Effects of Protected Cultivation Patterns on Soil Bacterial Diversity and Community Structure (Postprint)

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Abstract

To investigate the effects of organic and conventional greenhouse cultivation patterns and crop rotation on soil bacterial diversity and community structure, this study employed the Illumina HiSeq 2500 high-throughput sequencing platform to perform 16S rRNA sequencing on soil bacteria under different greenhouse cultivation patterns in Shunyi District, Beijing, in June 2016 (during the crop harvest period). The patterns included continuous leafy vegetable cropping, continuous solanaceous fruit cropping, and leafy vegetable-solanaceous fruit rotation under both organic and conventional greenhouse cultivation modes. Following sequencing quality control, a total of 17,278 operational taxonomic units (OTUs) and 318,851 valid sequences were obtained. The study compared differences in soil bacterial diversity, bacterial community composition, relative abundance, and the relationships between soil physicochemical properties and bacterial community diversity under different cultivation patterns and rotation systems. The results demonstrated that soil microbial community structure differed significantly between organic and conventional greenhouse cultivation modes, with soil bacterial diversity being higher under organic greenhouse cultivation than under conventional cultivation. Under organic greenhouse cultivation, the soil bacterial community structure showed significant differences between rotation and continuous cropping systems, whereas no significant differences were observed between these systems under conventional greenhouse cultivation. Under organic cultivation patterns, soil bacterial community diversity in rotation systems was higher than that in continuous cropping systems. The soil bacterial communities in greenhouse cultivation were dominated by Sphingomonas (5.05%) and Bacillus (4.84%), with a total of 14 genera having relative abundances greater than 0.5%. Organic greenhouse cultivation soils contained more bacteria that promote plant growth and organic matter decomposition, while conventional greenhouse cultivation soils harbored more bacteria that degrade chemical pesticides, prevent soil diseases, and promote nitrification processes. RDA analysis revealed that soil bacterial communities were primarily influenced by total phosphorus, available phosphorus, and organic matter. Tumebacillus, Candidatus Solibacter, and Acidothermus are all bacterial genera that decompose organic matter and utilize carbon sources, showing positive correlations with soil organic matter (SOM). These findings indicate that under greenhouse conditions, differences in soil microbial community structure between organic and conventional cultivation primarily stem from variations in fertilizer use, pest control measures, and management practices. Under organic greenhouse cultivation patterns, crop rotation is more conducive to exerting its role in improving soil nutrient cycling and controlling soil diseases and pests. These results provide a reference for studying differences in soil ecological quality under different cultivation patterns in greenhouse conditions at the microbial level.

Full Text

Abstract

To investigate the effects of organic and conventional facility planting modes and crop rotation on soil bacterial diversity and community structure, this study employed high-throughput sequencing technology using the Illumina Hiseq 2500 platform to perform 16S rRNA sequencing of soil bacteria in June 2016 (during the crop harvest period) under different facility planting modes in Shunyi District, Beijing. The modes included organic facility planting and conventional facility planting, each with leafy vegetable continuous cropping, Solanaceous vegetable continuous cropping, and leafy-Solanaceous vegetable rotation. After quality control, a total of 17,278 operational taxonomic units (OTUs) and 318,851 effective sequences were obtained. The study compared differences in soil bacterial diversity, community composition, relative abundance, and the relationships between soil physicochemical properties and bacterial community diversity across different planting modes and rotations. Results showed that soil microbial community structure differed significantly between organic and conventional facility planting, with higher bacterial diversity observed in organic facility soils. Under organic management, bacterial community structure showed clear differences between rotation and continuous cropping, whereas no significant differences were observed under conventional management. Bacterial community diversity was higher in rotation soils than in continuous cropping soils under organic facility planting. The soil bacterial community was dominated by *Sphingomonas* (5.05%) and *Bacillus* (4.84%), with 14 genera exhibiting relative abundance greater than 0.5%. Organic facility soils contained more bacteria promoting plant growth and organic matter decomposition, while conventional facility soils harbored more bacteria capable of degrading chemical pesticides, controlling soil-borne diseases, and promoting nitrification. Redundancy analysis (RDA) revealed that soil bacterial communities were primarily influenced by total phosphorus, available phosphorus, and organic matter. *Tumebacillus*, *Candidatus Solibacter*, and *Acidothermus*—all bacteria that decompose organic matter and utilize carbon sources—showed positive correlations with soil organic matter (SOM). These findings indicate that differences in soil microbial community structure between organic and conventional facility planting mainly stem from variations in fertilizer application, pest control measures, and management practices. Under organic facility planting, crop rotation better leverages its benefits for improving soil nutrient cycling and controlling soil-borne diseases. These results provide a reference for studying differences in soil ecological quality under different facility planting modes at the microbial level.

Keywords: facility planting; organic farming; crop rotation system; soil bacteria; community structure; diversity; high-throughput sequencing

Introduction

Facility planting is an intensive cultivation method that improves or creates controllable environmental conditions (such as solar greenhouses) for growing vegetables and melons, primarily using soil-based cultivation. Global facility planting area exceeds 3.9 million hectares, with China accounting for approximately 90% of this area. However, the "high input, high output" characteristic of conventional facility planting leads to substantial nutrient accumulation in facility soils, creating soil constraints such as secondary salinization, soil acidification, and soil-borne diseases. Facility planting methods and changes in soil physicochemical properties also affect soil microbial diversity and community structure. Soil microorganisms play crucial roles in agricultural ecosystems, participating in every aspect of crop-soil interactions, including soil carbon and nitrogen cycling, plant growth regulation, plant disease and pest control, and soil structure optimization.

In recent years, organic planting aimed at establishing and restoring biodiversity in agricultural ecosystems and achieving sustainable development has gained widespread attention. Studies have shown that organic planting significantly increases soil microbial diversity, thereby maintaining the stability of soil ecosystems, primarily due to organic fertilizer application providing abundant and diverse food resources for soil microbial growth and reproduction. Research indicates that organic fertilizer application increases the abundance of beneficial soil bacteria such as nitrogen-fixing bacteria, which convert elements from organic forms into plant-available forms, enhancing soil fertility and promoting nutrient cycling and plant growth. Additionally, crop rotation can balance nutrient utilization, improve soil physicochemical properties, and reduce soil-borne diseases. Studies have demonstrated that rotation increases soil microbial diversity and enhances the abundance of bacteria such as *Pseudomonadaceae* spp., which effectively decompose soil organic matter and prevent soil-borne diseases.

However, previous studies on the effects of organic planting and rotation on soil microbial diversity and community structure were not conducted under facility conditions. Facility planting subjects soils to high temperature and humidity conditions, which influence microbial diversity and community structure. Studies by Zeng Xibo et al. under facility conditions showed that organic planting significantly increased soil microbial diversity compared to conventional planting. Unlike open-field cultivation, organic facility planting can increase the abundance of bacteria such as Firmicutes, which help prevent soil-borne diseases. Nevertheless, research on soil microbial diversity and community structure under different planting modes (organic vs. conventional) in facility conditions remains limited.

Currently, investigating soil microbial diversity and community structure to reveal mechanisms underlying soil quality and functional differences under various agricultural practices has become a research hotspot. This study employed DNA extraction and high-throughput sequencing technology to examine the effects of different planting modes (organic vs. conventional) and crop rotation on soil bacterial diversity and community structure and their relationships with soil environmental factors in Shunyi District, Beijing, under facility conditions. By elucidating differences in soil bacterial community structure among different modes, this study aims to identify more rational facility planting patterns and provide a theoretical basis for improving the soil ecological environment and sustainable development of facility planting.

Materials and Methods

1.1 Study Site Description

The experimental site was located in a facility vegetable plantation in Shunyi District, Beijing (116°49 E, 40°04 N). The soil type was clay loam, with an average annual temperature of 11.5°C, annual sunshine duration of 2,750 hours, frost-free period of 191–199 days, average annual relative humidity of 50%, and average annual rainfall of approximately 625 mm. Soil samples collected in June 2016 revealed the following basic chemical properties for the 0–20 cm test soil layer: pH 7.45, electrical conductivity 88.65 $\mu S \cdot cm^{-1}$, organic matter 16.36 $g \cdot kg^{-1}$, total nitrogen 1.40 $g \cdot kg^{-1}$, total phosphorus 0.52 $g \cdot kg^{-1}$, total potassium 0.84 $g \cdot kg^{-1}$, available phosphorus 20.21 $mg \cdot kg^{-1}$, available potassium 134.06 $mg \cdot kg^{-1}$, nitrate nitrogen 3.48 $mg \cdot kg^{-1}$, and ammonium nitrogen 1.40 $mg \cdot kg^{-1}$. The plantation covered an area of 0.11 km^2 and consisted of seven greenhouses (100 m long × 7 m wide, 5 years old). Vegetable types included Solanaceous crops [tomato (*Solanum lycopersicum*), pepper (*Capsicum annuum*), eggplant (*Solanum integrifolium*)] and leafy vegetables [leek (*Allium tuberosum*), celery (*Coriandrum sativum*)].

1.2 Experimental Design

The experiment comprised six treatments: organic facility planting and conventional facility planting, each with leafy vegetable continuous cropping, Solanaceous vegetable continuous cropping, and leafy-Solanaceous vegetable rotation. Each treatment had three replicates, with one greenhouse serving as one replicate. Rotation involved two crops per year, planted from March–July and September–February. Leafy vegetable continuous cropping used leek, Solanaceous vegetable continuous cropping used tomato, and rotation alternated between leek and tomato.

Organic facility planting applied organic fertilizer as base fertilizer at 1,000–1,200 $\mathrm{kg \cdot hm^{-2}}$, with measured chemical properties: total nitrogen 1.94 $\mathrm{g \cdot kg^{-1}}$, total phosphorus 0.58 $\mathrm{g \cdot kg^{-1}}$, total potassium 1.40 $\mathrm{g \cdot kg^{-1}}$, and organic matter 182.45 $\mathrm{g \cdot kg^{-1}}$. Conventional facility planting used a 6:1 mixture of diammonium phosphate and garden-specific compound fertilizer as base fertilizer at 450 $\mathrm{kg \cdot hm^{-2}}$. The mixed fertilizer contained \$ $680g \cdot kg$^{-1}\$ total nutrients (P_2O_5 460 $\mathrm{g \cdot kg^{-1}}$, nitrogen 180 $\mathrm{g \cdot kg^{-1}}$, K_2O 70 $\mathrm{g \cdot kg^{-1}}$). Both modes received 3-4 topdressing applications of diammonium phosphate at 120 $\mathrm{kg \cdot hm^{-2}}$. For pest control, organic mode used insect nets, while conventional mode applied chemical insecticides (thiamethoxam, cyromazine) 3–5 times starting one week after transplanting. All greenhouses underwent 30–45 days of high-temperature sterilization in late July annually. Organic mode used bee pollination (bumblebees, 1,200 heads per 667 $\mathrm{m^2}$), while conventional mode used manual pollination. Both modes employed manual weeding. Conventional mode yield stabilized at approximately 60,000 $\mathrm{kg \cdot hm^{-2}}$ for Solanaceous crops, while organic mode yield was 80% of conventional but with higher quality and storage durability.

1.3 Sampling Method

Sampling was conducted after ten rotation cycles. The current season' s crops were planted in March 2016, and sampling occurred in June 2016 during the harvest period. For each treatment, 0–20 cm topsoil samples were collected using an S-shaped multipoint method. Soil cores (3 cm diameter, 20 cm depth) were taken near plant roots, with six cores per greenhouse combined and thoroughly mixed to form one composite sample. Each soil sample was divided into two portions: approximately 100 g stored in sterile bags in a dry ice box and transported to the laboratory for storage at -80°C, and about 800 g stored at -4°C for physicochemical analysis.

1.4 Soil Physicochemical Analysis

Soil physicochemical indices were measured according to literature methods [20-21]. pH and electrical conductivity (EC) were measured using a pH meter and conductivity meter (soil:water ratio 1:5). Ammonium nitrogen (NH_4^+-N) and nitrate nitrogen (NO_3^--N) were extracted with 0.5 $\mathrm{mol \cdot L^{-1}}$ K_2SO_4 solution for 1 hour and measured using a continuous flow analyzer. Soil organic matter (SOM) was determined by the oil bath heating-$K_2Cr_2O_7$ volumetric method. Total soluble nitrogen (TSN) was extracted with 0.5 $\mathrm{mol \cdot L^{-1}}$ K_2SO_4 solution for 1 hour and measured using a TOC analyzer nitrogen module. Total phosphorus (TP) was determined by the molybdenum-antimony anti-colorimetric method. Available phosphorus (AP) was extracted with 0.5 $\mathrm{mol \cdot L^{-1}}$ $NaHCO_3$ and measured spectrophotometrically. Available potassium (AK) was extracted with 1 mol · L^{-1} NH_4Ac and measured by flame photometry. Cation exchange capacity (CEC) was determined by the NH_4Cl-NH_4Ac method.

1.5 DNA Extraction and High-Throughput Sequencing

Three replicate soil samples from each treatment were thoroughly mixed to form a representative sample for bacterial analysis. Approximately 0.33 g of freeze-dried soil was used for total DNA extraction with a Fast DNA Spin Kit for Soil (MP Biomedicals, USA) following the manufacturer' s instructions. Extracted DNA quality was checked by 1% gel electrophoresis, and concentration was measured using a NanoDrop 2000 UV-Vis Spectrophotometer (Thermo Fisher Scientific, USA).

Bacterial 16S rRNA genes were amplified using universal primers 515F (5 -GTGCCAGCMGCCGCGGTAA-3) and 907R (5 -CCGTCAATTCCTTTGAGTTT-3). PCR conditions were: 98°C pre-denaturation for 1 min; 30 cycles of 98°C denaturation for 10 s, 50°C annealing for 30 s, 72°C extension for 30 s; and final extension at 72°C for 5 min. Products were detected by 2% agarose gel electrophoresis and sequenced on the Hiseq 2500 platform (Illumina, San Diego, CA, USA) by Novogene Bioinformatics Technology Co., Ltd. (Beijing).

1.6 Data Analysis

Raw sequences were assembled using Pandaseq (v2.7), and primers and adapters were removed using Trimmomatic (v0.30). Usearch (v8.0) was used to compare assembled and filtered sequences against a database to remove chimera sequences, yielding effective sequence data. The RDP classifier Bayesian algorithm was used for operational taxonomic unit (OTU) clustering at 97% similarity. Representative sequences for each OTU were taxonomically annotated to obtain species information and relative abundance distributions. Alpha diversity was calculated using Shannon, Simpson, and Chao1 indices. Beta diversity reflecting differences among samples was analyzed by principal component analysis (PCA) based on phylogenetic relationships and sequence relative abundance. Redundancy analysis (RDA) was performed to analyze correlations between soil bacterial community structure and environmental factors.

Results

2.1 Soil Physicochemical Properties Under Different Facility Planting Modes

Soil physicochemical analysis results are presented in Table 1 . The test soil was weakly acidic, with pH ranging from 6.23 to 6.71, showing significant differences among treatments ($P = 0.003$) but narrow variation. Organic matter, available potassium, nitrate nitrogen, and electrical conductivity showed highly significant differences among treatments ($P < 0.001$). Ammonium nitrogen content also differed significantly among the six treatments ($P = 0.004$). Electrical conductivity values were higher in conventional facility soils than in organic soils, indicating more severe salt accumulation under conventional management. Nitrate nitrogen content followed the same pattern, with excess nitrate likely being the main cause of soil salt accumulation. Organic matter content was higher in organic facility soils, demonstrating that organic facility planting significantly increased soil organic matter. Available potassium was higher in rotation treatments than in continuous cropping, likely because crop rotation facilitates soil nutrient accumulation.

2.2 High-Throughput Sequencing Results

High-throughput sequencing based on 16S rRNA yielded 318,851 effective sequences (average read length 418 bp) across all samples. Clustering analysis at 97% similarity produced 17,278 OTUs (Figure 1 [Figure 1: see original paper], Table 2). Coverage and rarefaction curves were used to assess the microbial diversity captured in the sequence libraries. Coverage for all six treatments exceeded 98.5% (Table 2), and rarefaction curves (Figure 1) plateaued, indicating that the sequence libraries adequately reflected bacterial community composition and diversity, essentially covering all bacterial populations in facility soils.

2.3 Soil Bacterial Alpha Diversity Under Different Facility Planting Modes

Table 2 lists soil bacterial alpha diversity indices calculated from OTU numbers (97% similarity). Under leafy vegetable continuous cropping, Solanaceous vegetable continuous cropping, and leafy-Solanaceous rotation, Shannon diversity indices were higher in organic facility soils than in conventional facility soils. For leafy vegetable continuous cropping and rotation, organic facility soils also showed higher Chao1 and Simpson diversity indices than conventional soils. In organic facility soils, rotation had higher Shannon diversity than continuous leafy or Solanaceous cropping, but lower Chao1 index compared to other treatments, with little difference in Simpson index. Under conventional facility planting, Solanaceous continuous cropping showed the highest Shannon, Simpson, and Chao1 indices. These results indicate that rotation more clearly increased soil bacterial diversity under organic facility management.

2.4 Principal Component Analysis of Soil Bacterial Communities

To explore differences in bacterial community structure among treatments, principal component analysis (PCA) was performed. After varimax orthogonal rotation ($P = 0.05$), two principal components were extracted, explaining 29.39% and 20.27% of variance, respectively (Figure 2 [Figure 2: see original paper]). Organic and conventional facility treatments were completely separated along PC1, with organic treatments on the positive axis and conventional treatments on the negative axis, indicating distinct bacterial community structures. Additionally, under organic management, rotation and continuous cropping showed clear separation along PC2 (continuous cropping on the positive axis, rotation on the negative axis), whereas conventional management showed no clear separation between rotation and continuous cropping.

2.5 Soil Bacterial Community Composition and Relative Abundance

Representative sequences from OTUs at 97% similarity were taxonomically analyzed using the RDP classifier Bayesian algorithm at the genus level. Fourteen genera had relative abundance >0.5% (Figure 3 [Figure 3: see original paper]): *Sphingomonas* (5.05%), *Bacillus* (4.84%), *Lysobacter* (1.49%), *Arthrobacter* (0.95%), *Bhargavaea* (0.79%), *Pseudomonas* (0.62%), *Bryobacter* (0.96%), *Agromyces* (0.62%), *Candidatus Solibacter* (0.59%), *Acidothermus* (0.53%), *Tumebacillus* (0.55%), *Candidatus Entotheonella* (0.57%), *Microvirga* (0.61%), and *Blastococcus* (0.51%). *Sphingomonas* and *Bacillus* were the dominant genera (>4% relative abundance), while all others were <1.5%.

Relative abundances of bacterial genera (>0.5%) differed between organic and conventional facility soils (Figure 4 [Figure 4: see original paper]). Seven genera were significantly more abundant in conventional soils: *Sphingomonas*, *Pseudomonas*, *Agromyces*, *Blastococcus*, *Lysobacter*, *Candidatus Entotheonella*, and *Microvirga*. Seven genera were significantly more abundant in organic soils: *Bacillus*, *Arthrobacter*, *Bhargavaea*, *Bryobacter*, *Candidatus Solibacter*, *Acidothermus*, and *Tumebacillus*. *Acidothermus* was unique to organic facility soils. Rotation soils showed significantly higher abundances of four genera compared to continuous cropping: *Bacillus*, *Lysobacter*, *Bryobacter*, and *Bhargavaea*.

2.6 Correlation Between Soil Bacterial Community Structure and Physicochemical Properties

Detrended correspondence analysis using CANOCO software indicated that RDA was appropriate (Figure 5 [Figure 5: see original paper]). Axis 1 explained 63.4% of variance and Axis 2 explained 28.3%. During RDA, five soil environmental factors were selected by manual forward selection: TP, AP, SOM, NH_4^+-N, and AK, which explained 98.7% of the variation in the original ten soil variables, essentially covering all soil environmental information. Euclidean distances among the six treatments showed clear separation between organic and conventional facility soils. Differences between rotation and continuous cropping were observed under both modes, but were more pronounced under organic management. TP and AP had the greatest influence on bacterial community structure. *Pseudomonas* and *Bryobacter* were positively correlated with TP and AP, while *Blastococcus* and *Candidatus Entotheonella* were negatively correlated. SOM also substantially affected bacterial community structure: *Tumebacillus*, *Candidatus Solibacter*, and *Acidothermus* were positively correlated with SOM, whereas *Agromyces*, *Lysobacter*, and *Sphingomonas* were negatively correlated. *Tumebacillus*, *Candidatus Solibacter*, and *Acidothermus* are bacteria that decompose organic matter and utilize carbon sources, thus thriving in organic-rich soils and showing positive correlations with SOM. Additionally, NH_4^+-N and AK influenced bacterial community structure, with *Bacillus* and *Arthrobacter* showing positive correlations.

Discussion

3.1 Effects of Facility Planting Mode (Organic/Conventional) on Soil Bacterial Community Structure

Principal component analysis revealed distinct bacterial community structures between organic and conventional planting modes. Alpha diversity indices indicated that organic facility planting increased soil bacterial community diversity compared to conventional planting, consistent with Ge et al.' s findings on tea plantation soil microbial diversity. Changes in available carbon sources due to different fertilization practices likely represent an important factor affecting soil bacterial diversity and community structure. Organic fertilizer application in organic facility planting provides substantial organic matter, forming diverse carbon types during decomposition that serve as varied food resources for microorganisms, thereby increasing microbial community diversity. RDA results also identified soil organic matter as a primary factor influencing bacterial community structure. Bacteria that decompose organic matter and utilize carbon sources—*Tumebacillus*, *Candidatus Solibacter*, and *Acidothermus*—were positively correlated with SOM content. Furthermore, long-term organic fertilizer application improves soil structure, providing favorable habitats for microbial growth and increasing microbial diversity. RDA analysis also demonstrated clear differences in bacterial community structure between organic and conventional modes, with soil phosphorus (total and available) and organic matter content being the main influencing factors. This suggests that facility soils may experience phosphorus deficiency, which reduces microbial diversity; fertilization increases phosphorus and improves soil N/P ratios, thereby enhancing microbial diversity. Additionally, differences in bacterial community diversity between the two facility planting modes may result from chemical inputs (pesticides and insecticides) and salt accumulation affecting soil microorganisms. Soil microbial communities, as micro-ecosystems, possess certain stability. Studies have shown that chemical pesticide use disrupts this stability as an external disturbance, causing a few adapted populations to proliferate while suppressing others.

The types and quantities of soil bacterial communities differed between organic and conventional facility soils. Genera significantly more abundant in conventional soils could be functionally categorized as: degraders of chemical insecticides and other aromatic organic compounds (*Sphingomonas*, *Pseudomonas*, *Agromyces*); stress-tolerant and disease-controlling bacteria (*Blastococcus*, *Lysobacter*); and nitrification-promoting bacteria (*Candidatus Entotheonella*, *Microvirga*). Conventional facility soils contained more microorganisms capable of degrading large organic pollutants, likely due to chemical insecticide use for pest management. Conventional soils also had more nitrification-promoting bacteria, resulting from excessive chemical fertilizer application and nitrogen accumulation. Microorganisms reciprocally affect their environment; nitrification-promoting bacteria convert large amounts of nitrogen to nitrate, whose accumulation is a major factor causing secondary salinization in facility soils and severely impacts vegetable yield and quality with increasing planting duration. Soil physicochemical analysis confirmed these findings, with higher electrical conductivity and nitrate nitrogen in conventional facility soils, indicating more severe salt accumulation. Additionally, conventional facility soils contained more stress-tolerant bacteria because chemical insecticides effectively controlled soil-borne diseases in the short term, resulting in significantly lower pest and disease incidence than in organic soils, consistent with Finckh et al.' s findings on potato cultivation. However, long-term insecticide use causes severe organic pollution and resistance, substantially reducing disease control effectiveness.

Genera significantly more abundant in organic soils could be functionally categorized as: plant growth-promoting bacteria (*Bacillus*); and organic matter-decomposing, carbon-utilizing bacteria (*Arthrobacter*, *Bhargavaea*, *Bryobacter*, *Candidatus Solibacter*, *Acidothermus*, *Tumebacillus*). Organic facility soils contained more carbon-decomposing and plant growth-promoting bacteria than conventional soils, consistent with Ye et al.' s conclusions. Organic fertilizer application in organic facility planting provides diverse food resources and more suitable growth environments for soil microorganisms. In contrast, heavy chemical fertilizer use in conventional facility planting causes rapid organic carbon decomposition without increasing total soil organic carbon accumulation, reducing soil microbial biomass carbon and creating carbon source limitations for microbial growth. Organic facility planting uses biological measures for pest control, avoiding organic pollution and providing favorable growth conditions. Organic fertilizer application not only supplies nutrients for crop growth but also improves soil physicochemical properties, benefits nutrient balance, and increases nutrient content. Numerous studies have shown that organic produce contains more vitamin C, phosphorus, potassium, and mineral elements (Fe, Mg) and has superior sensory quality and chemical composition compared to conventional produce.

3.2 Effects of Crop Rotation on Soil Bacterial Community Structure

Principal component analysis showed that under organic facility planting, bacterial community structure differed significantly between rotation and continuous cropping, whereas under conventional facility planting, no clear differences were observed. Alpha diversity analysis indicated that rotation soils had higher bacterial diversity (Shannon index) than continuous cropping soils under organic facility planting, but lower diversity (Shannon and Simpson indices) than Solanaceous continuous cropping under conventional facility planting. Hua et al. found that rotation increased soil bacterial diversity in open-field conditions. Rotation increases root exudate diversity, providing more carbon source types for microorganisms and thereby increasing microbial diversity. The lower bacterial diversity in rotation soils under conventional facility planting may be because high temperature and humidity conditions in facility soils affect conventional soil bacterial diversity more than organic soils. Additionally, heavy chemical inputs (fertilizers, pesticides, and insecticides) in conventional facility planting may reduce soil bacterial community diversity. These factors in conventional facility planting may have diminished the beneficial effects of rotation on soil bacterial communities, making organic facility planting more effective for enhancing rotation-induced bacterial diversity increases. Analysis of bacterial genera with >0.5% relative abundance showed that rotation significantly increased the abundance of plant growth-promoting (*Bacillus*), disease-controlling (*Lysobacter*), organic matter-decomposing (*Bhargavaea*), and carbon cycling-promoting (*Bryobacter*) genera compared to continuous cropping, consistent with Li et al.' s findings. This demonstrates that rotation better regulates soil microbial community structure, controls soil-borne diseases, promotes nutrient utilization, and prevents continuous cropping obstacles.

Conclusion

This study analyzed mixed samples from three replicates per treatment to explore soil bacterial community structure characteristics under different facility planting and rotation conditions from a microbial community perspective. Results showed that organic and conventional facility planting produced distinct soil bacterial community structures, with organic facility planting increasing soil bacterial diversity. Conventional facility soils contained more bacteria degrading chemical insecticides and aromatic organic compounds, controlling soil-borne diseases, and promoting nitrification, while organic facility soils contained more carbon-decomposing and plant growth-promoting bacteria. Crop rotation under organic facility planting better leveraged its benefits for improving soil nutrient cycling and controlling soil-borne diseases. Facility soil bacterial community structure was primarily influenced by three soil environmental factors: total phosphorus, available phosphorus, and organic matter. Bacteria that decompose organic matter and utilize carbon sources (*Tumebacillus*, *Candidatus Solibacter*, and *Acidothermus*) were positively correlated with soil organic matter content. The effects of different facility planting modes and rotations on soil bacterial community structure require further long-term study.

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