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Soil Microbial Community Changes under Continuous Cucumber Cropping in Greenhouse Systems

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Abstract Continuous cropping of greenhouse cucumbers is widely practiced in intensive vegetable production, but long-term monoculture often leads to soil degradation and continuous cropping obstacles. Soil microbial communities play a key role in maintaining soil fertility, nutrient cycling, and plant health. This study explores the changes in soil microbial community structure under greenhouse cucumber continuous cropping conditions. By combining soil physicochemical analysis with high-throughput sequencing techniques, the diversity and composition of soil microorganisms were examined under different continuous cropping durations. The results show that prolonged continuous cropping significantly alters microbial community structure, reduces microbial diversity, and increases the abundance of certain pathogenic microorganisms. Environmental factors such as soil pH, organic matter, and root exudates were identified as important drivers of these changes. The study highlights the importance of microbial regulation strategies, including bio-organic fertilizers and crop rotation, to improve soil health and promote sustainable greenhouse cucumber production.
Keywords Continuous cropping; Greenhouse cucumber; Soil microbial community; Microbial diversity; Soil health

1 Introduction

Greenhouse cucumber cultivation has become a vital component of modern horticulture due to its ability to provide high yields and quality produce throughout the year, independent of external climatic conditions. This intensive production system supports food security and economic development, especially in regions with limited arable land or unfavorable outdoor growing conditions. The controlled environment of greenhouses allows for optimized temperature, humidity, and light, which significantly enhances cucumber growth and productivity compared to open-field cultivation. As a result, greenhouse cucumber farming has expanded rapidly worldwide, becoming an essential practice for meeting increasing consumer demand and supporting sustainable agricultural intensification (Liu et al., 2020; Zhao et al., 2020).

However, continuous cropping of cucumbers in greenhouse systems often leads to serious obstacles that threaten long-term productivity and soil health. These continuous cropping obstacles include soil nutrient imbalances, accumulation of soil-borne pathogens, increased salinity, and autotoxicity caused by root exudates. Such adverse effects result in reduced crop yields and quality over time, posing significant challenges for sustainable greenhouse vegetable production. The decline in soil quality under continuous monocropping is closely linked to changes in the soil microbial community structure and function, which play critical roles in nutrient cycling and disease suppression. Understanding these changes is crucial for developing effective management strategies to mitigate continuous cropping problems and maintain productive greenhouse systems (Yao et al., 2006; Liu et al., 2020).

Soil microbial communities are key drivers of soil ecosystem functions and are highly sensitive indicators of soil health under continuous cropping regimes. Research on microbial community dynamics in continuously cropped cucumber soils reveals shifts in bacterial and fungal diversity, with decreases in beneficial microbes such as Bacillus and increases in potentially pathogenic fungi like Ascomycota. These microbial shifts correlate with changes in soil physicochemical properties such as pH, organic matter content, and nutrient availability.

Investigating the interactions between soil microbes and environmental factors provides insights into the mechanisms underlying continuous cropping obstacles. Moreover, manipulating microbial communities through practices like crop rotation, residue incorporation, or biochar amendment offers promising avenues to restore soil health and enhance cucumber yield sustainability in greenhouse systems (Zhao et al., 2020; Chen et al., 2022).

2 Soil Ecological Characteristics under Continuous Cropping of Greenhouse Cucumbers

2.1 Changes in soil physicochemical properties under continuous cropping conditions

Continuous cucumber cropping in greenhouse systems often leads to significant alterations in soil physicochemical properties, which can negatively impact soil health and crop productivity. Studies have shown that prolonged monoculture results in decreased soil pH, increased electrical conductivity (EC), and accumulation of total salts, indicating soil acidification and salinization trends that are detrimental to plant growth. For example, research along the Yellow River irrigation area demonstrated a consistent decline in pH and rise in total salt content with increasing years of continuous cucumber cultivation, alongside increases in organic matter and available nutrients such as nitrogen, phosphorus, and potassium during the early years of cropping (Huang et al., 2023). Similarly, long-term monocropping has been associated with elevated concentrations of organic matter and nutrients but also with adverse changes like soil acidification and nutrient imbalances that challenge sustainable production (Zhao et al., 2020).

Different cultivation patterns can modulate these physicochemical changes by influencing microbial communities and nutrient dynamics. Rotation systems such as paddy upland or garlic rotations have been found to mitigate soil acidification by maintaining higher pH levels compared to continuous cucumber monocropping. These rotations also promote beneficial shifts in microbial populations that contribute to improved soil quality. For instance, a study comparing six cultivation patterns over nine years found that rotation practices significantly altered bacterial and fungal community structures while alleviating the trend toward acidification seen under continuous cucumber cropping (Zhang et al., 2023). Such findings highlight the importance of diversified cropping systems for maintaining favorable soil physicochemical conditions in greenhouse cucumber production (Figure 1).

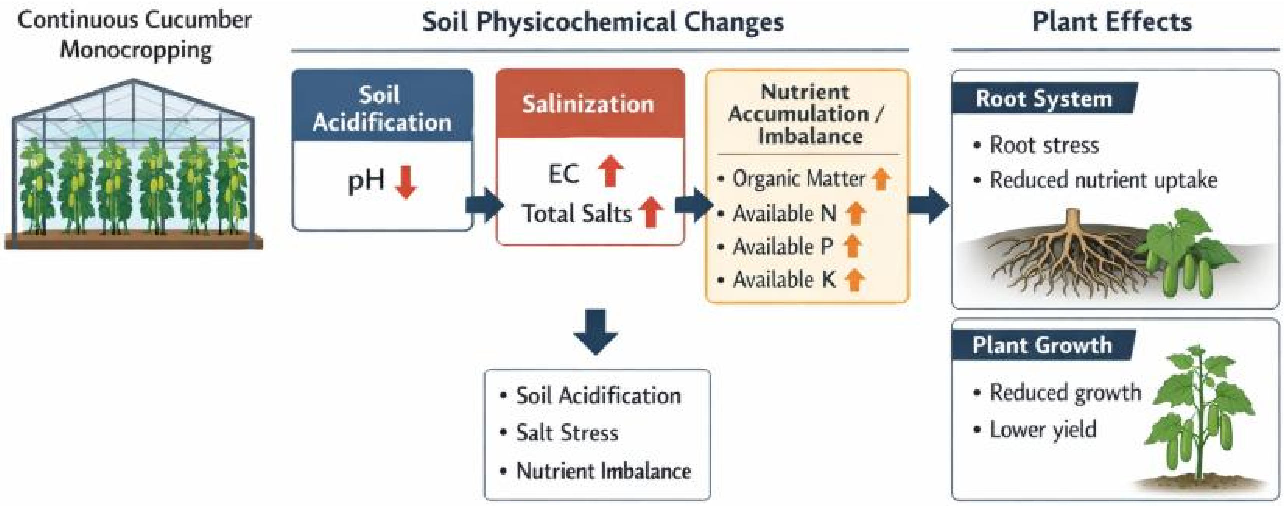

Figure 1 Conceptual illustration of how continuous cucumber monocropping in greenhouse systems alters soil physicochemical properties, including pH decline, salt accumulation, and nutrient imbalance, which ultimately influence cucumber root systems and plant growth performance

2.2 Effects of continuous cropping on soil nutrient cycling

Continuous cucumber cropping disrupts normal nutrient cycling processes within the soil ecosystem, often leading to nutrient accumulation or depletion that affects plant nutrition and microbial activity. While some nutrients like organic carbon, total nitrogen, available phosphorus, and potassium tend to increase initially due to fertilizer inputs and residue accumulation, their bioavailability may decline over time due to imbalances caused by monoculture practices. For example, studies have reported increased nutrient contents after several years of continuous cropping but also noted decreases in enzyme activities related to nutrient mineralization such as phosphatase and urease, which are critical for converting nutrients into plant-available forms (Zhao et al., 2017; Huang et al., 2025). This decoupling between nutrient presence and availability can impair efficient nutrient uptake by cucumbers.

Microbial communities play a central role in mediating nutrient cycling under continuous cropping conditions. Changes in microbial diversity and function influence key processes such as nitrogen fixation, phosphorus solubilization, and organic matter decomposition. Research indicates that beneficial microbial taxa involved in nitrogen and phosphorus cycling decline with prolonged monocropping while potentially pathogenic microbes increase. For instance, rotation systems that enrich microbiota antagonistic to pathogens also enhance functional genes associated with nitrogen and phosphorus cycling compared to continuous cucumber monoculture (Zhang et al., 2023; Xu et al., 2025). These microbial shifts directly affect nutrient transformations and availability, underscoring the need for management strategies that support healthy microbial-mediated nutrient cycling.

2.3 Changes in the stability of soil micro-ecosystems

The stability of soil micro-ecosystems is compromised under continuous cucumber cropping due to altered microbial community composition, reduced diversity, and disrupted interactions among microorganisms. Continuous monoculture tends to decrease fungal diversity while increasing certain bacterial groups linked with stress or disease conditions. For example, long-term mono-cropping has been shown to reduce beneficial bacterial phyla such as Actinobacteria while increasing Acidobacteria and Firmicutes; similarly, fungal communities shift toward dominance by Ascomycota species often associated with pathogenicity (Zhao et al., 2020). These changes weaken the resilience of the soil microbiome against environmental stresses and pathogen invasion.

Network analyses reveal that continuous cropping leads to more complex but less cohesive microbial interaction networks characterized by higher connectivity but reduced clustering among fungi, indicating destabilization of micro-ecosystem structure over time (Huang et al., 2025). Moreover, reductions in key enzyme activities further impair ecosystem functions essential for maintaining soil health. Interventions such as biochar amendment combined with intercropping have demonstrated potential for restoring micro-ecosystem stability by improving microbial diversity, reducing salinity stress, enhancing nutrient availability, and promoting beneficial microbial taxa (Shen et al., 2025). Maintaining stable micro-ecosystems is therefore critical for sustaining productive greenhouse cucumber cultivation under intensive continuous cropping regimes.

3 Structure and Function of Soil Microbial Communities

3.1 Composition characteristics of soil bacteria, fungi, and actinomycetes

Soil microbial communities under continuous cucumber cropping are characterized by shifts in the relative abundance and diversity of bacteria, fungi, and actinomycetes, which play distinct roles in soil processes. Bacterial communities often dominate in terms of abundance and are highly responsive to changes in soil physicochemical properties caused by monocropping. Key bacterial phyla such as Proteobacteria, Acidobacteria, and Actinobacteria fluctuate with cropping duration, with Actinobacteria often declining under continuous monoculture while Acidobacteria may increase, reflecting altered nutrient availability and soil conditions (Chen et al., 2024). Fungal communities also undergo compositional changes; Ascomycota typically become more dominant in continuous cropping systems, sometimes linked to increased pathogen presence, while beneficial groups like arbuscular mycorrhizal fungi (AMF) may decline without crop rotation or soil amendments (Labouyrie et al., 2023; Wooliver et al., 2025).

Actinomycetes, a group of filamentous bacteria important for organic matter decomposition and antibiotic production, tend to decrease in diversity and abundance under long-term monocropping due to soil degradation and reduced organic inputs. This decline can weaken natural disease suppression and nutrient cycling functions. However, management practices such as organic amendments or crop rotations can help restore actinomycete populations by improving soil structure and nutrient status (Chen et al., 2024; Mishra et al., 2025). Overall, continuous cucumber cropping leads to a less balanced microbial community composition with potential increases in pathogenic fungi and decreases in beneficial bacteria and actinomycetes that support soil health.

3.2 Functions of microbial communities in soil ecosystems

Microbial communities perform essential functions in soil ecosystems including nutrient cycling, organic matter decomposition, disease suppression, and maintenance of soil structure. Bacteria and fungi mediate carbon and nitrogen transformations through enzymatic activities that regulate mineralization and nutrient availability for plants. For example, bacterial communities strongly influence nitrogen cycling processes such as nitrification and denitrification, while fungal communities contribute significantly to phosphorus solubilization and organic matter breakdown (Zheng et al., 2019; Jiao et al., 2021). These functional roles are critical for sustaining cucumber growth under greenhouse conditions where nutrient demands are high.

Continuous cropping can disrupt these functions by altering microbial community composition and reducing functional diversity. Declines in key enzyme activities related to carbon degradation (e.g., β-glucosidase) or nitrogen cycling (e.g., urease) have been observed under monoculture systems, impairing nutrient turnover rates (Zheng et al., 2019). Moreover, shifts toward pathogenic fungal dominance reduce the capacity for natural disease suppression. Conversely, diverse microbial communities with balanced bacterial-fungal interactions enhance multifunctionality by supporting multiple nutrient cycles simultaneously (Jiao et al., 2021). Thus, maintaining functional microbial diversity is vital for ecosystem resilience and productivity in continuous cucumber cropping systems.

3.3 Relationship between microbial diversity and soil health

Microbial diversity is positively correlated with overall soil health because diverse communities provide redundancy in ecosystem functions that buffer against environmental stresses and disturbances. High microbial richness supports stable nutrient cycling processes, improves soil structure through aggregate formation, and suppresses pathogens via competitive exclusion or antagonism (Banerjee and Van Der Heijden, 2022; Chen et al., 2024). In greenhouse cucumber systems subjected to continuous cropping, declines in microbial diversity often coincide with reduced soil fertility indicators such as enzyme activities and increased disease incidence.

Research shows that soils with greater bacterial and fungal diversity exhibit enhanced multifunctionality including improved carbon sequestration and nitrogen retention compared to less diverse soils (Zheng et al., 2019; Jiao et al., 2021). However, the relationship between diversity and function is complex; community composition often has a stronger influence on specific functions than mere species richness alone (Jiao et al., 2021). Management practices that promote microbial diversity-such as crop rotation or organic amendments-can restore degraded soils by reestablishing beneficial taxa that improve nutrient availability and plant health (Mishra et al., 2025). Therefore, preserving or enhancing microbial diversity is crucial for sustaining long-term soil health under intensive greenhouse cucumber cultivation.

4 Effects of Continuous Cropping of Greenhouse Cucumbers on Soil Microbial Community Structure

4.1 Effects of continuous cropping duration on microbial community diversity

The duration of continuous cropping in greenhouse cucumber systems significantly influences soil microbial community diversity, often leading to complex shifts in bacterial and fungal populations. Short-term continuous cropping may initially increase bacterial richness due to nutrient inputs and root exudates stimulating microbial growth, but prolonged monoculture typically results in decreased bacterial diversity and altered community composition as soil nutrients become imbalanced and autotoxic compounds accumulate (Li et al., 2024; Chen et al., 2025). Fungal diversity often shows a contrasting pattern, with some studies reporting increased fungal richness under continuous cropping, potentially due to the proliferation of pathogenic fungi favored by monoculture conditions (Qiu et al., 2025; Zhang et al., 2025).

Long-term continuous cropping also affects the balance between deterministic and stochastic processes governing microbial community assembly. Deterministic factors such as soil pH, nutrient availability, and crop root exudates strongly shape microbial communities in early years, but with extended monoculture, stochastic processes gain influence, leading to less predictable community structures (Figure 2) (Chen et al., 2025; Wang et al., 2025).

These changes in assembly dynamics coincide with declines in soil organic matter and enzyme activities critical for nutrient cycling, further impacting microbial diversity and ecosystem function under continuous cucumber cultivation.

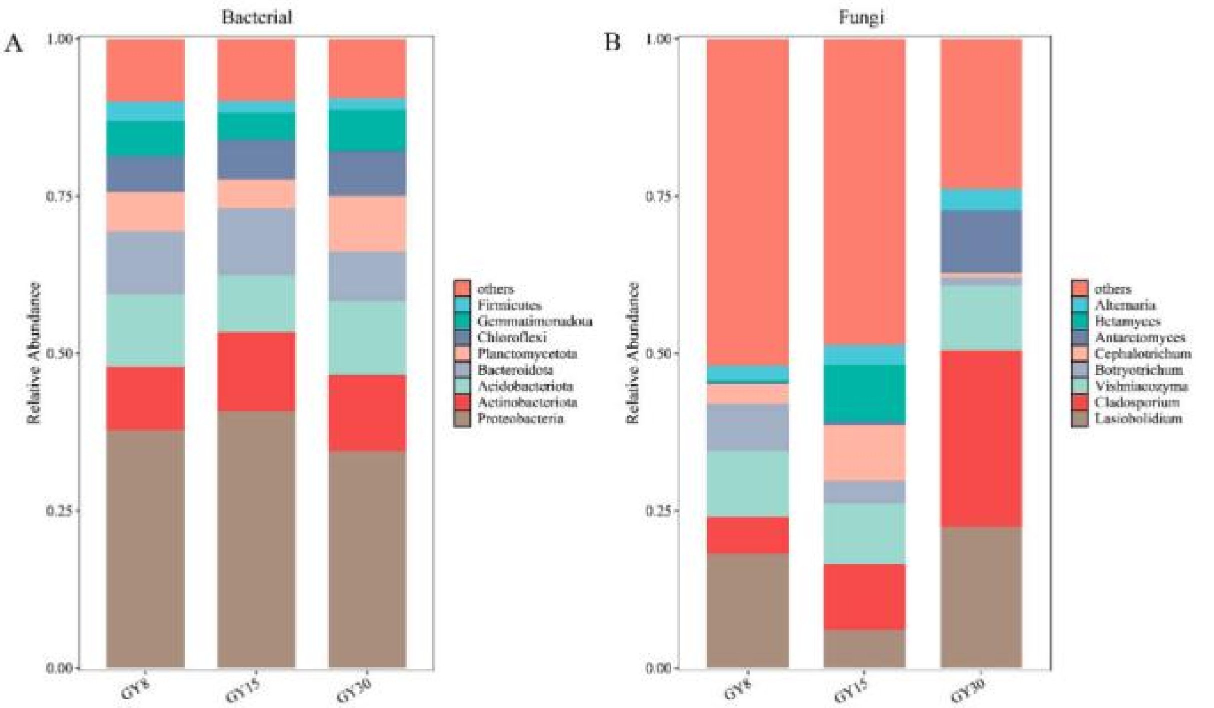

Figure 2 (A) Comparative analysis of bacterial relative abundances at the phylum level. (B) Comparative analysis of relative fungal abundance at the genus level (Adopted from Chen et al., 2025)

4.2 Dynamic changes of beneficial microorganisms and pathogenic microorganisms

Continuous cucumber cropping induces dynamic shifts between beneficial and pathogenic microorganisms in the soil, often resulting in reduced populations of plant-growth-promoting microbes alongside increases in pathogens. Beneficial bacteria such as those involved in nitrogen fixation or organic matter decomposition tend to decline over time due to nutrient depletion and unfavorable soil conditions caused by monocropping (Yang et al., 2025). Similarly, populations of beneficial fungi like arbuscular mycorrhizal fungi decrease, weakening symbiotic relationships that enhance nutrient uptake and disease resistance.

Conversely, pathogenic microorganisms including certain fungal genera (e.g., Fusarium, Alternaria) and bacterial pathogens tend to increase with continuous cropping duration, contributing to higher disease incidence and reduced crop yields (Chen et al., 2025). The accumulation of pathogen-associated genes correlates with disease severity in long-term monoculture soils, highlighting the risk posed by unchecked pathogen proliferation (Wang et al., 2025). Management strategies such as microbial fertilizer application or crop rotation have been shown to partially restore beneficial microbes while suppressing pathogens, improving soil health under continuous cropping regimes (Qiu et al., 2025).

4.3 Variation characteristics of the abundance of different microbial groups

The abundance of specific microbial groups varies markedly with continuous cucumber cropping duration, reflecting shifts in soil environmental conditions and resource availability. Bacterial phyla such as Proteobacteria often decrease over time while Acidobacteria increase, indicating a shift toward microbes adapted to lower nutrient levels and more acidic soils common under long-term monoculture (Ding et al., 2024; Li et al., 2024). Actinomycetes generally decline with prolonged cropping due to reduced organic matter inputs but can be stimulated by amendments that improve soil quality (Yang et al., 2025).

Fungal communities show increased relative abundance of pathogenic taxa like Cladosporium and Alternaria during extended continuous cropping periods, while beneficial fungal groups decline or fluctuate depending on management practices (Zhang et al., 2025). Co-occurrence network analyses reveal that bacterial network complexity decreases over time whereas fungal networks may partially recover or become more modular, suggesting differential adaptability among microbial groups to continuous cropping stress (Chen et al., 2025; Wang et al., 2025). These variations underscore the importance of monitoring specific microbial taxa to understand soil health trajectories under intensive greenhouse cucumber production.

5 Driving Factors of Changes in Soil Microbial Communities

5.1 Regulatory effects of root exudates on microbial communities

Root exudates play a crucial role in shaping soil microbial communities by providing carbon sources and signaling molecules that selectively stimulate or inhibit specific microbial taxa. These exudates include sugars, amino acids, organic acids, and secondary metabolites that influence microbial growth and activity in the rhizosphere, thereby affecting community composition and function. The diversity and quantity of root exudates can vary with plant species, developmental stage, and environmental conditions, leading to dynamic shifts in microbial populations around cucumber roots under continuous cropping (Philippot et al., 2023). Such selective pressures can promote beneficial microbes involved in nutrient cycling or suppress pathogens, but continuous monoculture may alter exudate profiles unfavorably, reducing microbial diversity and increasing pathogen prevalence.

Moreover, root exudates contribute to feedback loops that modify soil properties and microbial habitats. Microbial metabolism of exudates can change soil pH, nutrient availability, and organic matter content locally, which further influences microbial community assembly and interactions (Philippot et al., 2023). These microbially mediated modifications create heterogeneous niches that support diverse microbial functions essential for plant health. However, under continuous cucumber cropping, altered exudation patterns combined with soil degradation may disrupt these feedbacks, leading to simplified microbial networks and impaired ecosystem services.

5.2 Effects of fertilization and agronomic management practices

Fertilization regimes and agronomic practices significantly impact soil microbial community structure by altering nutrient availability and soil physicochemical conditions. Organic amendments generally enhance microbial diversity and functional gene abundance by supplying complex carbon substrates that support diverse heterotrophic microbes (Zheng et al., 2019). In contrast, excessive use of chemical fertilizers can reduce microbial richness by favoring fast-growing copiotrophic bacteria while suppressing oligotrophic taxa adapted to low-nutrient environments. The balance between these inputs influences the abundance of key functional groups involved in nitrogen cycling, carbon turnover, and disease suppression.

Agronomic practices such as crop rotation, tillage intensity, and irrigation also modulate microbial communities by affecting soil moisture regimes, aeration, and root-soil interactions. For example, crop rotation introduces varied root exudates and residues that maintain higher microbial diversity compared to continuous monocropping (Figure 3) (Li et al., 2022; Bai et al., 2023). Reduced tillage preserves soil structure and fungal hyphal networks critical for nutrient transport. Together, these management factors interact with fertilization to shape the resilience and multifunctionality of soil microbiomes under greenhouse cucumber cultivation.

5.3 Influence of soil environmental factors

Soil environmental factors including pH, organic matter content (SOM), moisture levels, and nutrient status are primary drivers of soil microbial community composition and diversity. Soil pH strongly influences bacterial diversity by affecting enzyme activities and nutrient solubility; many bacterial taxa have narrow pH optima leading to shifts in dominant phyla as pH changes (Zhou et al., 2020). Fungal communities tend to be less sensitive to pH but respond more to organic matter quality and moisture availability. High SOM supports greater microbial biomass and functional potential by providing energy sources for heterotrophs (Zheng et al., 2019; Huang et al., 2024).

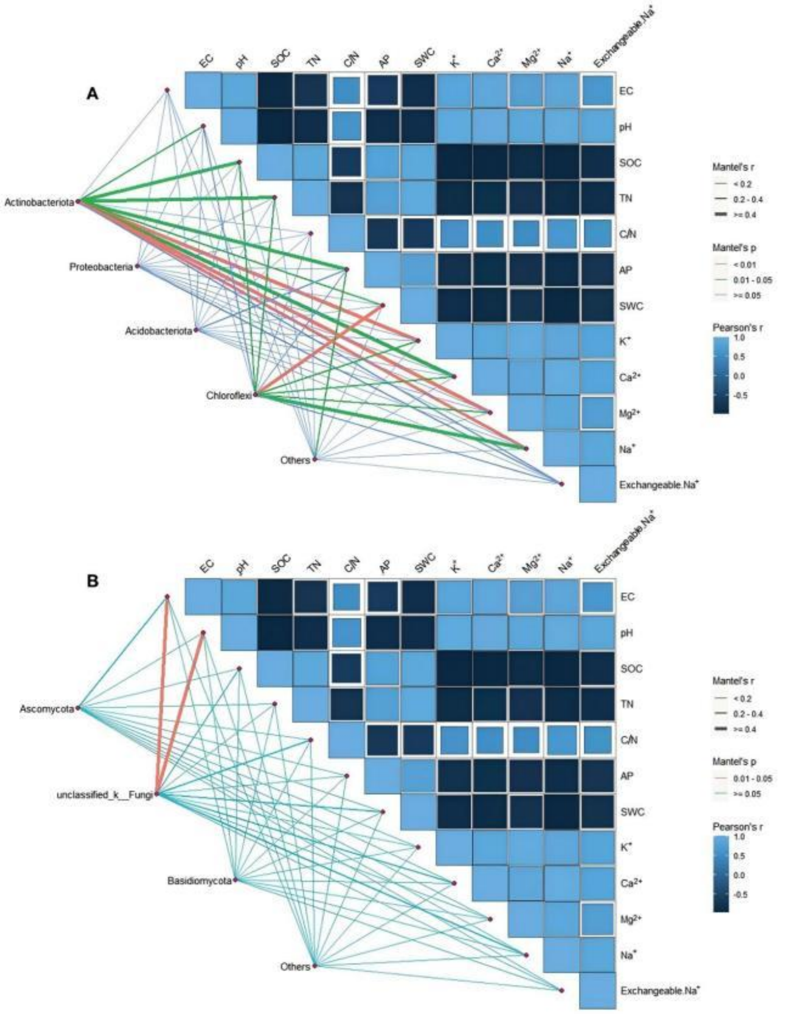

Figure 3 Partial Mantel test examined the relationship between dominant phyla of soil bacteria (A) and fungi (B) (relative abundance > 5%) and soil environmental factors. The edge width corresponds to the Mantel's r statistic for the corresponding distance correlation, and the edge color indicates statistical significance (Adopted from Bai et al., 2023)

Moisture regulates oxygen diffusion and substrate accessibility in soils; both drought stress and waterlogging can reduce microbial diversity by selecting for tolerant species (Lladó et al., 2018; Bai et al., 2023). Nutrient imbalances caused by continuous cropping often lead to declines in SOM and altered C:N ratios that constrain microbial growth. Structural equation modeling studies highlight that these abiotic factors collectively shape bacterial communities more strongly than fungal ones due to differences in ecological niches (Huang et al., 2024). Managing these environmental parameters is therefore critical for sustaining healthy soil microbiomes under intensive greenhouse cucumber production.

6 Case Study: Analysis of Soil Microbial Community Changes in a Greenhouse Cucumber Continuous Cropping System

6.1 Overview of the study area and experimental design

The study was conducted in a calcareous soil region of northern China, where greenhouse cucumber monocropping has been practiced for varying durations, including 1, 8, 15, and 22 years. The experimental design involved collecting soil samples from greenhouses with these different continuous cropping histories to assess how prolonged cucumber cultivation affects soil microbial communities. This approach allowed for a comparative analysis of microbial diversity and community structure changes over time under intensive greenhouse conditions (Zhao et al., 2020; Huang et al., 2023). Soil physicochemical properties such as pH, organic matter, electrical conductivity (EC), and nutrient concentrations were also measured to link microbial shifts with environmental factors.

In addition to the temporal gradient of continuous cropping years, the study incorporated high-throughput sequencing techniques targeting bacterial 16S rRNA and fungal 18S rRNA gene fragments to characterize microbial communities comprehensively. This molecular approach provided detailed insights into taxonomic composition and relative abundances of key microbial groups across different cropping durations. The integration of soil chemical analyses with sequencing data enabled identification of potential drivers behind microbial community changes associated with continuous cucumber monoculture (Figure 4) (Liu et al., 2020; Zhao et al., 2020).

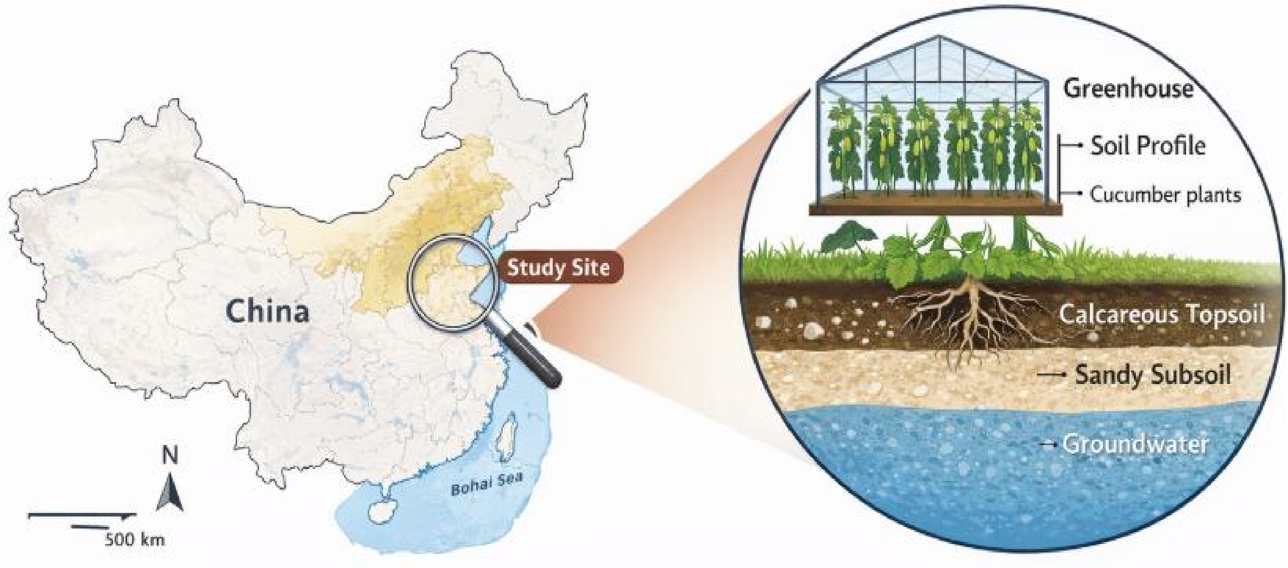

Figure 4 Location of the study site in a calcareous soil region of northern China and schematic representation of greenhouse cucumber monocropping systems used for soil sampling (Adopted from Liu et al., 2020)

6.2 Sequencing and data analysis results of microbial community structure

Sequencing results revealed significant alterations in both bacterial and fungal community structures as continuous cropping years increased. Bacterial diversity showed a decline in dominant phyla such as Actinobacteria, while Acidobacteria and Firmicutes increased significantly after eight or more years of monocropping. For fungi, the relative abundance of Ascomycota increased markedly with longer cultivation periods, indicating a shift toward fungal groups often associated with disease development (Zhao et al., 2020). These compositional changes coincided with decreases in soil pH and fungal diversity but increases in soil organic matter and nutrient concentrations like total nitrogen and available phosphorus.

Beta diversity analyses demonstrated that bacterial community composition changed significantly with consecutive cucumber cultivation but alpha diversity remained relatively stable. Notably, some beneficial bacterial genera involved in nitrogen cycling decreased over time, while others related to functional adaptation increased. Co-occurrence network analysis indicated that long-term continuous cropping weakened species interactions within bacterial communities, resulting in less complex networks that may reduce ecosystem stability (Liu et al., 2020; Chen et al., 2022). Overall, these findings highlight that continuous cucumber cropping reshapes microbial communities by favoring certain taxa while suppressing others critical for soil health.

6.3 Relationship between continuous cropping years and soil microbial community changes

The duration of continuous cucumber cropping was strongly correlated with shifts in soil microbial communities through its effects on soil environmental factors such as pH, organic matter content, and nutrient availability. Redundancy analysis identified soil organic matter and nitrate nitrogen as key drivers influencing bacterial community variation, whereas pH alongside organic matter significantly affected fungal community structure (Zhao et al., 2020; Huang et al., 2023). As continuous cropping progressed, increasing salinity and acidification contributed to declines in microbial diversity and altered functional potentials.

Furthermore, extended monoculture led to reductions in beneficial microbes including Bacillus and Sphingomonas genera known for nutrient cycling and pathogen suppression, while pathogenic fungi antagonistic to plant health became more abundant (Chen et al., 2022). These microbial shifts were linked to observed decreases in enzyme activities related to nutrient turnover and overall soil quality deterioration. The study underscores the importance of managing continuous cropping duration alongside soil amendments or crop rotations to mitigate negative impacts on the soil microbiome and sustain greenhouse cucumber productivity.

7 Strategies for Alleviating Continuous Cropping Obstacles and Microbial Regulation

7.1 Application of bio-organic fertilizers and microbial inoculants

Bio-organic fertilizers and microbial inoculants have emerged as effective tools to mitigate continuous cropping obstacles by enhancing soil fertility and restoring beneficial microbial communities. These amendments supply organic matter and introduce beneficial microbes such as Bacillus, Trichoderma, and nitrogen-fixing bacteria, which improve nutrient cycling, suppress soil-borne pathogens, and promote plant growth. Studies on cowpea demonstrated that treatments with microbial agents increased soil organic matter, nitrate nitrogen, and potassium content while enriching beneficial bacterial taxa like Bradyrhizobium, leading to improved crop yield and quality (Zhu et al., 2025). Similarly, biochar-based organic fertilizers have been shown to increase microbial diversity and the abundance of beneficial genera such as Arthrobacter and Pseudomonas, while reducing harmful fungi like Fusarium, thereby alleviating continuous cropping stress in tobacco soils (Chen et al., 2025).

The mechanisms underlying these benefits include enhanced microbial network complexity and stability, which support resilient soil ecosystems capable of resisting pathogen invasion. Bio-organic amendments also improve soil physicochemical properties such as pH and nutrient availability, creating a more favorable environment for microbial proliferation (Hu et al., 2025). The combined effects of nutrient enrichment and microbial community regulation contribute to improved plant health and productivity under continuous cropping systems. Thus, integrating bio-organic fertilizers with targeted microbial inoculants represents a promising strategy for sustainable greenhouse cucumber production.

7.2 Crop rotation, intercropping, and soil improvement measures

Crop rotation and intercropping are well-established agronomic practices that alleviate continuous cropping obstacles by diversifying root exudates and disrupting pathogen life cycles. Rotation systems have been shown to enhance soil nutrient levels-including organic matter, ammonium nitrogen, phosphorus, and potassium-and increase enzyme activities critical for nutrient cycling such as acid phosphatase and β-glucosidase (Chen et al., 2025). These improvements correlate with shifts in rhizosphere microbial communities toward higher abundances of beneficial bacteria (e.g., Actinobacteria) and fungi (e.g., Basidiomycota), which suppress pathogens like Fusarium responsible for wilt diseases. Intercropping similarly promotes microbial diversity by providing varied carbon sources that sustain a broader range of microorganisms.

Soil improvement measures including the application of biochar or specialized soil conditioners further support these practices by enhancing soil structure, moisture retention, and nutrient availability. Biochar amendments derived from agricultural residues can increase pH, organic matter content, available potassium, and sulfur in continuous cropping soils while promoting beneficial microbes such as Sphingomonas and Bacillus (Hu et al., 2025). These combined approaches create a more balanced soil ecosystem that resists degradation caused by monoculture cropping. Therefore, integrating crop diversification with targeted soil amendments is essential for maintaining healthy microbial communities in greenhouse systems.

7.3 Application prospects of microecological regulation in greenhouse agriculture

Microecological regulation-manipulating the soil microbiome to optimize plant-soil interactions-holds great promise for overcoming continuous cropping challenges in greenhouse agriculture. Advances in synthetic microbiology enable the design of tailored microbial consortia that enhance nutrient acquisition, disease resistance, and stress tolerance by reshaping the native soil community structure. For example, plants can recruit specific growth-promoting bacteria through root exudates containing metabolites like nobiletin that stimulate beneficial microbes producing phytohormones such as indole-3-acetic acid (IAA), thereby improving root development under continuous cropping stress (Haiyan et al., 2025).

Future applications may combine bio-organic amendments with precision microbiome engineering to establish stable, disease-suppressive soils adapted to intensive greenhouse conditions. This approach requires comprehensive understanding of microbe-microbe and plant-microbe interactions within the complex rhizosphere environment. Integrating multi-omics technologies with ecological modeling will facilitate the identification of keystone taxa critical for ecosystem function and guide effective interventions (Wang et al., 2024). Overall, microecological regulation represents a sustainable strategy to enhance productivity while mitigating the negative impacts of continuous cucumber monoculture in greenhouses.

8 Conclusions and Future Research Directions

Continuous cucumber monocropping in greenhouse systems leads to significant shifts in soil microbial communities, characterized by decreased bacterial and fungal diversity alongside altered community composition. Key bacterial phyla such as Actinobacteria tend to decline, while Acidobacteria, Firmicutes, Chloroflexi, and Gemmatimonadetes increase with prolonged cropping duration. Similarly, fungal communities show an increase in Ascomycota abundance, often linked to pathogenicity, while beneficial fungi such as Chaetomium and Mortierella decrease over time. These microbial changes coincide with soil physicochemical alterations including reduced pH, increased electrical conductivity, and accumulation of organic matter and nutrients like nitrogen and phosphorus. The restructuring of microbial networks also reflects weakened species interactions and reduced ecosystem stability under long-term monoculture.

Moreover, continuous cropping negatively impacts functional groups involved in nutrient cycling and disease suppression. Beneficial genera such as Bacillus and Sphingomonas decline, which correlates with reduced enzyme activities critical for soil health. Soil metabolic functions related to amino acid biosynthesis and fatty acid metabolism are also disrupted as cropping years increase. These microbial and functional shifts contribute to soil sickness symptoms observed in cucumber production systems, including yield decline and increased disease incidence. Overall, the evidence indicates that continuous cucumber cropping induces a complex cascade of biotic and abiotic changes that undermine soil quality and sustainability.

Despite advances in understanding microbial responses to continuous cucumber cropping, several limitations remain in current research. Most studies focus on taxonomic shifts using high-throughput sequencing but provide limited insight into the functional roles of altered microbial communities or their direct effects on plant health. Functional predictions based on marker genes or metabolomics remain preliminary, necessitating more integrative multi-omics approaches to elucidate microbe-mediated mechanisms underlying continuous cropping obstacles. Additionally, many investigations are region-specific with variable soil types and management practices, limiting the generalizability of findings across diverse greenhouse systems. Temporal dynamics beyond a few years are insufficiently explored; long-term monitoring is needed to capture progressive microbial succession and resilience potential. Furthermore, interactions between microbes, plants, and environmental factors such as soil chemistry require deeper mechanistic studies to identify keystone taxa or metabolites driving system stability or degradation. Finally, practical strategies for microbiome manipulation remain underdeveloped due to incomplete knowledge of how introduced amendments or crop rotations reshape native communities sustainably. Addressing these gaps will be critical for developing effective interventions that restore soil health and productivity in continuous cucumber greenhouse cultivation.

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Conflict of Interest Disclosure

The author affirms that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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