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Effects of Different Organic Fertilization Regimes on Soil Physicochemical Properties and Bacterial Community Assembly to Promote Greenhouse-Cultivated Aloe vera Growth

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Abstract

Sustainable production of greenhouse-cultivated aloe largely depends on soil quality and rhizosphere microbial stability. Organic fertilization is widely applied to improve farmland soil environment, whereas the long-term effects of different organic fertilizer regimes on soil fertility, plant growth and rhizosphere bacterial community assembly remain poorly documented in intensive aloe cultivation systems. This four-year greenhouse trial was conducted to systematically investigate how different organic fertilization practices regulate soil physicochemical properties, aloe growth performance, and rhizosphere bacterial diversity. Four treatments were established, including earthworm manure (QY), aloe-specific organic fertilizer (LY), conventional organic fertilizer (PY), and non-fertilized control (CK). Plant growth traits, soil fertility parameters, and rhizosphere bacterial community composition and diversity were comprehensively determined and compared across treatments. Long-term application of organic fertilizer significantly improved soil nutrient conditions and *Aloe vera* biomass, with the QY treatment shows the significant improvement effect. Soil organic matter (SOM) content increased by 40.76% under QY treatment. Fertilization regimes significantly reshaped bacterial community structure and diversity. Strong positive correlations were detected between dominant bacterial species and key soil nutrients. SOM and AP were verified as the primary edaphic drivers governing phylum-level bacterial community variation. QY and LY organic fertilizer treatments increased microbial community heterogeneity, while PY and CK fertilization treatments maintained relatively stable microbial community structure. These results indicate that earthworm manure (QY treatment) shows greater potential in improving soil quality and maintaining microbial ecological stability, making it an ideal fertilization strategy for healthy and sustainable *Aloe vera* production.

1. Introduction

Aloe vera (L.) Burm. f., a typical medicinal and edible crop belonging to the Asphodelaceae family, has been extensively utilized in functional food, healthcare products, and pharmaceutical formulations. Its mesophyll tissue of leaves is rich in bioactive gel and contains a variety of phytochemicals, among which polysaccharides, emodin, anthraquinones and flavonoids are the main bioactive constituents. Aloe-derived polysaccharides are well established for their antiviral, anti-inflammatory and immunomodulatory activities [6], accumulating preclinical and clinical evidence further substantiates their therapeutic potential in respiratory viral infections and oncological indications. Although significant progress has been made in relevant basic research, the industrial promotion and clinical standardization of aloe polysaccharide products continue to encounter substantial challenges. Variations in cultivated germplasm, geographical conditions, harvest timing and downstream processing methodologies result in inconsistent structural features and purity levels of the extracted polysaccharides, thereby further contributing to suboptimal data reproducibility and unreliable quality control. These practical bottlenecks significantly restrict the large-scale and standardized development of industries related to aloe.

In the cultivation of medicinal plants, the accumulation of secondary bioactive metabolites is predominantly contingent upon the growth status in the field. In greenhouses, the rhizosphere soil centered on soil biological characteristics are key factors regulating the growth and metabolite synthesis of *Aloe vera* plants. Microbial communities within the rhizosphere exert a profound regulatory on soil ecological health and crop productivity. Both the vegetative growth and secondary metabolic processes in plants are co-regulated by the physicochemical conditions and biological characteristics of soil. Soil microorganisms serve as pivotal participants in terrestrial biogeochemical cycles, facilitation the decomposition of organic matter and the transformation of nutrient within farmland soil. The rhizosphere microbial communities are involved in the degradation of soil organic matter and the activation of nitrogen, phosphorus and potassium nutrients, thereby effectively enhancing soil nutrient availability and promoting plant nutrient uptake (Klemedtsson et al. 1987; Singh et al. 1989; Srivastava et al. 1991). Changes in the structure and species composition of microbial communities are highly sensitive to variations in the rhizosphere environment, commonly used as a reliable biological indicator for assessing soil ecological stability. Furthermore, beneficial rhizosphere microorganisms can inhibit the proliferation of soil-borne pathogens, alleviate stress in the root microenvironment, and sustain the structural equilibrium of the community, all of which are crucial for maintaining the healthy growth of medicinal plants (Bhattacharyya et al. 2011; Wu et al. 2017).

Fertilization management constitutes one of the most prevalent anthropogenic interventions that modify the composition, abundance and functional structure of soil microbial communities within agroecosystems (Yu et al. 2008). Existing studies consistently show that the applying organic fertilizer significantly improves soil physicochemical properties and soil enzyme activity, while also enhancing the rhizosphere microhabitat conditions (Timo et al. 2004). A substantial body of research has investigated soil microbial and physicochemical responses to organic fertilization regimes; however, the majority of existing studies are limited to short-term experimental observations. The cumulative ecological impacts resulting from long-term, continuous application of organic fertilization are often underappreciated. Such knowledge gaps are especially pronounced in intensive protected cultivation system. Greenhouse cultivation is characterized by relatively enclosed growing environments and prolonged mono-cropping practices-conditions that readily predispose soils to nutrient imbalances and progressive degradation of the soil micro-ecosystem. To date, the effects of long-term organic fertilization strategies on rhizosphere bacterial community diversity and their subsequent influence on Aloe vera growth remain poorly understood. Addressing this knowledge gap is critical for optimizing field management practices and sustaining soil ecological health in protected environment aloe cultivation.

A four-year field experiment was conducted in a commercial greenhouse to investigate the effects of different organic fertilization regimes on the growth of Aloe vera under protected cultivation. Plant growth indices and soil physicochemical properties were assessed using standardized analytical methods, and high-throughput 16S rRNA gene sequencing was employed to characterize the compositional and structural diversity of rhizosphere soil bacterial communities. This study systematically investigates the regulatory effects of long-term continuous organic fertilization on soil nutrient dynamics, rhizosphere microbial community assembly and aloe growth performance. The results offer evidence-based theoretical insights to guide the optimization of fertilization strategies and enhance soil ecological functionality in intensive protected-culture systems for Aloe spp.

2. Methods

2.1 Experimental site and Experimental design

The experiment was carried out in the biological greenhouse of Huifeng Campus, Chuzhou University, Langya District, Chuzhou City, Anhui Province (118°18'16.06"E, 32°16'13.61"N). The initial physical and chemical properties of the 0–20 cm soil layer were: Soil organic matter (SOM), 21.5 g/kg; total nitrogen (TN), 1.73 g/kg; alkaline nitrogen (AN), 102.7 mg/kg; total phosphorus (TP), 1.24 g/kg; available phosphorus (AP), 97.8 mg/kg; total potassium (TK), 15.6 g/kg; available potassium (AK), 196 mg/kg; and pH, 6.75.

The experiment was designed as a randomized block design with four different fertilization treatments. Each treatment was repeated three times for a total of 12 experimental plots. Each plot was 12 m^2 in area with walkways and drainage ditches that were 0.5 m wide. Since 2019 *Aloe vera* L. has been grown under four fertilization regimes: earthworm manure (QY), aloe specific fertilizer (LY), conventional organic fertilizer (PY) and unfertilized control (CK).

2.2 Soil sample collection

Soil samples for the aloe experiment were taken in May 2024 using a modified procedure (Liu et al. 2018). An S-shaped five-point sampling was used with a soil auger. From each experimental plot, soil was sampled from the 0–20 cm layer around the roots of *Aloe vera* L. with each sample having a diameter of approximately 3–5 cm. The soil collected was put in sealed bags with a total of 12 samples. Each sample was then divided into three equal parts: one part was air-dried under natural conditions for determination of soil physicochemical properties; a second part was kept at 4°C for bacterial enumeration; and the remaining part was kept at -20°C in 2 mL centrifuge tubes for high-throughput sequencing analysis of soil bacterial communities.

2.3 Determination of soil physical and chemical properties

Soil physicochemical properties were determined by standard analytical methods as described by Bao (2010). SOM were determined by the potassium dichromate-sulfuric acid method. TN was determined using the Kjeldahl distillation procedure, TP was determined using the perchloric acid-sulfuric acid procedure, and TK was determined using the acid dissolution followed by flame spectrophotometry procedure. AN was determined using alkali-hydrolyzed diffusion method, AP by molybdenum-antimony colorimetric method and AK by leaching turbidity method. Soil pH was measured by a potentiometric method.

2.4 Determination of soil bacterial community diversity

Total microbial DNA from the *Aloe vera* L. rhizosphere soil extracted with the E.Z.N.A™ Mag-Bind Soil DNA Kit (OMEGA, USA, No. M5635-02). DNA concentrations were measured with Qubit and samples that passed quality control were used for library construction. The first-round PCR amplification was carried out with DNA amounts, as determined by Qubit 3.0. The bacterial 16S rRNA gene was PCR amplified with primers 341F (5'-CCTACGGGNGGCGCGCAG-3') and 805R (5'-GACTACHVGGTATCTAATCC-3'). During the 2nd round amplification, Illumina bridge PCR compatible primers were incorporated. Library size was checked by 2% agarose gel electrophoresis while library concentration was determined by Qubit 3.0 to obtain uniform cluster generation and high-quality sequencing data.

Paired-end reads from next generation sequencing were used for operational taxonomic unit (OTU) clustering and taxonomy analysis. Identified OTUs were used to calculate microbial diversity indices and assess sequencing depth. Common alpha-diversity indices were Shannon index, Chao1 index and Ace index (Zhuykova et al. 2022). The data that support the findings of this study have been deposited into CNSA (https://db.cngb.org/cnsa/) with accession number CNP0008762.

2.5 Statistical Analyses

The mean and standard deviation of variables per plot were calculated using Excel 2010. Statistical analyses were conducted with the method of analysis of variance, followed by Duncan's multiple range test at a level of significance of 0.05, with IBM Statistical Package 27.1 (IBM Corporation, New York City, NY, USA).

3. Results

3.1 Effects of different organic fertilizer applications on soil physicochemical properties

SOM is one of the most important factors in soil fertility. Compared with the CK, SOM contents of treatments using aloe-specific LY and QY were significantly higher (Table 1). Specifically, organic matter of LY and QY treatments was 33.24% and 40.76% higher than CK, respectively, with differences statistically significant at 0.05 level. No significant difference was found between LY and QY. Although the conventional organic PY had a slight increase in organic matter, this change was not statistically significant.

Soil nitrogen, phosphorous, and potassium contents also differed significantly between fertilizer treatments (Table 1). TK and TP also showed similar trends with the QY treatment having the highest levels. However, no significant differences were found among the QY, LY, and PY treatments, and all were significantly higher than CK ($P < 0.05$). No significant differences in TP were found between all treatments. Available nutrients, which are directly absorbable by crops, were especially affected by fertilization. AN levels in LY and QY treatments were significantly higher than in CK and PY ($P < 0.05$) and PY had the least amount of AN. For AP, QY treatment was significantly higher than CK ($P < 0.05$) with an increase of 42.34% and no significant differences were observed among the other treatments. With respect to AK incidence, both LY and QY treatment groups exhibited significantly higher AK prevalence compared with PY and CK control groups ($P < 0.05$), with respective increases of 33.33% and 28.07%. Therefore, relative to the PY treatment, both LY and QY treatments demonstrated superior efficacy in enhancing soil fertility and increasing the bioavailability of essential nutrients.

3.2 Effects of different fertilization treatments on growth traits of Aloe vera

The influence of four fertilization treatments (CK, PY, LY, and QY) on vegetative growth parameters-plant height, crown width, leaf length, leaf width, and leaf number-is summarized in Fig. 1. Among all measured traits, only plant height showed a statistically significant treatment effect, with the QY treatment yielding the maximum value (39 cm), representing a 31.0% and 36.8% increase over the CK (28 cm) and LY (29 cm) groups, respectively. In contrast, although the QY treatment consistently ranked highest for leaf length (34 mm) and leaf number (12.0), followed by PY (35 mm, 12.0), LY (32 mm, 11.8), and CK (34 mm, 11.5), these inter-group differences did not reach statistical significance (all $P > 0.05$), indicating only marginal promoting effects of organic amendments on these two traits.

Notably, crown width and leaf width exhibited an opposing declining trend under organic fertilizer application, with the CK group showing the broadest crown (58 cm) and leaf width (9.5 mm), whereas the QY treatment displayed the narrowest values (52 cm and 8.2 mm, respectively). This unexpected suppression suggests that organic inputs may inadvertently restrict lateral expansion, possibly due to resource allocation trade-offs favoring vertical growth over radial biomass accumulation. In summary, the findings of this study demonstrate that QY treatment exerts selective and specific promoting effects on the agronomic traits of Aloe vera plants, this fertilizer can significantly increase plant height, while exhibiting neutral or negative regulatory effects on other morphological indicators.

3.3 Analysis of soil bacterial sequences and their diversity indices

Using Illumina MiSeq sequencing, a total of 1,282,643 raw sequences was obtained from 12 soil samples. After quality control procedures, including read trimming and filtering, 1,116,148 high-quality bacterial tags remained with an average of 93,012 tags per sample. Following the removal of chimeric sequences and clustering at a 97% similarity threshold, 4,798 bacterial OTUs were identified, with the QY treatment having the highest OTU count.

In this study, the Shannon index, Chao 1 index and ACE index were employed to evaluate the bacterial α diversity, so as to comprehensively characterize the diversity and richness of community. Specifically, the LY and QY treatments exhibited considerably higher Shannon values relative to the PY and CK groups ($P < 0.05$). The Good's coverage of all sequenced samples reached 0.99, indicating sufficient sequencing depth and reliable representation of the rhizosphere bacterial community composition in the present study. Overall comparison of multiple alpha-diversity metrics further confirmed that the QY treatment substantially improved bacterial richness and diversity, yielding the most diverse and abundant bacterial community among the four experimental groups (Table 2).

3.4 Dynamic changes of bacterial communities in soil

Principal sequencing profiling revealed distinct taxonomic clustering of rhizosphere bacterial communities at the phylum level across CK, PY, LY and QY fertilization treatments. Ten dominant phyla were identified across all samples: Proteobacteria, Actinobacteria, Acidobacteria, Firmicutes, Bacteroidetes, Planctomycetes, Chloroflexi, Gemmatimonadetes, Candidatus Saccharibacteria and Cyanobacteria. Collectively, these phyla accounted for over 90% of the total bacterial relative abundance (Fig. 2). Proteobacteria dominated the bacterial assemblages in all treatment groups. Its relative abundance reached 55.82%, 41.38%, 48.62% and 61.29% in CK, PY, LY and QY, respectively, with the QY treatment presenting the highest proportion of Proteobacteria among all experimental groups.

No significant differences in the relative abundance of Actinobacteria were detected across all fertilization treatment groups. In the PY treatment, Firmicutes and Bacteroidetes account for the higher composition, with relative abundances reaching 15.86% and 20.79%, respectively. The above results indicate that different organic fertilization regimes can significantly alter the composition and relative abundance of rhizosphere bacterial communities at the phylum level.

3.5 Correlation analysis between soil physicochemical properties and rhizosphere soil bacterial diversity

To identify the key edaphic factors driving the assembly of rhizosphere bacterial communities in *Aloe vera* soil, we performed a correlation analysis between the dominant OTUs and nine soil environmental variables, including soil organic matter (SOM), total nitrogen (TN), total phosphorus (TP), total potassium (TK), alkali-hydrolyzable nitrogen (AN), available phosphorus (AP), available potassium (AK), electrical conductivity (EC), and soil pH (Fig. 3).Correlation analysis showed that SOM was strongly and positively correlated with the majority of dominant OTUs ($r > 0.8$), indicating that soil organic carbon serves as a core substrate resource governing bacterial community niche construction and assembly in aloe rhizosphere. In comparison, TN and TP exhibited weak-to-moderate negative correlations with several predominant OTUs, suggesting that excessive nitrogen and phosphorus accumulation may induce nutrient stoichiometric imbalance and further constrain bacterial community proliferation. For rapidly available soil nutrients, AP showed a slight positive correlation with dominant OTUs, while AN and AK presented negligible and irregular correlations. These results implied that plant-available N and K were not the primary limiting factors shaping core bacterial taxa under the current fertilization regime. Although soil pH and EC are widely recognized as critical microbial community regulators in terrestrial ecosystems, both variables only weakly correlated with most bacterial OTUs in the present study. This indicated that, within the range of field observation, soil pH and salinity exerted relatively minor selective pressure on bacterial community variation. In summary, SOM was the predominant environmental filter shaping rhizosphere bacterial assemblages, followed by soil total phosphorus. Other soil physicochemical properties only exerted secondary or marginal effects on bacterial community distribution in facility-cultivated aloe soil.

3.6 Redundancy analysis of bacterial community composition in response to environmental variables

To explore the relationships between soil physicochemical variables and phylum-level bacterial community composition under varied organic fertilization practices, redundancy analysis (RDA) was conducted using dominant bacterial phyla (relative abundance > 1%) and nine quantified soil edaphic indices. The RDA model effectively interpreted the variation in bacterial phylum composition across treatments, with the first two axes jointly explaining 80.0% of the total constrained community variation (RDA1: 61.84%; RDA2: 18.16%), and the entire model accounting for 82.0% of overall community variability (Fig. 4).

Ordination results showed that biological replicates of all four fertilization treatments were centrally distributed in the ordination space, demonstrating that different organic fertilization modes did not trigger significant overall differentiation in phylum-level bacterial community composition. However, obvious discrepancies in replicate dispersion were observed among treatments. The replicates of QY and LY treatments displayed scattered spatial distribution, implying higher community heterogeneity of soil bacterial phyla under these two fertilization regimes. In contrast, the samples of CK and PY exhibit a higher degree of aggregation, indicating that the species composition of the samples from these two treatments is characterized by relatively stable and homogeneity at the phylum level.

Environmental vector interpretation indicated that soil organic matter (SOM) and available phosphorus (AP) were the pivotal environmental variables driving the variation of phylum-level bacterial composition, which was consistent with the foregoing correlation analysis. Both SOM and AP exhibited positive loadings on the two main RDA axes. The SOM vector was highly associated with QY treatment replicates, revealing that SOM accumulation was the dominant factor shaping the bacterial phylum composition of QY-fertilized soil. The AP vector was located between QY and LY treatment replicates, suggesting that available phosphorus moderately regulated the phylum-level community structure of both fertilization groups with no single treatment-specific dominance.

In summary, RDA result confirmed that long-term organic fertilizer application primarily altered the distribution and stability of soil rhizosphere bacterial communities at the phylum level. The QY and LY fertilization modes effectively increased the heterogeneity of phylum-level species composition, while CK and PY maintained stable bacterial community structures. SOM and AP served as the core edaphic drivers filtering the assembly of rhizosphere bacterial phyla, further illustrating that

soil organic carbon and available phosphorus availability are key factors modulating the phylum-level species composition of aloe rhizosphere soil under facility organic fertilization.

4. Discussion

This study demonstrated that aloe-specific organic fertilization (LY and QY) substantially improved rhizosphere soil fertility under facility cultivation conditions. Compared with the control treatment, SOM content increased significantly by 33.24% and 40.76% under LY and QY applications, respectively ($P < 0.05$; Table 1), highlighting the capacity of targeted organic amendments to promote soil carbon sequestration. Application of organic fertilizers facilitates the reconstruction of rhizosphere microbial networks, promotes the decomposition and transformation of phosphorus and potassium in soil, and simultaneously optimizes soil physicochemical properties, including soil pH, AN, AP, and AK (Liu et al. 2014; Shen et al. 2015; Tang et al. 2023). The ameliorated soil microenvironment further improves root nutrient absorption efficiency for nitrogen, phosphorus, and potassium, ultimately establishing a stable and beneficial rhizosphere ecological environment for aloe growth.

Fertilization management is a key driver modulating the diversity and structural assembly of soil bacterial communities in agroecosystems (Fan et al. 2021; Sun et al. 2015; Tang et al. 2020). Consistent with previous studies, the present results confirmed that LY and QY organic fertilization significantly enhanced soil bacterial diversity compared with PY and CK treatments ($P < 0.05$). The analysis results of species composition at the phylum level indicate that there are significant differences in community among different treatment groups. Proteobacteria dominated the rhizosphere bacterial community in all groups, with the highest relative abundance observed in the QY treatment (61.29%), followed by CK (55.82%), LY (48.62%), and PY (41.38%). No significant treatment effects were detected for Actinobacteria abundance. In contrast, the Firmicutes and Bacteroidetes showed treatment-specific enrichment in PY treatment (Fig. 2), with their relative abundances (15.86% and 20.79%) reaching the highest levels. These differential distribution patterns indicate that different organic fertilization regimes impose distinct selective pressures on specific bacterial phyla, thereby reshaping rhizosphere community structure.

The superior bacterial diversity and richness detected in LY and QY treatments can be primarily attributed to the favorable C/N ratio of earthworm manure-based organic fertilizers. The balanced supply of carbon and nitrogen substrates provides rhizosphere bacteria in *Aloe vera* with sufficient energy and essential nutrients to support their survival, proliferation, and metabolic activity. This conclusion is consistent with previous studies, which have verified that earthworm manure amendment effectively improves soil bacterial diversity in medicinal plant cultivation systems (Xu et al. 2007; Wang et al. 2024). Moreover, the consistent increased ACE and Chao1 indices across all organic fertilization treatments further confirms that organic substrate supplementation enhances both the richness and diversity of rhizosphere bacterial communities in soil from facility-cultivated *Aloe vera*.

Organic fertilization improves soil physicochemical properties and supplies abundant microbial substrates, thereby optimizing rhizosphere microhabitat conditions and promoting bacterial community succession. The resulting shifts in microbial community composition enhance soil nutrient availability, thereby facilitating crop growth and establishing a positive feedback loop among soil properties, microbial communities, and plant productivity (Lou et al. 2023; Shu et al. 2022). In this study, the close correlations among SOM accumulation, bacterial community assembly, and aloe growth performance further confirmed that rational organic fertilization improves soil quality and regulates rhizosphere micro-ecology by modulating bacterial community characteristics in intensive greenhouse cultivation systems.

Further correlation and redundancy analyses clarified the core edaphic drivers of bacterial community variation at the phylum level. SOM and AP were identified as the primary environmental factors shaping the composition of rhizosphere bacterial communities, with SOM acting as the predominant ecological factor governing rhizosphere soil microbial communities. Although different organic fertilization regimes did not induce substantial overall separation of bacterial communities, distinct differences in replicate dispersion indicated that specialized QY and LY fertilization increased

community heterogeneity, while conventional PY fertilization and blank control maintained relatively stable and homogeneous bacterial assemblages. These above differences indicate that diversified organic fertilization reshapes microbial niche differentiation and community assembly processes, rather than merely altering community taxonomic composition. The comprehensive findings of this study demonstrate that long-term targeted organic fertilization can optimize soil nutrient conditions, enhance bacterial community diversity, and stabilize rhizosphere microecological functions. The results of this study can provide a theoretical basis for the screening and optimization of fertilization strategies in the sustainable cultivation of greenhouse grown *Aloe vera*.

Long-term application of organic fertilizers can effectively promote the accumulation of soil organic matter for *Aloe vera* under facility cultivation, enhances the availability of soil potassium and phosphorus, and comprehensively improve the diversity and richness of rhizosphere bacterial communities. Changes in soil physicochemical properties induced by organic fertilizer application further promote the enrichment of beneficial bacterial taxa, facilitate positive microbial ecological succession and stabilize soil ecological functions. Overall, the targeted organic fertilization practices, particularly the QY treatment, outperforms conventional organic fertilization and non-fertilization management in optimizing rhizosphere microenvironment and maintaining a healthy soil microbial community. Future research should focus on exploring the regulatory mechanisms of combined organic and inorganic fertilization ratios on soil microbial community assembly and rhizosphere micro-environmental homeostasis, so as to further refine scientific and efficient fertilization regimes for intensive aloe greenhouse cultivation.

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Declarations

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Data Availability Statements: The authors confirm that the data supporting the findings of this study are available within the article.

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Author Contribution

X.S. designed the experiment, T.T. wrote the main manuscript text, T.T. and W.Z. prepared figures and tables. All authors reviewed the manuscript.

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Tables

Table 1 The effect of different organic fertilizers on the physicochemical properties of soil

Treatments	Organic matter (g/kg)	Total nitrogen (g/kg)	Total phosphorus (g/kg)	Total potassium (g/kg)	Alkali-hydrolyzed nitrogen (g/kg)	Available phosphorus (g/kg)	Available potassium (g/kg)	pH value
CK	17.00 ± 1.64 b	1.30 ± 0.21 b	0.66 ± 0.25 b	16.67 ± 0.43 a	98.24 ± 1.45 b	77.42 ± 5.89 b	187.00 ± 15.56 b	7.00 ± 0.18 a
PY	17.48 ± 2.17 b	1.51 ± 0.34 ab	1.00 ± 0.28 ab	16.77 ± 0.24 a	84.55 ± 2.24 c	88.40 ± 22.56 ab	162.67 ± 16.26 b	7.10 ± 0.05 a
LY	22.65 ± 0.99 a	1.79 ± 0.05 a	1.14 ± 0.09 a	17.10 ± 0.15 a	175.03 ± 70.27 a	99.94 ± 15.48 ab	249.33 ± 4.16 a	6.96 ± 0.12 a
QY	23.93 ± 2.83 a	1.88 ± 0.26 a	1.45 ± 0.06 a	16.63 ± 0.15 a	158.60 ± 22.25 a	110.20 ± 2.47 a	239.50 ± 27.58 a	7.00 ± 0.10 a

Note: Different letters within the same column indicate significant differences between treatments at the 0.05 level.

Table 2 Soil bacterial sequencing and community alpha diversity indices under different organic fertilizer treatments

Treatments	OTUs	Shannon	Chao I	Ace	Coverage
CK	727.00 ± 67.01 c	4.30 ± 0.10 b	741.24 ± 101.36 c	742.29 ± 106.48 c	1.00 ± 0.00 a
PY	813.00 ± 190.92 c	4.85 ± 0.28 b	835.77 ± 203.32 c	835.54 ± 202.81 c	1.00 ± 0.00 a
LY	1642.50 ± 4.50 b	5.49 ± 0.10 a	1675.16 ± 31.52 b	1680.59 ± 36.10 b	1.00 ± 0.00 a
QY	2126.50 ± 249.61 a	5.59 ± 0.81 a	2227.10 ± 369.60 a	2226.06 ± 1386.27 a	1.00 ± 0.00 a

Note: Different letters within the same column indicate significant differences between treatments at the 0.05 level.

Figures

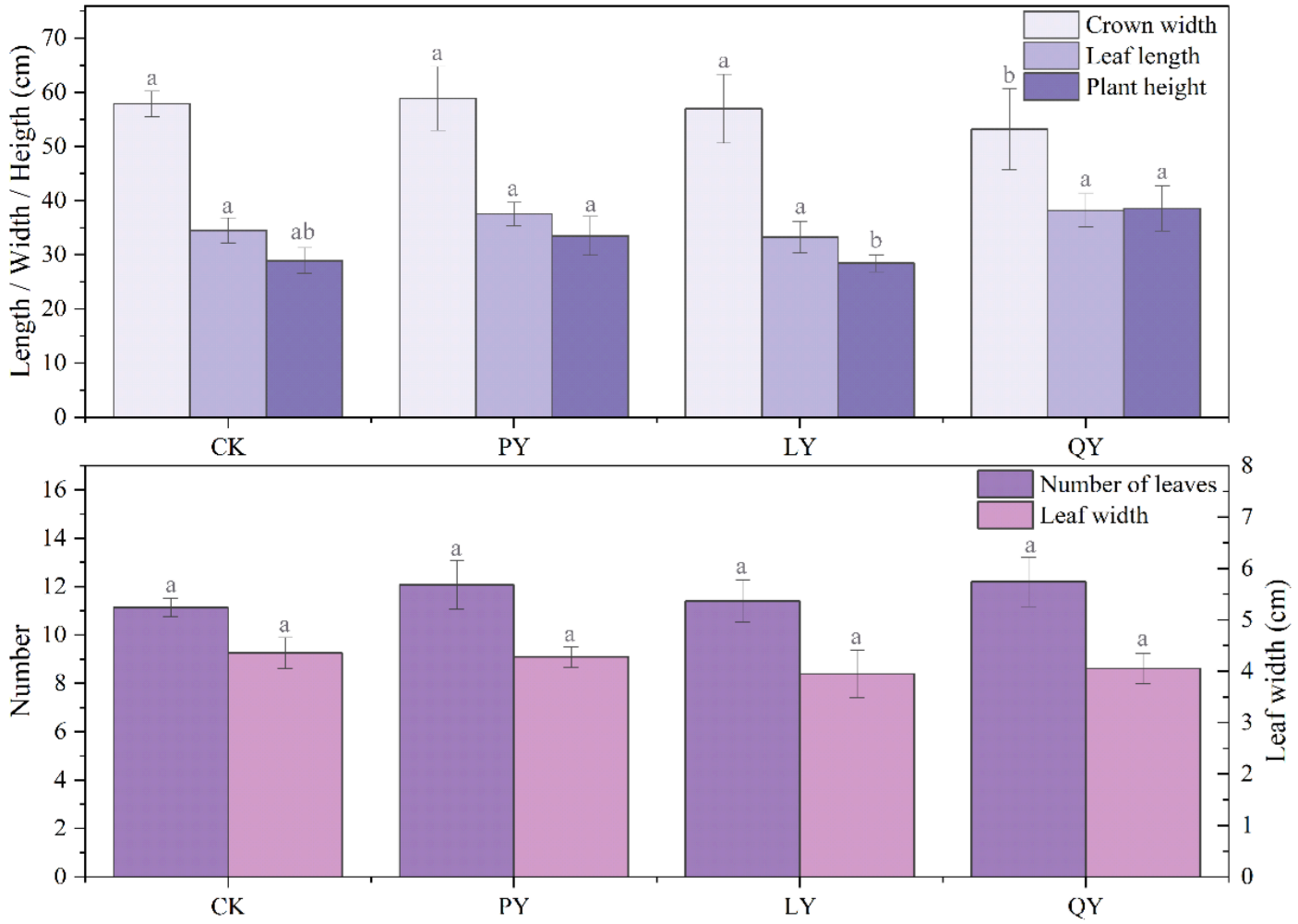

Figure 1

Physiological indicators for cultivating aloe under different organic fertilizer treatments. QY, earthworm manure;LY, Aloe-specific fertilizer; PY, general organic fertilizer; CK, no organic fertilizer. The same as follow. Different letters indicate significant differences between treatments at the 0.05 level.

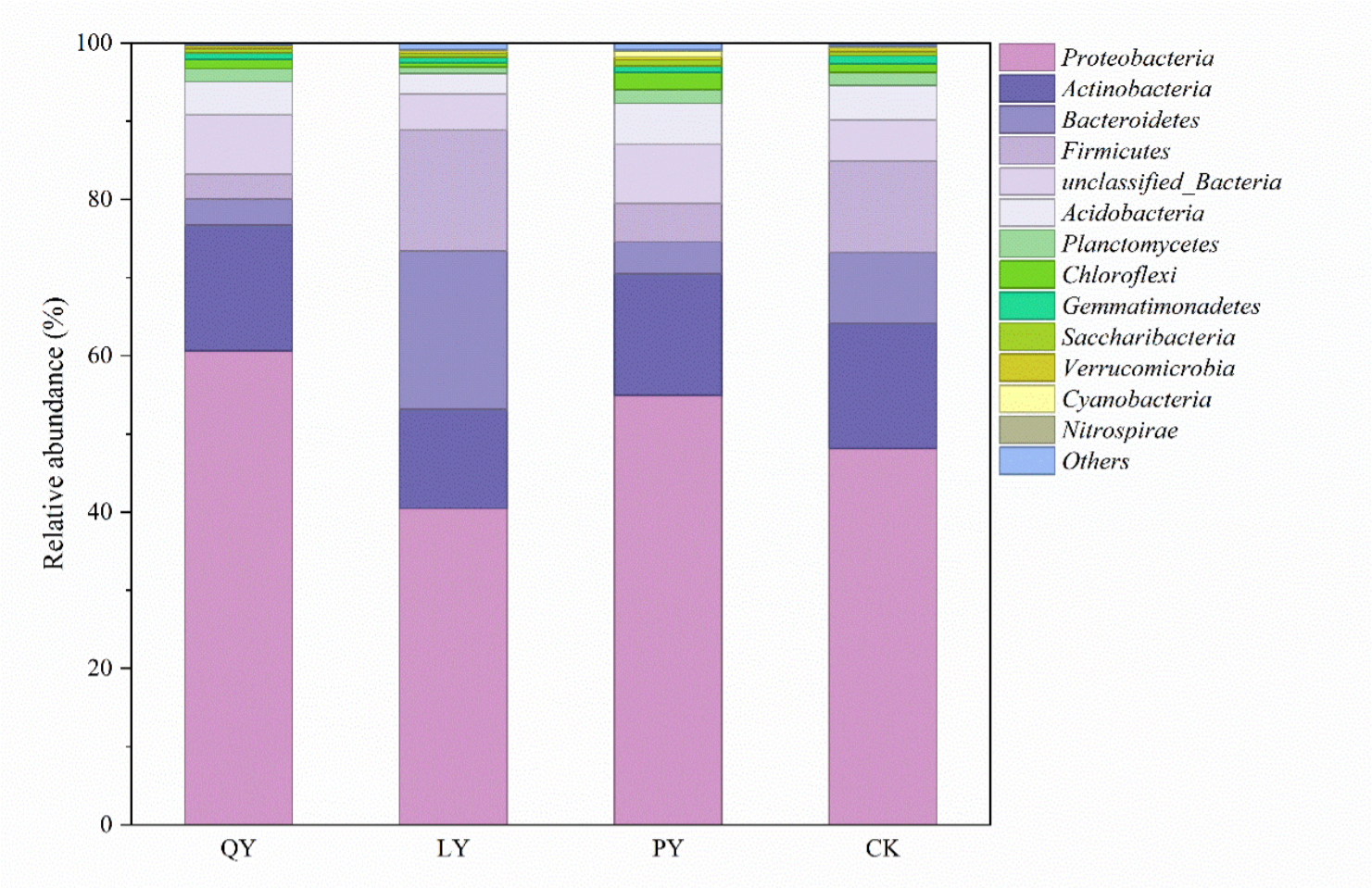

Figure 2

The relative abundance of bacterial phylum under different organic fertilizer treatments.

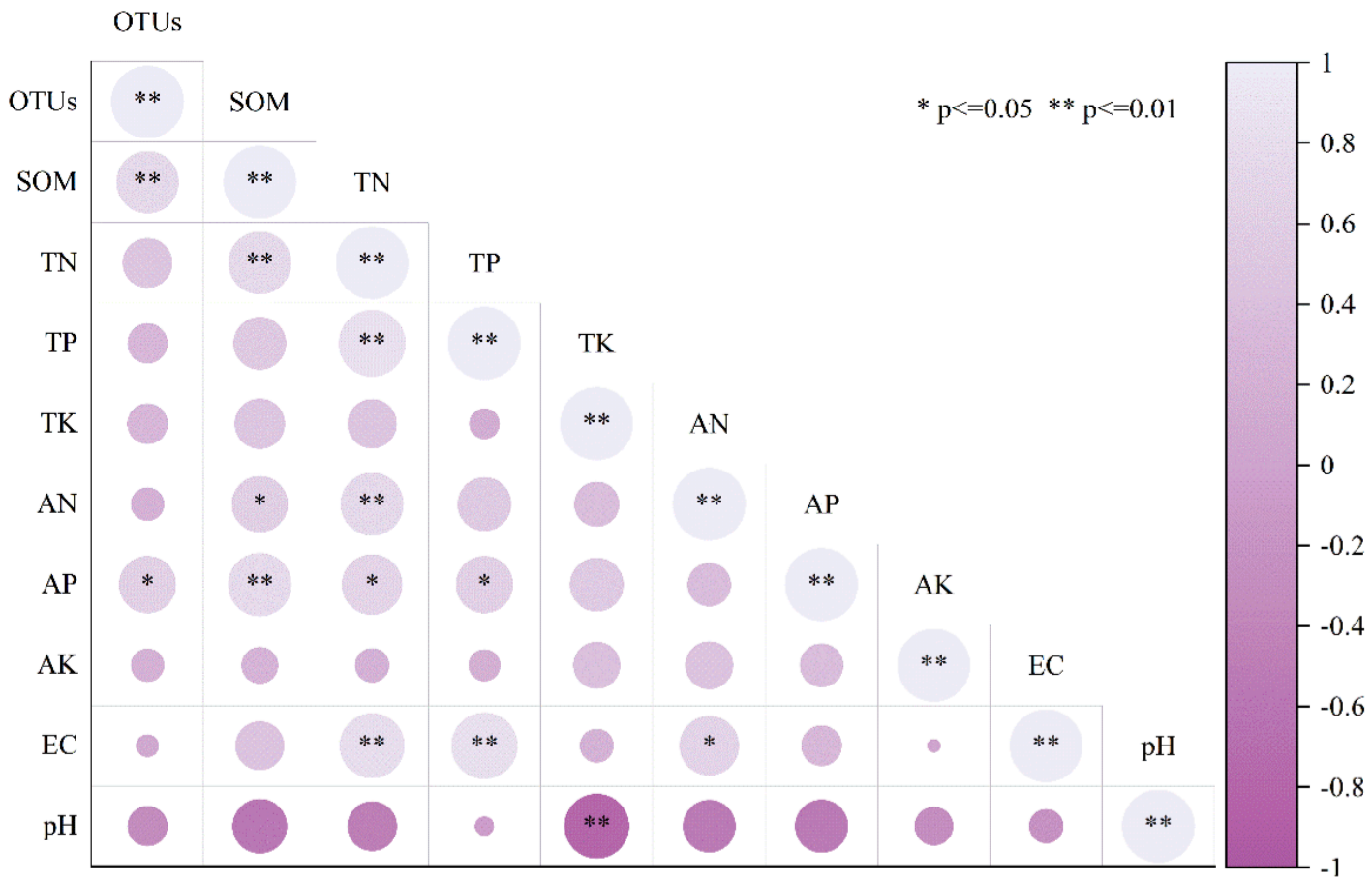

Figure 3

Correlation analysis between soil physicochemical properties and OTUs. SOM, soil organic matter; TN, total nitrogen; TP, total phosphorus; TK, total potassium; AN, alkali-hydrolyzed nitrogen; AP, available phosphorus; AK, available potassium.

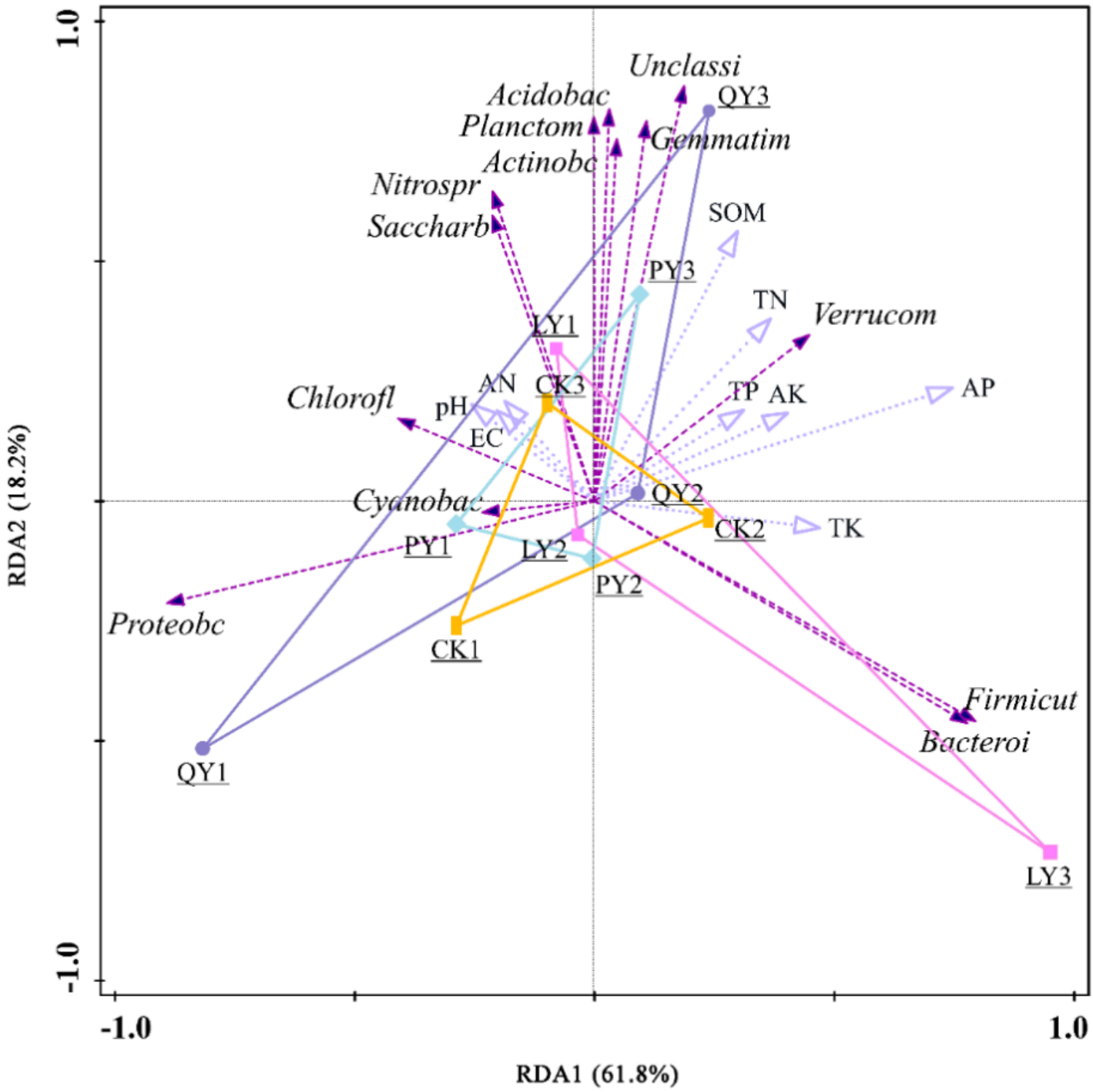

Figure 4

Redundancy analysis (RDA) of the relationship between the analyzed soil samples and environmental variables.