53 ± 1,85 d
	P (%)	0.008 ± 0.001 abc	0.003 ± 0.00 a	0.027 ± 0.001 bc	0.017 ± 0.002 abc	0.001 ± 0.000 a	0.001 ± 0.000 a
	CH ($\mu g\ C\ g^{-1}$ soil)	13,67 ± 1,43 a	14,91 ± 0,60 a	316,2 ± 57,6 c	78,21 ± 16,6 ab	26,63 ± 14,1 a	49,62 ± 1,72 ab
	PF ($\mu g\ C\ g^{-1}$ soil)	14,92 ± 1,36 a	18,61 ± 1,58 a	149,4 ± 18,1 c	117,3 ± 32,7 bc	19,30 ± 3,46 a	48,06 ± 6,47 ab
t2	EC ($mScm^{-1}$)	0,489 ± 0,06 abc	1,225 ± 0,01 d	1,154 ± 0,24 d	1,295 ± 0,19 d	0,075 ± 0,01 a	0,053 ± 0,00 a
	pH	7,626 ± 0,10 bc	7,406 ± 0,09 ab	7,423 ± 0,09 b	7,496 ± 0,02 b	7,57 ± 0,04 b	6,98 ± 0,07 a
	TOC (%)	2,152 ± 0,06 ab	2,534 ± 0,27 ab	2,389 ± 0,42 ab	2,526 ± 0,13 ab	1,086 ± 0,20 a	3,432 ± 0,08 abc
	AW (%)	9,205 ± 0,03 ab	8,290 ± 0,17 ab	7,879 ± 0,61 a	9,103 ± 0,63 ab	9,856 ± 1,36 ab	11,83 ± 0,20 ab
	TN	0,307 ± 0,03 ab	0,356 ± 0,02 abc	0,423 ± 0,06 bc	0,469 ± 0,04 bc	0,187 ± 0,02 a	0,293 ± 0,01 ab

	(%)						
	C:N	7,14 ± 0,64 ab	7,15 ± 0,86 ab	5,63 ± 0,39 ab	5,43 ± 0,32 a	5,69 ± 0,40 ab	11,73 ± 0,67 cd
	P (%)	0.006 ± 0.00 ab	0.002 ± 0.00 a	0.028 ± 0.01 c	0.013 ± 0.00 abc	0.000 ± 0.00 a	0.001 ± 0.00 a
	CH ($\mu g\ C\ g^{-1}$ soil)	25.81 ± 1.99 a	28.04 ± 1.15 a	139.8 ± 19.6 b	106.6 ± 22.2 ab	20.85 ± 0.42 a	55.63 ± 1.99 ab
	PF ($\mu g\ C\ g^{-1}$ soil)	16.91 ± 2.11 a	20.37 ± 2.23 a	142.0 ± 45.8 c	67.38 ± 12.2 abc	15.59 ± 2.19 a	62.37 ± 2.34 abc

Notes: EC: electrical conductivity; TOC: total organic carbon; AW: available plant water; TN: total nitrogen; C/N: carbon to nitrogen ratio; P: assimilable phosphorus; CH: carbohydrates; PF: polyphenols; soil conditions: CV - soil treated with vermicompost; CC - soil treated with compost of greenhouse crop residues; CK - soil treated with manure from chickens; CS - soil treated with organic compost derived from mixture of chicken and sheep manure; CON - cultivated and untreated soil; NAT - natural and uncultivated soil); sampling dates: t1 - immediately after treatment; t2 - 3 months after treatment; lowercase letters indicate significant differences in the interaction 'soil condition x sampling date' after Tukey's test ($p < 0.05$).

3.2. Changes in biochemical properties among soil conditions

3.2.1. Changes in soil basal respiration

Figure 1.SI reports the daily values of soil basal respiration throughout the monitoring period. Considering these values, it was evident that only soils treated with CC and CON plots had significantly lower SBR than reference sites (NAT soils). When compared with CON, SBR was significantly higher in all treatments with organic soil amendments except CC soils and NAT plots, and the soils treated with CK and CS showed the highest values (Figure 2).

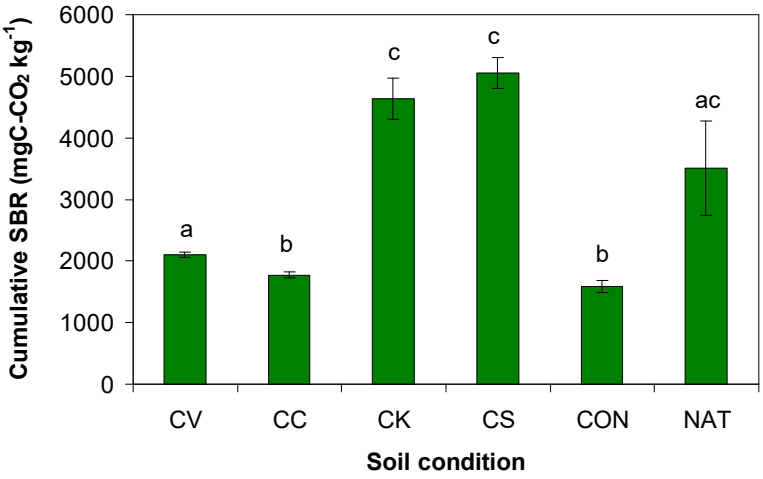

Figure 2**:** Basal respiration of soil (mean ± standard error, n = 3) measured under 6 conditions and 2 sampling dates.

Legend: soil conditions: CV - soil treated with vermicompost; CC - soil treated with compost of greenhouse crop residues; CK - soil treated with manure from chickens; CS - soil treated with organic compost derived from mixture of chicken and sheep manure; CON - cultivated and untreated soil; NAT - natural and uncultivated soil); sampling dates: t1– immediately after treatment; t2 – 3 months after treatment; lowercase letters indicate significant differences in the interaction 'soil condition x sampling date' after Tukey's test ($p < 0.05$).

3.2.2. Changes in enzymatic activities

The differences in the enzymatic activities among the 6 soil conditions were always significant according to ANOVA, and the same was found over time, except for PA (Table 1.SI). More specifically, at survey 't1', only the soils treated with CK and CS showed significant increases in DHA and BGA compared with all other plots. These values decreased over time and at survey 't2'

only an increase in DHA was noticed for CK soils. No significant differences in PA content were found among all soil conditions at both survey dates except between CON and NAT plots and in UA at time 't1'. In contrast, for the last survey, UA only increased significantly in CS plots (Figure 3).

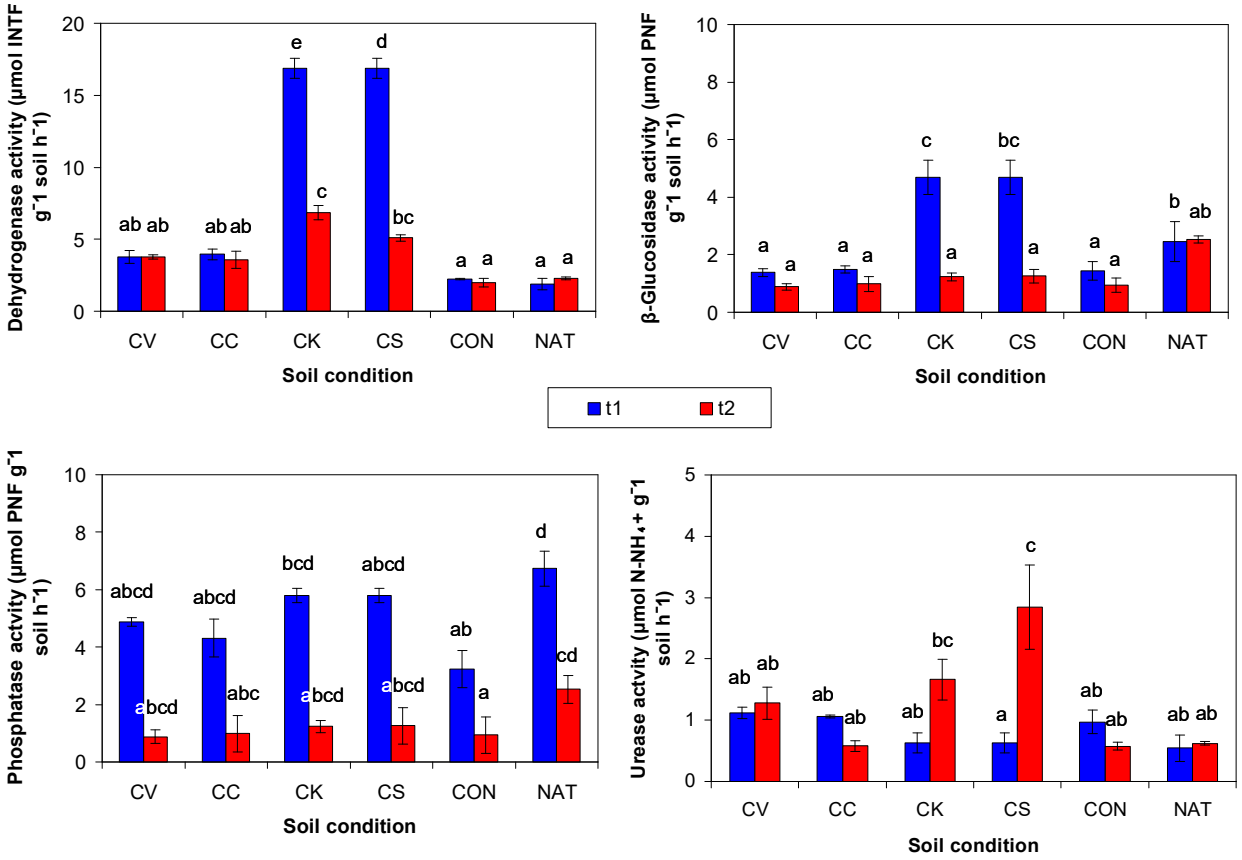

Figure 3: Enzymatic activities (mean ± standard error, n = 3) measured under 4 soil conditions and 2 sampling dates.

Legend: soil conditions: CV - soil treated with vermicompost; CC - soil treated with compost of greenhouse crop residues; CK - soil treated with manure from chickens; CS - soil treated with organic compost derived from mixture of chicken and sheep manure; CON - cultivated and untreated soil; NAT - natural and uncultivated soil); sampling dates: t1- immediately after treatment; t2 – 3 months after treatment; lowercase letters indicate significant differences in the interaction 'soil condition x sampling date' after Tukey's test ($p < 0.05$).

3.3. Changes in composition and diversity of bacterial communities among soil conditions

The ANOVA revealed that both the richness and evenness of bacterial communities (the latter measured by Pielou index) were significantly different among the soil conditions analyzed whereas only the evenness significantly varied over time (Table 1.SI). The CC, CK and CS

364 treatments of soil resulted in the lowest values of bacteria richness and Pielou index. In the survey at
365 ‘t1’, these values were significantly different from CON plots but not NAT soils; in the final survey,
366 only bacteria richness measured in CK and CS plots was significantly lower than CON soils (Figure
367 4).
368

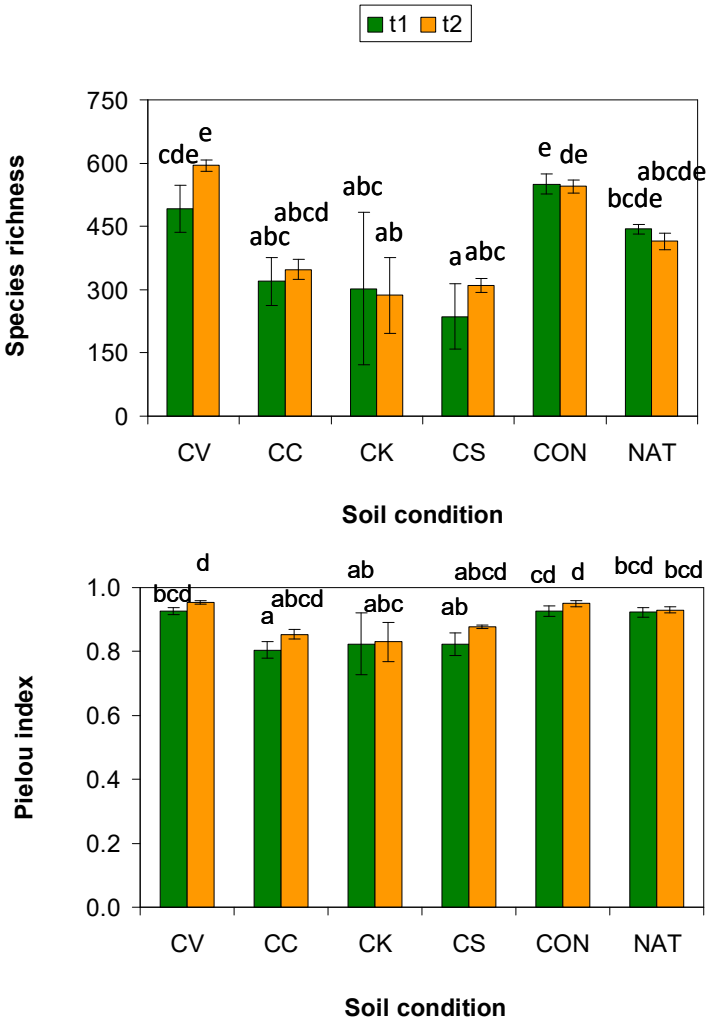

Figure 4: Bacterial richness and evenness (expressed as Pielou index) measured under 6 soil conditions and 2 sampling dates.

Legend: soil conditions: CV - soil treated with vermicompost; CC - soil treated with compost of greenhouse crop residues; CK - soil treated with manure from chickens; CS - soil treated with organic compost derived from mixture of chicken and sheep manure; CON - cultivated and untreated soil; NAT - natural and uncultivated soil); sampling dates: t1- immediately after treatment; t2 – 3 months after treatment; lowercase letters indicate significant differences in the interaction ‘soil condition x sampling date’ after Tukey’s test ($p < 0.05$).

369 The number of sequences in the bacterial domain was 787,733, 14 showed a relative
370 frequency over 0.1% and 10 showed a relative frequency greater than 0.5%. ANOVA showed that

the relative abundance of all bacterial *phyla* was significantly different among the 6 soil conditions whereas only the *Actinobacteria, Planctomycetes, Firmicutes, Chloroflexi* and *Verrumicrobia* phylum were significantly variable over time (Table 1.SI). In treated soils, bacterial communities changed compared with CON and NAT plots at both, 't1' and 't2' survey dates (Figure 5). Compared with NAT plots, only the *Acidobacteria* and *Gemmatimonadetes* phylum were significantly different whereas significant differences were found between treated and CON soils only for *Deinococcus-Thermus*. The most abundant phyla in treated soils were *Proteobacteria* and *Bacteroidetes* whereas again *Proteobacteria* and *Acidobacteria* prevailed in CON and NAT soils. The *Deinococcus-Thermus* phylum was only found in treated soils (Figure 5).

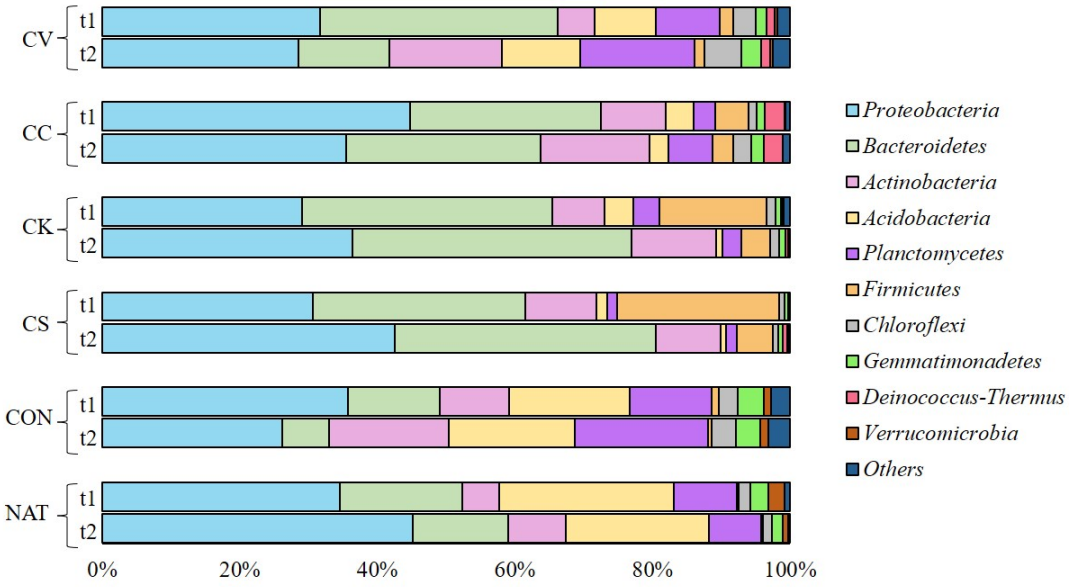

Figure 5: Relative frequency of bacterial phyla (abundance over 0.5%) measured under 6 soil conditions and 2 sampling dates.

Legend: soil conditions: CV - soil treated with vermicompost; CC - soil treated with compost of greenhouse crop residues; CK - soil treated with manure from chickens; CS - soil treated with organic compost derived from mixture of chicken and sheep manure; CON - cultivated and untreated soil; NAT - natural and uncultivated soil); sampling dates: t1- immediately after treatment; t2 – 3 months after treatment.

In this study, 191 bacterial taxa were identified in soil samples at the genus or next available higher taxonomic level with relative abundance over 0.1%. *Luteimonas* genus was favored over time (from 't1' to 't2') in CK and CS treatments, while decreasing in CV. In CON and NAT soils, *Luteimonas* was in low concentrations at both survey dates. The *Sphingobacterium* genus was prevalent in the CK and CS soils whereas in the CV, CC, CON and NAT soils, its presence was very low or null. The *Flavobacteriaceae* family and the *Salinimicrobium* genus were prevalent in treated

soils and absent in CON and NAT soils. The *Xanthomonadaceae* family was found in higher and lower percentages in CC and in CK and CS soils, respectively, being absent in CON and NAT soils; and the same was noted for the *Galbibacter* genus (Figure 6 and Table 3.SI).

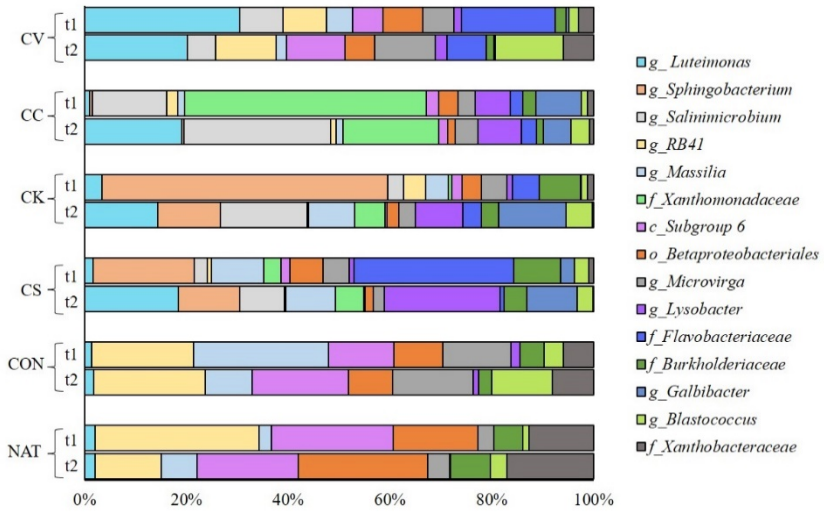

Figure 6: Relative frequency of bacterial genus (or the next available higher taxonomic level) of the 15 most abundant genera measured under 6 soil conditions and 2 sampling dates.

Legend: soil conditions: CV - soil treated with vermicompost; CC - soil treated with compost of greenhouse crop residues; CK - soil treated with manure from chickens; CS - soil treated with organic compost derived from mixture of chicken and sheep manure; CON - cultivated and untreated soil; NAT - natural and uncultivated soil); sampling dates: t1- immediately after treatment; t2 – 3 months after treatment.

3.4. Relationships among physical, chemical, biochemical and microbiological properties

The PCA, applied at the 2 survey dates, provided 3 principal components explaining 73.7% (survey date 't1') and 81% ('t2') of the total variance in the original variables. PC1 and PC2 explained 48.5% and 16.3% ('t1'), and 51.3% and 22.8% ('t2') of this variance, respectively. At both survey dates, high negative loadings were found between most physical and chemical properties of soils, and the first PCs, while these loadings were high but generally positive with microbiological properties and bacterial diversity. Of the biochemical properties of soils, only DHA and PA influenced PC1 and PC2 at both survey dates. Only the C:N ratio was an influential loading for PC3. It is notable that the loadings of the microbiological properties were quite similar for PC1 at both dates. By contrast, the effects of the physical, chemical and biochemical soil properties varied

between the 2 surveys. The pH, TOC and BGA influenced this PC at ‘t1’ whereas UA had a high loading at ‘t2’ (Figures 7a and 7b, and Table 2.SI).

According to the gradients in the studied variables along the first PC, a clear distinction among the different soil conditions can be observed at both survey dates. More specifically, at ‘t1’ survey, NAT and CON plots were associated with high values of bacteria richness and evenness as well as to specific *phyla* (e.g., *Chloroflexi, Gemmatimonadates, Actinobacteria, Planctomycetes, Verrucomicrobia*) and the relative abundance of many bacteria phyla whereas the soils treated with CK and CS were characterized by high values of EC, TOC, CH, PF, P, and TN as well as of BGA and DHA. Over time (survey ‘t2’), a gradient CC and CK < CC < NAT < CV < CON was observed along the PC1, which is influenced by several physical, chemical and biochemical properties of soil whereas a noticeable discrimination among the abandoned agricultural plots (treated or not) and NAT plots was evident along the PC2, associated with high loadings of TOC, C:N, BGA and PA and a few bacterial phyla (Figure 7c and 7d).

The PCA coupled with AHCA evidenced clear distinctions among the 6 soil conditions. These 2 techniques grouped the plots into 3 clusters. At survey date ‘t1’, a first cluster grouped CON and NAT plots while a second and third group mainly consisted of CV and CC soils and CK and CS plots. This clustering changed over time, and, at survey ‘t2’, the first cluster contained only NAT plots, the second group CV and CON soils, and the third CC, CK and CS plots (Figures 7c, 7d and 8).

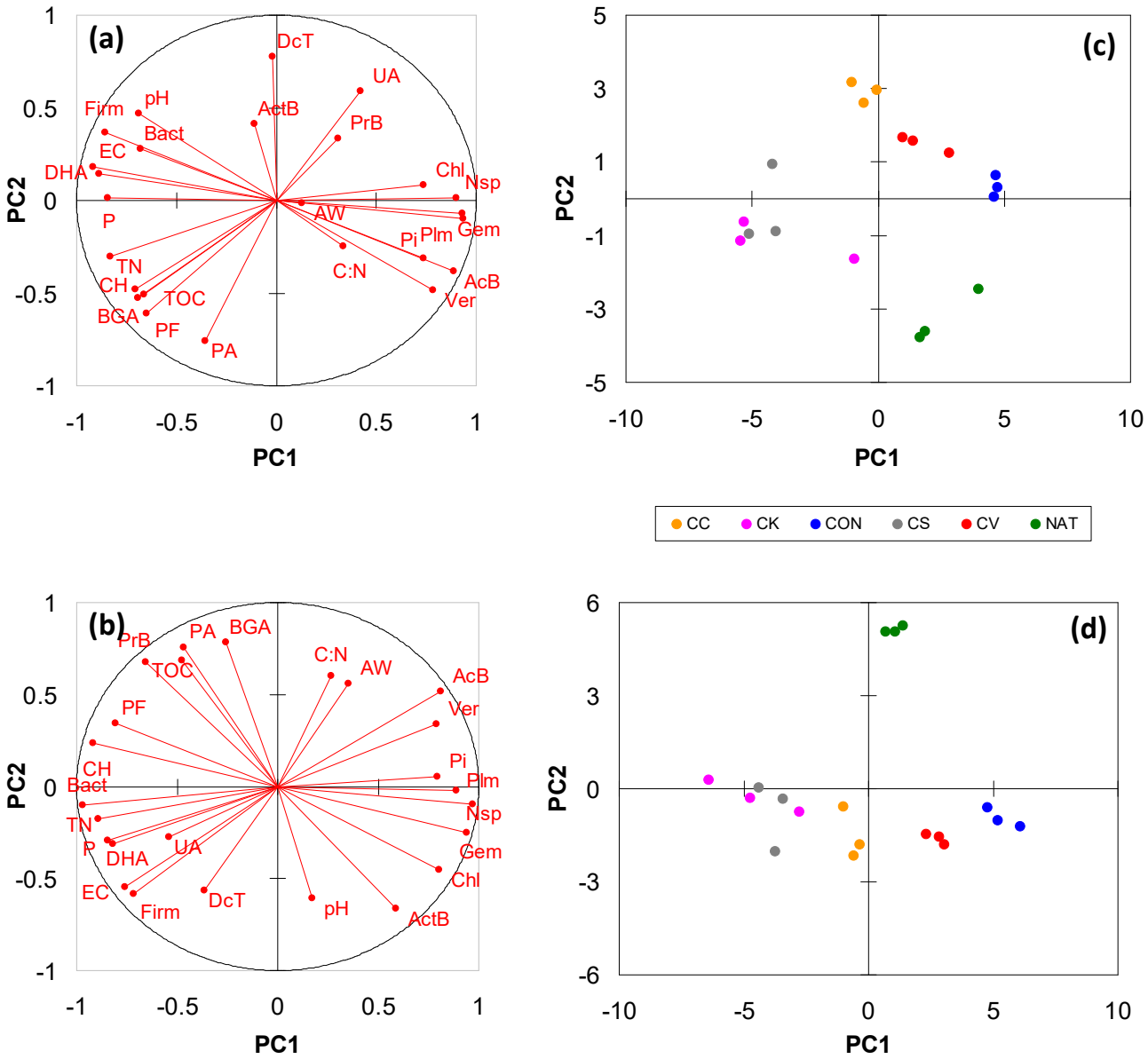

Figure 7: Loadings of the original variables (physical, chemical and biochemical properties as well as bacteria phyla and diversity) (a is sampling date 't1', and b is sampling date 't2') and scores (c is sampling date 't1', and d is sampling date 't2') on the first 2 principal components (PC1 and PC2) provided by PCA.

Legend: soil conditions: CV - soil treated with vermicompost; CC - soil treated with compost of greenhouse crop residues; CK - soil treated with manure from chickens; CS - soil treated with organic compost derived from mixture of chicken and sheep manure; CON - cultivated and untreated soil; NAT - natural and uncultivated soil); sampling dates: t1- immediately after treatment; t2 – 3 months after treatment; soil properties: EC - electrical conductivity; TOC - total organic carbon; AW - available plant water; TN - total nitrogen; C/N - carbon to nitrogen ratio; P - assimilable phosphorus; CH - carbohydrates; PF - polyphenols; DHA - dehydrogenase activity; BGA - β-glucosidase activity; PA - alkaline phosphatase activity; UA - urease activity; PrB - Proteobacteria; Bact - Bacteroidetes; ActB - Actinobacteria; AcB - Acidobacteria; Plm - Planctomycetes; Firm - Firmicutes; Chl - Chloroflexi; Gem -Gemmatimonadetes; DcT - Deinococcus-Thermus; Ver - Verrucomicrobia: Nsp - number of species; Pi: Pielou index.

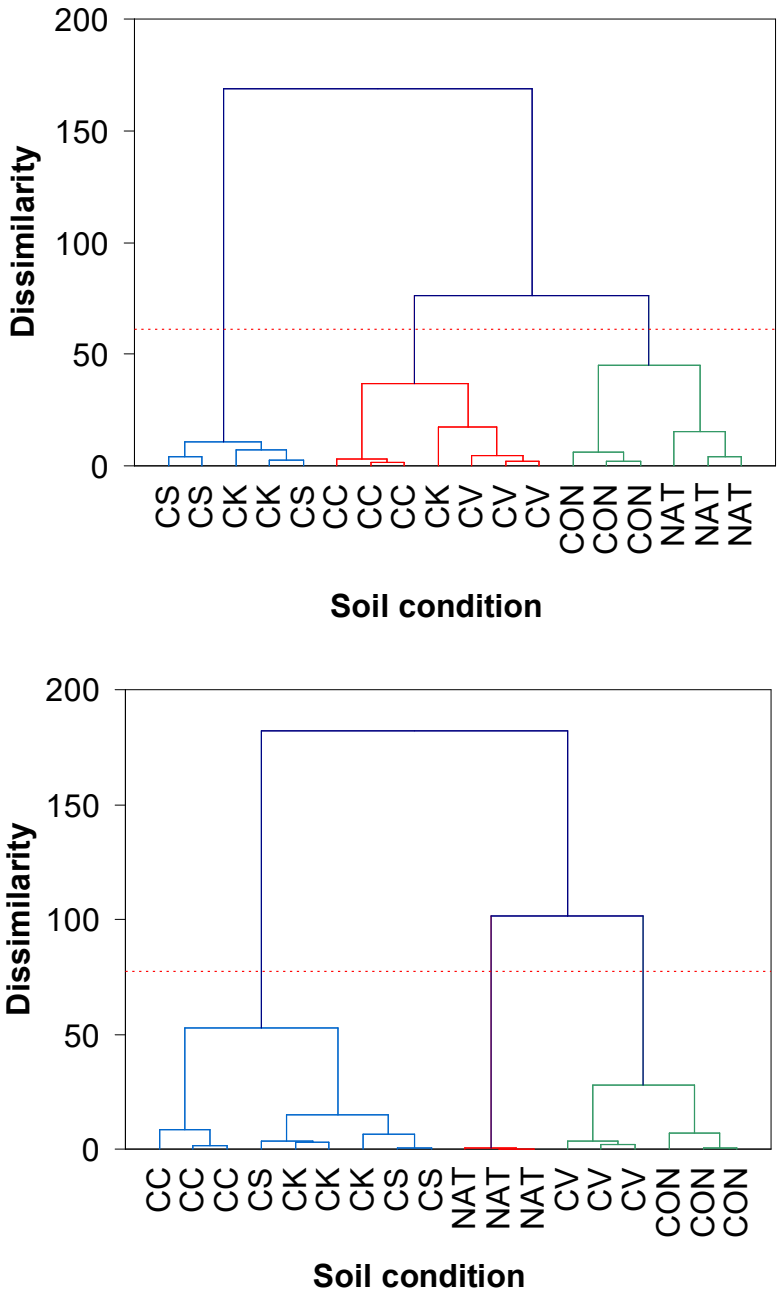

Figure 8: Dendrogram provided by the agglomerative hierarchical cluster analysis (AHCA).

Legend: soil conditions: CV - soil treated with vermicompost; CC - soil treated with compost of greenhouse crop residues; CK - soil treated with manure from chickens; CS - soil treated with organic compost derived from mixture of chicken and sheep manure; CON - cultivated and untreated soil; NAT - natural and uncultivated soil); sampling dates: t1- immediately after treatment (upper figure); t2 – 3 months after treatment (lower figure).

430

3.5. Analysis of indicator taxa of bacterial community in the different soil conditions

According to ISA, 120 bacterial *taxa* of the 204 counted were significantly ($p < 0.05$) associated with the different soil conditions (treated, control and reference). Some bacterial *taxa* were indicator species only at survey dates 't1' or 't2' whereas others were at both dates (Table S3.SI). In more detail, 24 bacterial *taxa* were potential indicators for CV (e.g., *Luteimonas, Gillisia* and *Vitellibacter* genus), 23 for CC (e.g., *Halomonas, Membranicola* and *Mycobacterium* or *Lysobacter* at 't1'), 3 for CK (e.g., *Brevundimonas* and *Lysobacter* at 't2'), 5 for CS (*Azoarcus, Roseomonas, Atopostipes, Promicromonospora* and *Leifsonia*). CON and NAT soils showed close associations with 28 and 37 bacterial soil *taxa*, respectively (Table S3.SI). Other *generas*, such as *Microvirga, Massilia, Gaiella* or *Sphingomonas*, were among the best indicators of CON soils, and *Luteibacter, Reyranella, Phenylobacterium, Terrimonas* and *Flavitalea* were among the best indicators of NAT plots (Figure 9).

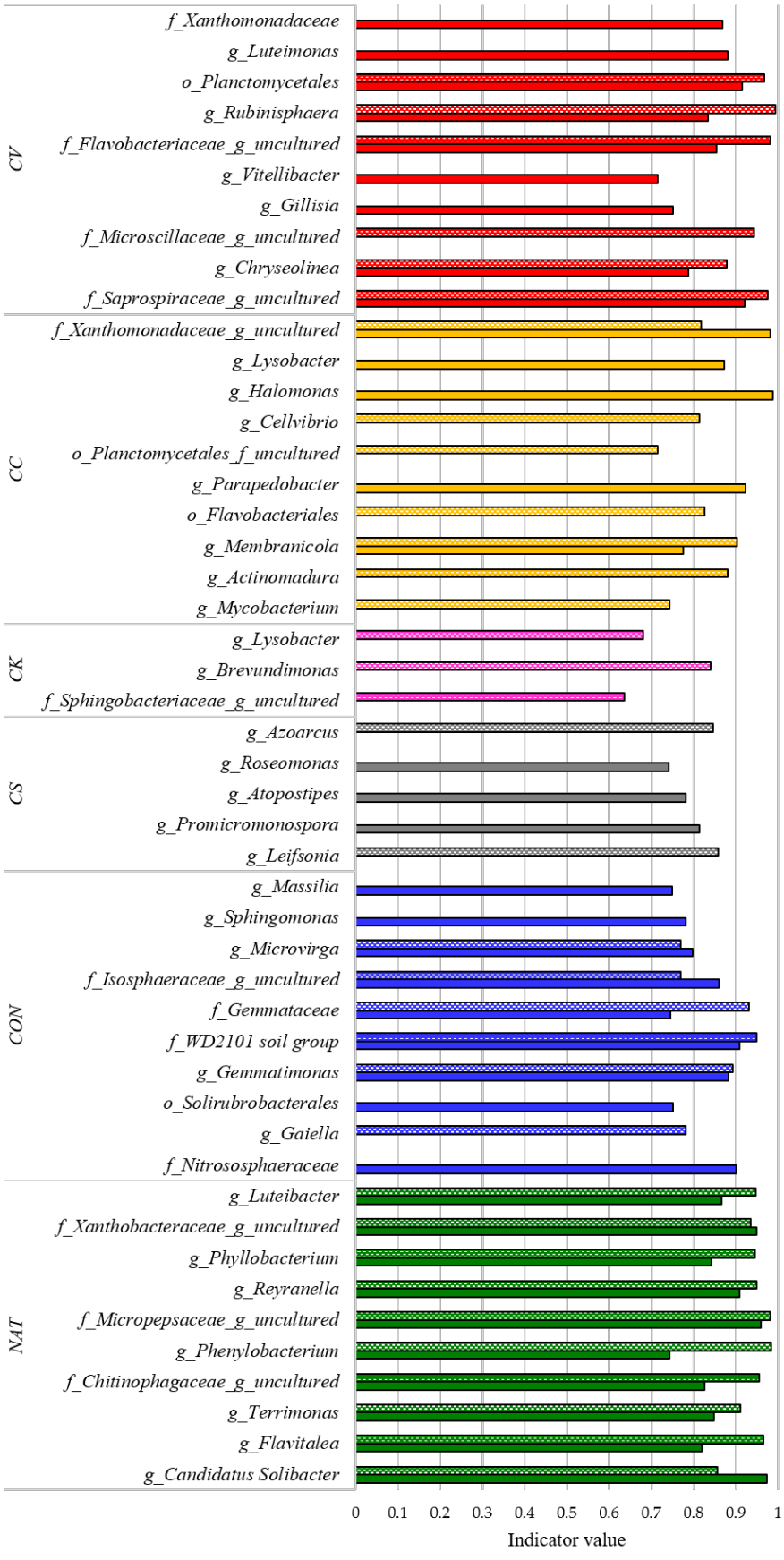
CV
f_Xanthomonadaceae
g_Luteimonas
o_Planctomycetales
g_Rubinisphaera
f_Flavobacteriaceae_g_uncultured
g_Vitellibacter
g_Gillisia
f_Microscillaceae_g_uncultured
g_Chryseolinea
f_Saprospiraceae_g_uncultured
CC
f_Xanthomonadaceae_g_uncultured
g_Lysobacter
g_Halomonas
g_Cellvibrio
o_Planctomycetales_f_uncultured
g_Parapedobacter
o_Flavobacteriales
g_Membranicola
g_Actinomadura
g_Mycobacterium
CK
g_Lysobacter
g_Brevundimonas
f_Sphingobacteriaceae_g_uncultured
CS
g_Azoarcus
g_Roseomonas
g_Atopostipes
g_Promicromonospora
g_Leifsonia
CON
g_Massilia
g_Sphingomonas
g_Microvirga
f_Isosphaeraceae_g_uncultured
f_Gemmataceae
f_WD2101 soil group
g_Gemmatimonas
o_Solirubrobacterales
g_Gaiella
f_Nitrososphaeraceae
NAT
g_Luteibacter
f_Xanthobacteraceae_g_uncultured
g_Phyllobacterium
g_Reyranella
f_Micropepsaceae_g_uncultured
g_Phenylobacterium
f_Chitinophagaceae_g_uncultured
g_Terrimonas
g_Flavitalea
g_Candidatus Solibacter
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
Indicator value

Figure 9: Indicator bacteria associated with the different soil conditions at 2 soil sampling dates ('t1' and 't2'). The graph shows 48 bacterial taxa of 120 resulting from the indicator species analysis; the full results are presented in Table 3.SI.

Legend: soil conditions: CV - soil treated with vermicompost; CC - soil treated with compost of greenhouse crop residues; CK - soil treated with manure from chickens; CS - soil treated with organic compost derived from mixture of chicken and sheep manure; CON - cultivated and untreated soil; NAT - natural and uncultivated soil); sampling dates: t1- immediately after treatment; t2 – 3 months after treatment.

445

446 *3.6. Soil quality index*

447

448 According to ANOVA, both soil condition ($F = 34.367$, $p < 0.001$) and time ($F = 12.710$, $p <$
449 0.01) as well as their interaction ($F = 2.896$, $p < 0.05$) were significant factors of variability for SQI.
450 At the 't1' survey date, the CON soils and the plots treated with CC and CV organic amendment
451 showed the lowest SQI (1.19 ± 0.05, 1.15 ± 0.04 and 1.21 ± 0.04, respectively); the highest value
452 was estimated for CK plots (2.60 ± 0.054). The 2 latter values were significantly different from all
453 other soil conditions. It is worth noting that the reference soils (NAT) showed an intermediate SQI
454 (1.76 ± 0.13) between those extremes (Figure 10).

455 Over time, the SQI significantly increased for all soil conditions, and the highest and lowest
456 values were again estimated for CK (2.84 ± 0.34) and CON (1.31 ± 0.04) soils. At this survey date
457 ('t2'), all soils treated with the different organic soil amendments showed a higher SQI (between
458 1.78 ± 0.07 for CC and 2.84 ± 0.34 for CK) than both CON (1.31 ± 0.04) and NAT (1.51 ± 0.04)
459 plots, although only the values of SQI estimated for CK (2.84 ± 0.34) and CS (2.41 ± 0.20) soils
460 were significantly different (Figure 10).

461

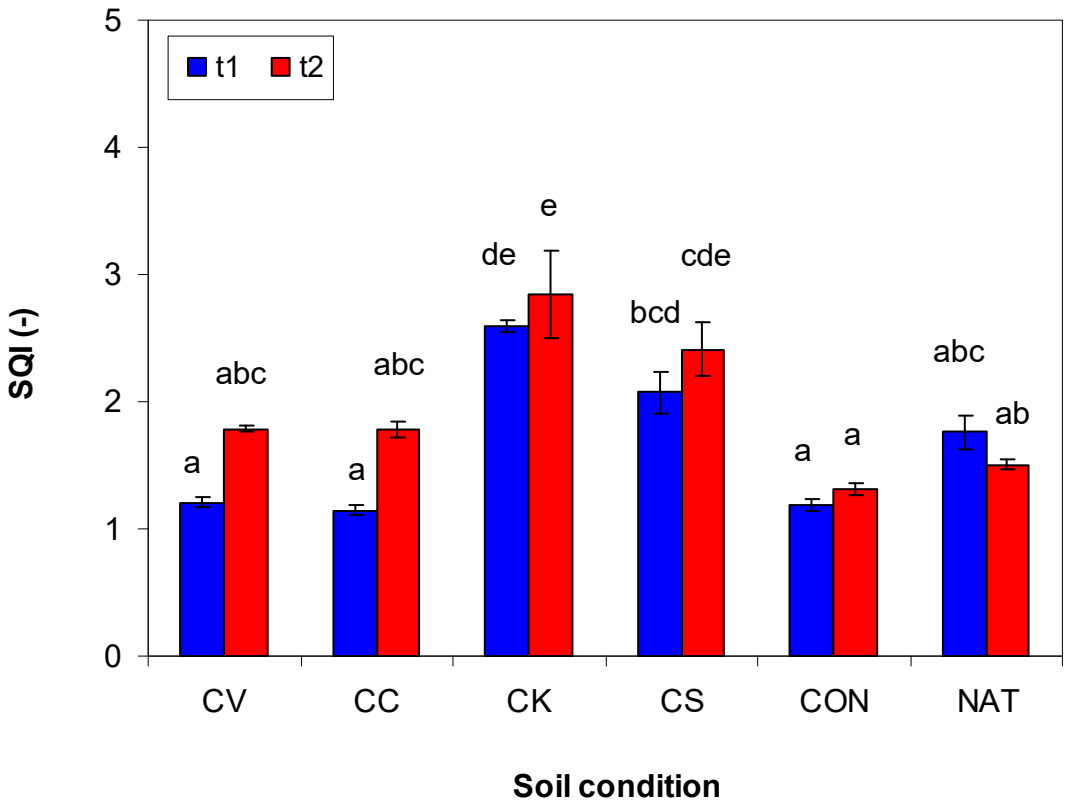

Figure 10: Soil quality index under different soil conditions at 2 soil sampling dates ('t1' and 't2').

Legend: soil conditions: CV - soil treated with vermicompost; CC - soil treated with compost of greenhouse crop residues; CK - soil treated with manure from chickens; CS - soil treated with organic compost derived from mixture of chicken and sheep manure; CON - cultivated and untreated soil; NAT - natural and uncultivated soil); sampling dates: t1- immediately after treatment; t2 – 3 months after treatment; lowercase letters indicate significant differences in the interaction 'soil condition x sampling date' after Tukey's test ($p < 0.05$).

4. Discussion

4.1. Changes in physical and chemical properties among soil conditions

Comparison of physical and -chemical properties of soils treated with organic soil amendments with the same parameters measured at the CON and NAT sites shows an increase in EC, presumably because of mineral elements supplied with compost (González-Ubierna et al., 2012; Hueso-González et al., 2018). Also present is increased pH, which can be attributed to production of OH- by organic ligands because of the mineralization of nitrogen (do Carmo et al., 2016). Three months after compost application, the EC values remained significantly higher (except for CV treatment), contrasting with other studies showing decreases in EC over time (González-Ubierna et

al., 2012; Soria et al., 2021). Presumably, the amounts of ions supplied with compost were released over time and were too high to be leached by precipitation, which is generally scarce in the dry period between April and July (dates of surveys 't1' and 't2'). The increase detected immediately after compost application requires attention because it may lead to an increased salinity of soils with a consequent increase in the osmotic potential of plants. The pH values are in accordance with some national standards (e.g., Italy), which suggest that the pH of the compost destined for agronomic purposes should be between 6.0 and 8.5 (Bouhia et al., 2021b).

All organic conditioners, except vermicompost, increased the TOC and TN contents of the soil (although not always significantly), and this increase is expected because the substrates for compost contain both vegetal and animal residues that determine their chemical composition with possible enrichment of the natural soil contents (Soria et al., 2021). It should be noted that the TOC content in the soils supplied with OM from compost was not far from the levels of NAT soils. The soils amended with animal-derived compost, which can result in additional input of C with a consequent increase in the mineralization of TOC (Kuzyakov et al., 2000), showed a decrease in TOC 3 months after application whereas TOC was stable over time after treatments with vermicompost and compost from crop residues. These slight changes in TOC indicate higher soil stability in CV and CC treatments, thanks to a balance between carbon inputs and outputs, which are a result of the decomposition and formation of OM in the soil (Rousk et al., 2015). Soil treated with manure compost contributed to a larger amount of labile OM—and significantly higher CH and PF content—compared with the other 2 amendments, and this increase can be considered an early indicator of carbon changes (Haynes, 2000). However, it should also be considered that an adequate organic amendment provides a balance between labile and reclaiming forms of OM and should ensure a long-term stock of nutrients. Additionally, high mineralization could result in long-term depletion of these stocks, which could also have a negative impact on soil health and their functionality (Soria et al., 2021). Other authors found that, 6 months after the application of organic amendments from recycled waste, TOC, TN, P and labile OM forms increased significantly compared with untreated soils (Rodríguez-Berbel et al., 2021). In another investigation conducted on abandoned agricultural soil, Rodríguez-Berbel et al. (2023) showed significant changes in the nutrient content and bacterial composition of soils treated with 4 organic amendments compared with the untreated control and natural soil, especially 3 months after application. According to these authors, compost from greenhouse crop residue is the optimal treatment for the short-term recovery of physical–chemical properties, nutrient contents, and bacterial composition of agriculture-degraded soils in semiarid areas.

4.2. Changes in biochemical properties among soil conditions

According to Tejada et al. (2006), the addition of organic amendments to the soil can influence the activities of enzymes, which are key indicators of soil quality (Bandick and Dick, 1999). Characterization of these biochemical properties shows that the different organic amendments applied to abandoned agricultural soils significantly influenced enzymatic activity and basal soil respiration in the first 3 months through changes in soil physical and chemical properties. In particular, an increase in soil basal respiration is expected in soils treated with compost of animal origin whereas OM is significantly increased. Moreover, these changes, which were the result of complex interactions among individual soil parameters, were different between soils amended with manure on one side and vermicompost and compost from vegetal residues on the other. Soil treatment with CK and CS significantly improved SBR even over the natural values shown by the reference sites. Treatments with manure showed intense enzyme activity related to C cycling (BGA and DHA) immediately after compost application whereas the activity rates in CV and CC treatments were lower and limited only to PA. This increased enzymatic activity is associated with higher CH, PF, TN, P and TOC contents in treated soils. These results suggest that the increase in OM and nutrient contents because the supply of organic amendments of animal origin TN and P, indirectly contributes to increased microbial activity through improved soil quality (Lal, 2015). Other authors have reported that the addition of organic manures increases microbial biomass, improving enzymatic activity and soil respiration (Zhen et al., 2014) as well as DHA and BGA (Subramanian et al., 2016). Furthermore, Rodríguez-Berbel et al. (2021) reported increased enzymatic activities together with basal respiration, 6 months after applying organic soil amendments in limestone quarries. However, the increase in enzymatic activities was not stable over time; after 3 months this increase vanished, probably because of the depletion of the organic substrates provided by the amendment. This noticeable reduction led to an increase in mineralization processes and as a result, to a progressive decrease in enzymatic activities (Delgado et al., 2012). It is worth highlighting that an increase in PA between the 2 survey dates was noted also in NAT and CON soils, which indirectly confirms that this increase cannot be associated with the compost application. Other authors report comparatively higher PA in amended soils than in control sites, and this could be because of the composition of nutrients provided by the amendment, which may favor an increase in the synthesis of phosphatase (Delgado et al., 2012). Moreover, the application of compost of animal origin also helps to significantly increase UA some months after treatment, and this may be because of the nitrogen fixation into the soil. This result is consistent with the findings of Antonious et al. (2020), who found an increase in UA 4 months after applying chicken manure. This indicates the

transformation of nitrogen into ammonium ions because of enhanced microbial activity after amendment application. The low C:N ratio confirms nitrogen mineralization because of plant-available nitrogen releases (Brust, 2019).

The soils treated with vermicompost and compost from vegetal residues showed different microbiological activities although the OM and nutrient contents were higher (but not significantly) 3 months after application whereas CH and PF were similar to control. High SBR could be indicative of CO_2 emission to the atmosphere because of the initial priming effect (Soria et al., 2021), with a concomitant effect on the feedback of greenhouse gases to the atmosphere. The application of CC and CV compost did not significantly increase SBR (in contrast to what observed for manure addition), which was also low in the control soil. Both CV and CC soils had a SBR that was higher than in soils with increased mineralization of OM (Creamer et al., 2014), but the basal respiration rates were lower than CS and CK composts. The higher SBR and concomitant mineralization of OM in soils treated with animal amendments could be disadvantageous compared to compost of plant origin and vermicompost because they might not maintain adequate levels of OM in the long term and favor a higher emission of CO_2. Moreover, the enzymatic activities associated with the carbon, nitrogen and phosphorus cycles for both treatments were similar in the control soils at both survey dates and therefore much lower than the corresponding values measured for the other organic conditioners or the NAT soils. The chemical composition of the compost produced from vegetable waste corresponds to recalcitrant OM, which is rich in lignocellulosic compounds that are resistant to biodegradation (Soria et al., 2022). By contrast, a higher enzymatic activity could be expected in soils treated with vermicompost because the content of compounds of animal origin is higher. However, the vermicomposting process using earthworms could have led to greater stability of the OM (Chatterjee et al., 2020). The ingestion of easily decomposable organic residues by earthworms favors the oxidation of unstable OM and improves the availability of nutrients for plants (Chatterjee et al., 2020).

4.3. Changes in composition and diversity of bacterial communities among soil conditions

The higher availability of OM and nutrients as well as the increased enzymatic activity led to a successful recovery of bacterial and fungal communities in amended soils (Blanco-Canqui et al., 2013; Kammann et al., 2015). Moreover, the significantly higher content of CH and PF stimulates the presence of native soil bacteria that mineralize these easily biodegradable compounds and

increase the enzymatic activity (Mondini et al., 2006) of new micro-organisms supplied by the amendment itself (Rodríguez-Berbel et al., 2021). The organic soil amendments create a bacterial hot spot after their application in response to the entry of exogenous labile carbon compounds (Kuzyakov et al., 2000; Kuzyakov and Blagodatskaya, 2015) and could be responsible for the high SBR rate detected in both animal composts. It is notable that, in general, the addition of CC and CV compost to soil increased bacteria richness and evenness over the levels shown by the control soils and close to the reference sites. The reverse effects were noted for the other substrates of animal origin, which showed a decrease in bacteria *phylum* and a dominance of some species over others.

According to Rodríguez-Berbel et al. (2021), soil amendment with organic substrates leads to changes in composition of bacterial communities at the *phylum* and *genus* levels. Furthermore, these changes are associated with several physical, chemical and biochemical soil properties in restored and untreated soils. Miralles et al. (2020) found a close link between the relative abundance of several bacterial *taxa* on the one hand and organic carbon and pH on the other. In another study, Miralles et al. (2020) reported that several soil bacteria *taxa* show significant correlations with pH, TN, TOC, P and EC. In our study this statement is corroborated by the associations between the labile carbon compounds and some enzymatic activities as well as by the characteristics of bacterial communities, shown by PCA. Evidently, the diversity and composition of soil microbial communities in semiarid environments are controlled by the chemical properties of soils (Miralles et al., 2020b). It is possible that the presence of certain metabolites in soils, their effects on moisture, several physical properties of soil and their association with different microclimates may favor a more selective environment for certain bacteria (Miralles et al., 2020a). In abandoned farmlands, Company et al. (2022) found that secondary succession of micro-organisms significantly affects the physical, chemical and microbiological properties; enzymatic activities; and diversity and taxonomic composition of bacterial communities in soils, with changes detected in TOC, microbial biomass carbon, SBR, PA and DHA and therefore in soil quality.

4.4. Relationships among physical, chemical, biochemical and microbiological properties and evaluation of overall soil quality

Consistent with Yang et al. (2020), the evaluation of soil properties and microbial communities resulting from application of organic amendments in abandoned agricultural soils under semiarid conditions has been conducted combining the microbiological, physical and chemical properties of soils using PCA and AHCA. This technique revealed that the applications of the

different organic soil amendments led to a distinction among the treated soils, the NAT sites and the CON plots. Immediately after compost application, the bacterial richness and evenness as well the presence of many common bacteria *phyla* made the NAT and CON soils similar to each other. These soils were clearly differentiated from the soils treated with manure (CK and CS), which were associated with high EC, organic compounds and carbon, nutrients as well as enzymatic activities. This is confirmed by the estimation of the SQI, which was significantly different between the CK and CS soils on the one hand and the other soil conditions on the other. The SQI indicates that overall soil quality was highest for the soils treated with manure.

Three months after the treatments, the NAT soils showed stable carbon content and enzymatic activities, which instead decreased in CON sites, although the latter maintained very similar bacterial communities. Moreover, the soils treated with CK, CS and CC organic amendments evidenced similar soil properties and microbial communities, associated with high nutrients and labile organic compounds. By contrast, the application of vermicompost made the treated soils more similar at the CON sites compared with the other treatments. The overall soil quality, expressed in terms of SQI, was clearly higher for the soils treated with chicken manure. In any case, excluding the application of CK compost, the treatments with organic soil amendments, regardless of the substrate origin (vegetal or animal) did not result over time in a significantly different soil quality compared to both CON and NAT sites.

Other studies, conducted in semiarid soils degraded by mining confirm that the organic soil amendments can change the chemical properties after treatment, influencing the microbial communities of soils restored using this practice (Rodríguez-Berbel et al., 2020).

4.5. Practical implications and future research

Overall, this study has demonstrated that under semiarid conditions, the application of organic soil amendments significantly changed some properties of cultivated and abandoned soils. This was mainly because the supply of organic compounds and nutrients that supported high enzymatic activities and modifications of bacterial communities evolved to lower richness and evenness. The effects of the organic soil amendments of animal origin were beneficial to the fertility and functionality of the treated soils from their first application, whereas treatment with compost produced from organic residues exerted the same effects some months after the application. It is notable that the application of the compost derived from chicken manure resulted in the highest soil quality on both survey dates. This means that the use of organic soil amendments of animal origin are preferable in terms of the restoration effectiveness of degraded croplands. By contrast, soil

supply with vermicompost led to lower and non-significant changes in the physical, chemical and biological properties. This indicates that this compost should not be prioritized as soil remediation strategy over other organic soil amendments, at least in the experimental conditions.

Because this study has monitored the effects of soil amendments on soil quality in the short term, we suggest a longer observation period to better understand the stable dynamics of OM, nutrients, enzymatic activities, bacterial communities' composition and, above all, soil basal respiration, which may provide long-term indications to farmers and agronomists about an appropriate decision regarding the selection of the best amendment in degraded croplands under semiarid conditions.

5. Conclusions

The short-term evaluation of soil quality after application of 4 organic soil amendments to abandoned cultivated soils has shown differentiated effects among the treatments and a different evolution in the main physical, chemical and biochemical soil properties, enzymatic and bacterial communities over time.

In response to the first research question regarding the soil properties that are modified by the application of each organic soil amendment, this study has shown that, compared with untreated soils and immediately after application, the compost of animal origin increased pH, EC and TN as well as the enzymatic activities associated with the carbon cycle but decreased bacterial richness and evenness. Over time, all the measured properties recovered the values found in the untreated soils, except for EC and TN, whose increase was stable over time, and bacteria richness, which remained lower. In addition, the compost from greenhouse crop residue increased EC and pH; the other effects were not significant throughout the monitoring period. The application of vermicompost did not affect the soil properties compared to the control soil.

In response to the second research question, the effects of organic soil amendments on soil properties and bacterial composition were not stable over time, and the changes detected immediately after treatment recovered after a few months.

The application of the compost derived from chicken manure resulted in the highest soil quality at both survey dates whereas the soil treatments with the other organic soil amendments did not result in a significantly different soil quality over time compared to both CON and NAT sites. This answer the third research question about the most effective organic soil amendment, indicating that, in general, the compost from animal manure is preferable to other substrates.

Overall, the results of this study may be useful to land planners and agronomists in selecting suitable organic soil amendments to restore degraded areas. However, more research is needed to explore the effects of organic soil amendments over a longer time and under different environmental conditions.

Acknowledgments

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Supplementary information

Table 1.SI - Results of 2-way ANOVA applied to physical, chemical and biochemical properties as well as bacteria phylum and diversity for different soil conditions at 2 sampling dates.

Factor	Degrees of freedom	Sum of squares	Mean squares	F	Pr > F
	EC				
Soil condition	5	7.736	1.547	35.791	< 0.0001
Sampling date	1	0.282	0.282	6.524	0.017
Soil condition x Sampling date	5	0.242	0.048	1.118	0.377
	pH				
Soil condition	5	1.287	0.257	11.439	< 0.0001
Sampling date	1	4.013	4.013	178.349	< 0.0001
Soil condition x Sampling date	5	0.682	0.136	6.061	0.001
	TOC				
Soil condition	5	28.719	5.744	7.563	0.000
Sampling date	1	11.968	11.968	15.758	0.001
Soil condition x Sampling date	5	2.508	0.502	0.660	0.657
	AW				
Soil condition	5	48.577	9.715	4.752	0.004
Sampling date	1	17.212	17.212	8.418	0.008
Soil condition x Sampling date	5	11.861	2.372	1.160	0.357
	TN				
Soil condition	5	0.330	0.066	16.306	< 0.0001
Sampling date	1	0.003	0.003	0.663	0.423
Soil condition x Sampling date	5	0.008	0.002	0.413	0.835
	C/N				
Soil condition	5	170.626	34.125	16.703	< 0.0001
Sampling date	1	66.941	66.941	32.765	< 0.0001
Soil condition x Sampling date	5	4.080	0.816	0.399	0.844
	P				

Soil condition	5	0.003	0.001	12.499	< 0.0001
Sampling date	1	0.000	0.000	0.081	0.778
Soil condition x Sampling date	5	0.000	0.000	0.084	0.994
	CH				
Soil condition	5	196536.649	39307.330	33.470	< 0.0001
Sampling date	1	3752.740	3752.740	3.195	0.086
Soil condition x Sampling date	5	44726.983	8945.397	7.617	0.000
	PF				
Soil condition	5	82739.973	16547.995	17.720	< 0.0001
Sampling date	1	463.473	463.473	0.496	0.488
Soil condition x Sampling date	5	3707.971	741.594	0.794	0.565
	DHA				
Soil condition	5	478.775	95.755	182.222	< 0.0001
Sampling date	1	76.019	76.019	144.664	< 0.0001
Soil condition x Sampling date	5	152.826	30.565	58.166	< 0.0001
	BGA				
Soil condition	5	19.116	3.823	10.728	< 0.0001
Sampling date	1	12.193	12.193	34.214	< 0.0001
Soil condition x Sampling date	5	13.369	2.674	7.503	0.000
	PA				
Soil condition	5	43.973	8.795	11.091	< 0.0001
Sampling date	1	0.345	0.345	0.435	0.516
Soil condition x Sampling date	5	0.049	0.010	0.012	1.000
	UA				
Soil condition	5	3.652	0.730	3.598	0.014
Sampling date	1	2.265	2.265	11.155	0.003
Soil condition x Sampling date	5	10.227	2.045	10.074	< 0.0001
	PrB				
Soil condition	5	556.941	111.388	11.193	< 0.0001
Sampling date	1	15.182	15.182	1.526	0.229
Soil condition x Sampling date	5	759.655	151.931	15.267	< 0.0001
	Bact				

Soil condition	5	3497.758	699.552	22.598	< 0.0001
Sampling date	1	96.662	96.662	3.123	0.090
Soil condition x Sampling date	5	813.592	162.718	5.256	0.002
	ActB				
Soil condition	5	200.186	40.037	8.197	0.000
Sampling date	1	242.592	242.592	49.669	< 0.0001
Soil condition x Sampling date	5	99.103	19.821	4.058	0.008
	AcB				
Soil condition	5	2474.074	494.815	77.804	< 0.0001
Sampling date	1	11.242	11.242	1.768	0.196
Soil condition x Sampling date	5	51.291	10.258	1.613	0.195
	Pim				
Soil condition	5	936.710	187.342	48.853	< 0.0001
Sampling date	1	60.895	60.895	15.880	0.001
Soil condition x Sampling date	5	130.424	26.085	6.802	0.000
	Firm				
Soil condition	5	965.383	193.077	8.377	0.000
Sampling date	1	266.449	266.449	11.560	0.002
Soil condition x Sampling date	5	464.952	92.990	4.034	0.008
	Chl				
Soil condition	5	53.751	10.750	20.090	< 0.0001
Sampling date	1	3.742	3.742	6.992	0.014
Soil condition x Sampling date	5	8.194	1.639	3.062	0.028
	Gem				
Soil condition	5	36.534	7.307	15.927	< 0.0001
Sampling date	1	0.273	0.273	0.596	0.448
Soil condition x Sampling date	5	4.538	0.908	1.978	0.118
	DcT				
Soil condition	5	35.255	7.051	50.471	< 0.0001
Sampling date	1	0.117	0.117	0.841	0.368
Soil condition x Sampling date	5	0.434	0.087	0.621	0.685
	Ver				

Soil condition	5	12.329	2.466	27.354	< 0.0001
Sampling date	1	0.548	0.548	6.081	0.021
Soil condition x Sampling date	5	3.299	0.660	7.318	0.000
	Nsp				
Soil condition	5	447267.535	89453.507	19.412	< 0.0001
Sampling date	1	6019.174	6019.174	1.306	0.264
Soil condition x Sampling date	5	20960.201	4192.040	0.910	0.491
	Pi				
Soil condition	5	0.092	0.018	13.675	< 0.0001
Sampling date	1	0.007	0.007	5.076	0.034
Soil condition x Sampling date	5	0.003	0.001	0.430	0.823

Notes: EC: electrical conductivity; TOC: total organic carbon; AW: available plant water; TN: total nitrogen; C/N: carbon to nitrogen ratio; P: assimilable phosphorus; CH: carbohydrates; POL: polyphenols; DHA: dehydrogenase activity; BGA: β-glucosidase activity; PA: alkaline phosphatase activity; UA: urease activity; PrB: Proteobacteria; Bact: Bacteroidetes; ActB: Actinobacteria; AcB: Acidobacteria; Plm: Planctomycetes; Firm: Firmicutes; Chloroflexi: Chl; Gem: Gemmatimonadetes; DcT: Deinococcus-Thermus; Ver: Verrucomicrobia: Nsp: number of species; Pi: Pielou index; soil conditions: CV - soil treated with vermicompost; CC - soil treated with compost of greenhouse crop residues; CK - soil treated with manure from chickens; CS - soil treated with organic compost derived from mixture of chicken and sheep manure; CON - cultivated and untreated soil; NAT - natural and uncultivated soil); sampling dates: t1 - immediately after treatment; t2 - 3 months after treatment.

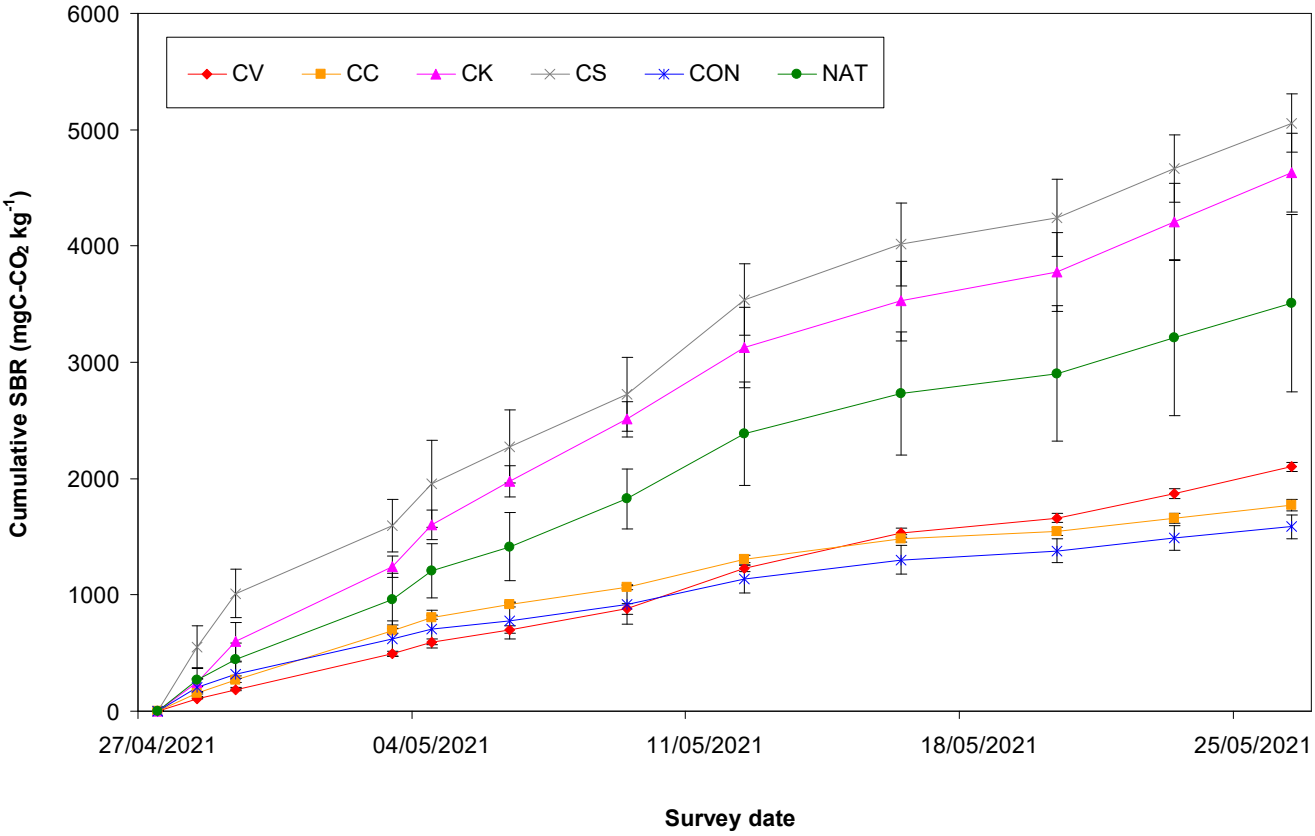

Figure 1.SI - Daily values of basal respiration of soil (mean ± standard error, n = 3) measured under 6 conditions at 2 sampling dates ('t1' and t2').

Legend: soil conditions: CV - soil treated with vermicompost; CC - soil treated with compost of greenhouse crop residues; CK - soil treated with manure from chickens; CS - soil treated with organic compost derived from mixture of chicken and sheep manure; CON - cultivated and untreated soil; NAT - natural and uncultivated soil); sampling dates: t1- immediately after treatment; t2 – 3 months after treatment.

Table 2.SI - Factor loadings of the original variables (physical, chemical and biochemical properties as well as bacteria phylum and diversity) (a, sampling date 't1', and b, sampling date 't2'), and scores (c, sampling date 't1', and d, sampling date 't2') on the first 2 Principal Components (PC1 and PC2) provided by PCA.

Variables	**Sampling date**					
	t1			**t2**		
	PC1	PC2	PC3	PC1	PC2	PC3
EC	-0.920	0.179	-0.012	-0.760	-0.547	0.187
pH	-0.687	0.470	-0.043	0.173	-0.608	-0.246
TOC	-0.663	-0.508	-0.400	-0.477	0.687	0.344
AW	0.128	-0.012	0.042	0.350	0.559	-0.089
TN	-0.831	-0.300	-0.145	-0.892	-0.177	0.139
C:N	0.333	-0.246	-0.534	0.265	0.604	0.491
P	-0.846	0.012	-0.180	-0.846	-0.292	-0.190
CH	-0.705	-0.479	0.210	-0.920	0.237	-0.202
PF	-0.650	-0.610	0.099	-0.807	0.346	-0.271
DHA	-0.890	0.145	-0.082	-0.821	-0.313	-0.160
BGA	-0.694	-0.524	-0.087	-0.257	0.782	-0.015
PA	-0.354	-0.758	-0.322	-0.469	0.756	-0.025
UA	0.420	0.592	-0.534	-0.542	-0.275	-0.486
PrB	0.310	0.337	-0.225	-0.655	0.679	0.121
Bact	-0.682	0.281	-0.455	-0.970	-0.098	0.013
ActB	-0.111	0.415	0.738	0.586	-0.663	0.137
AcB	0.887	-0.380	-0.032	0.810	0.516	0.061
Plm	0.936	-0.096	0.093	0.971	-0.097	0.034
Firm	-0.855	0.368	0.247	-0.717	-0.582	-0.051
Chl	0.736	0.081	-0.200	0.804	-0.453	0.144
Gem	0.932	-0.068	0.101	0.939	-0.250	0.131
DcT	-0.018	0.776	-0.508	-0.367	-0.563	0.638
Ver	0.784	-0.482	0.033	0.789	0.341	-0.420
Nsp	0.900	0.012	-0.007	0.887	-0.021	-0.066
Pi	0.738	-0.313	-0.267	0.793	0.053	-0.408

Notes: EC: electrical conductivity; TOC: total organic carbon; AW: available plant water; TN: total nitrogen; C/N: carbon to nitrogen ratio; P: assimilable phosphorus; CH: carbohydrates; POL: polyphenols; DHA: dehydrogenase activity; BGA: β-glucosidase activity; PA: alkaline phosphatase activity; UA: urease activity; PrB: Proteobacteria; Bact: Bacteroidetes; ActB: Actinobacteria; AcB: Acidobacteria; Plm: Planctomycetes; Firm: Firmicutes; Chloroflexi: Chl; Gem: Gemmatimonadetes; DcT: Deinococcus-Thermus; Ver: Verrucomicrobia: Nsp: number of species; Pi: Pielou index; sampling dates: t1- immediately after treatment; t2 - 3 months after treatment.

Table 3.SI - Results of the analysis of the indicator species of the genus or the next higher taxonomic level identified for each soil condition.

Soil condition	**Bacterial taxa**	**Value**	
		Sampling date	
		t1	t2
CV	g_*Acidobacteria bacterium SCN 69 37*	-	0.929**
	g_Ornithinimicrobium	0.798*	0.988**
	f_Prolixibacteraceae_g_*uncultured*	0.936**	0.937**
	f_Saprospiraceae_g_*uncultured*	0.922**	0.975**
	f_Saprospiraceae	0.892**	0.962**
	g_*Chryseolinea*	0.787*	0.879**
	f_Microscillaceae_g_*uncultured*	-	0.943**
	g_*Gillisia*	0.751*	-
	g_*Muricauda*	0.83*	-
	g_*Pricia*	0.9**	0.958**
	g_*Vitellibacter*	0.716*	-
	f_Flavobacteriaceae_g_*uncultured*	0.855*	0.982**
	o_Flavobacteriales	0.96**	-
	f_A4b_g_uncultured bacterium	0.82*	0.973**
	g_anaerobic bacterium MO CF2	-	0.976**
	f_Pirellulaceae	-	0.96**
	f_Gimesiaceae_g_*uncultured*	-	0.974**
	g_*Rubinisphaera*	0.835*	0.993**
	o_Planctomycetales	0.915**	0.967**
	f_Rhodobacteraceae	-	0.881**
	f_Sandaracinaceae_g_*uncultured*	-	0.888**
	f_Unknown Family_g_*uncultured*	0.896**	0.981**
	g_*Luteimonas*	0.88*	-
	f_Xanthomonadaceae	0.869*	-
CC	g_*Mycobacterium*	-	0.744**
	f_Bogoriellaceae	0.998**	0.877**
	g_*Enteractinococcus*	-	0.877**

	g_*Actinomadura*	-	0.88**
	g_*Membranicola*	0.776*	0.903**
	g_*Galbibacter*	0.713*	-
	g_*Myroides*	0.869*	-
	g_*Salinimicrobium*	0.875**	-
	o_Flavobacteriales	-	0.826*
	g_*Anseongella*	0.856**	0.956**
	g_*Parapedobacter*	0.924**	-
	f_Balneolaceae_g_*uncultured*	0.98**	0.819*
	g_*Paraburkholderia tropica*	0.928**	0.923**
	f_JG30 KF CM45	0.951**	0.874**
	g_*Truepera*	0.869**	-
	g_*Staphylococcus*	0.978**	0.871**
	o_Planctomycetales_f_uncultured	-	0.715*
	f_Fodinicurvataceae_g_*uncultured*	0.991**	0.937**
	g_*Marinobacter*	0.721*	-
	g_*Cellvibrio*	-	0.814**
	g_*Halomonas*	0.987**	-
	g_*Lysobacter*	0.872**	-
	f_Xanthomonadaceae_g_*uncultured*	0.982**	0.819**
CK	f_Sphingobacteriaceae_g_*uncultured*	-	0.637*
	g_*Brevundimonas*	-	0.841*
	g_*Lysobacter*	-	0.681*
CS	g_*Leifsonia*	-	0.859**
	g_*Promicromonospora*	0.813*	-
	g_*Atopostipes*	0.782*	-
	g_*Roseomonas*	0.741*	-
	g_*Azoarcus*	-	0.847**
CON	f_Nitrososphaeraceae	0.901**	-
	g_*uncultivated soil bacterium clone S111*	0.828**	-
	g_*uncultured bacterium 126*	0.784**	-
	g_*uncultured bacterium 92*	0.801*	-
	g_*Gaiella*	-	0.782*

	o_Gaiellales_f_uncultured	-	0.868**
	o_Solirubrobacterales	0.751*	-
	g_*Chitinophaga*	-	0.784**
	g_*Segetibacter*	-	0.897**
	g_*UTCF1*	0.891***	0.882**
	g_*Gemmatimonas*	0.883**	0.892**
	f_Gemmatimonadaceae	0.822**	-
	g_*planctomycete WY108*	0.844**	0.847**
	f_*WD2101 soil group_g_uncultured*	-	0.955**
	f_*WD2101 soil group_g_uncultured*	0.848**	0.941**
	f_*WD2101 soil group_g_uncultured*	0.879**	0.84**
	f_*WD2101 soil group*	0.908**	0.95**
	g_*Gemmata*	-	0.915**
	f_Gemmataceae_g_*uncultured*	-	0.907**
	f_Gemmataceae	0.746*	0.931**
	f_Isosphaeraceae_g_*uncultured*	0.86**	-
	f_Isosphaeraceae	0.818**	-
	g_*Microvirga*	0.798*	0.77**
	g_*Psychroglaciecola*	0.871**	-
	f_Beijerinckiaceae	0.842**	-
	g_*Sphingomonas*	0.781*	-
	g_*Candidatus Alysiosphaera*	0.853**	-
	g_*Massilia*	0.75*	-
NAT	g_*Candidatus Solibacter*	0.974***	0.856**
	o_Subgroup 7	-	0.842**
	c_Subgroup 17	-	0.864**
	g_*Acidobacteria bacterium W27*	0.913**	0.878**
	g_*uncultured bacterium 213*	0.869**	-
	g_*uncultured bacterium 259*	0.93**	0.907**
	g_*uncultured bacterium DA023*	0.915***	-
	g_*Flavitalea*	0.821**	0.966**
	g_*Terrimonas*	0.849**	0.91**
	f_Chitinophagaceae_g_*uncultured*	0.827**	0.956**

	f_Chitinophagaceae	0.874**	0.794*
	f_Microscillaceae	0.782**	0.964**
	g_*SH PL14*	0.806*	-
	o_Planctomycetales_f_*uncultured*	0.721*	-
	g_*Caulobacter*	-	0.944**
	g_*Phenylobacterium*	0.743*	0.983**
	g_*Dongia*	-	0.915**
	o_Elsterales_f_*uncultured*	-	0.866**
	f_Micropepsaceae_g_*uncultured*	0.96**	0.982**
	g_*Reyranella*	0.908**	0.95**
	g_*Methylobacterium*	-	0.885**
	f_KF JG30 B3	0.972**	0.982**
	g_*Allorhizobium Neorhizobium Pararhizobium Rhizobium*	-	0.961**
	g_*Phyllobacterium*	0.842*	0.945**
	f_Rhizobiaceae	0.764*	-
	g_*Rhodoplanes*	0.909**	-
	f_Xanthobacteraceae_g_*uncultured*	0.95**	0.936**
	f_Xanthobacteraceae	-	0.914**
	g_*Acidovorax*	-	0.915**
	g_*IS 44*	0.959**	0.896**
	g_*Candidatus Accumulibacter*	0.891**	-
	f_SC I 84	-	0.889**
	o_Betaproteobacteriales	-	0.961**
	g_Acidibacter	0.818*	-
	f_Steroidobacteraceae	0.855**	-
	g_*Luteibacter*	0.866**	0.948**
	g_*Candidatus Udaeobacter*	0.818*	-

Notes: soil conditions: CV - soil treated with vermicompost; CC - soil treated with compost of greenhouse crop residues; CK - soil treated with manure from chickens; CS - soil treated with organic compost derived from mixture of chicken and sheep manure; CON - cultivated and untreated soil; NAT - natural and uncultivated soil); sampling dates: t1 - immediately after treatment; t2 – 3 months after treatment; significance at probability level: * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; no asterisks represent non-significant correlations ($p > 0.05$).