ISSN: 2710-0723

Regulation of Soil Microbial Diversity on the Stability of Farmland Ecosystem

Ma Lin[1,2,3,4,5,*]

[1] Shaanxi Agricultural Development Group Co., Ltd., Xi'an 710075, China

[2] Institute of Land Engineering and Technology, Shaanxi Provincial Land Engineering Construction Group Co., Ltd., Xi'an 710075, China

[3] Key Laboratory of Degraded and Unused Land Consolidation Engineering, Ministry of Natural Resources, Xi'an 710075, China

[4] Shaanxi Engineering Research Center of Land Consolidation, Xi'an 710075, China

[5] Key Laboratory of Cultivated Land Quality Monitoring and Conservation, Ministry of Agriculture and Rural Affairs, Xi'an 710075, China

*Corresponding Author: Ma Lin

Abstract

In this paper, the regulatory effect of soil microbial diversity on the stability of farmland ecosystem under different agricultural management measures was systematically discussed through comparative experimental design. Select typical intensive farmland in major grain producing areas in China, and set up four treatments: conventional management (CON), organic agriculture (ORG), ecological enhancement (ECO), and natural restoration (NAT). Continuously monitor soil physical and chemical properties, microbial community structure, and ecosystem stability indicators. The results showed that ORG and ECO treatments significantly increased soil organic matter, total nitrogen content, and pH value ($p<0.05$), and significantly enhanced the Shannon Wiener diversity index of bacteria and fungi. The analysis of microbial community structure shows that ecological management measures restore the community to its natural state. The complexity of the microbial co-occurrence network is highest under ECO treatment, and key groups such as Proteobacteria and arbuscular mycorrhizal fungi are significantly correlated with system stability. Structural equation modeling (SEM) further reveals that microbial diversity is a core factor in regulating ecosystem stability, indirectly optimizing agricultural ecological stability by enhancing soil function and strengthening system resistance and resilience. The study emphasizes that enhancing soil microbial diversity is a key path to achieving sustainable agricultural development, ensuring food security, and ecological balance.

Keywords

Soil Microbial Diversity; Farmland Ecosystem; Stability.

1. Introduction

Farmland ecosystem is the foundation of global food security and human well-being, but it faces many challenges such as overuse of chemical fertilizers, abuse of pesticides, frequent pests and diseases. These problems not only lead to environmental pollution, but also seriously threaten the sustainability of farmland ecosystem. As the core component of farmland ecosystem, the health status of soil is directly related to crop yield, quality and the stability of ecosystem. In recent years, more and more studies show that soil microbial diversity plays a vital role in maintaining soil health and ecosystem function.

Soil microorganism is one of the oldest, most diverse and most complex biological groups on the earth. They participate in various biogeochemical processes in soil, such as nutrient cycling, organic matter decomposition, plant growth promotion and disease suppression. Soil microbial diversity includes not only species diversity, but also functional diversity and gene diversity [1]. However, due to the complexity of soil microorganisms and the limitation of research methods, our understanding of the relationship between soil microbial diversity and farmland ecosystem stability is still limited.

Nevertheless, some studies show that soil microbial diversity is closely related to the versatility of farmland ecosystem [2]. For example, soils with high microbial diversity usually have stronger nutrient cycling ability and higher crop yield. [3] In addition, some specific microbial communities can effectively inhibit the occurrence of soil-borne diseases, thus improving the stress resistance of crops [4]. However, different agricultural management measures, such as fertilization, farming and planting patterns, will have a significant impact on soil microbial diversity, and then affect the stability of farmland ecosystem [5].

Therefore, it is of great significance to discuss how soil microbial diversity regulates the stability of farmland ecosystem for formulating sustainable agricultural management strategies, increasing crop yield and reducing negative environmental impacts. The purpose of this study is to reveal the changing law of soil microbial diversity under different agricultural management measures through experiments and data analysis, and to explore how these changes affect the stability of farmland ecosystem.

2. Research Method

2.1. Research Area and Experimental Design

Select the representative intensive farmland areas in China's main grain producing areas. The natural backgrounds such as climate and soil types in this area are basically the same. Using the design of "Comparative Experiment", adjacent plots with different management measures were selected in the same area (to reduce the difference of soil background), and the following treatment groups were set up:

① Conventional Management Group (CON): The high fertilizer and high pesticide management model commonly adopted by local farmers serves as a control.

② Organic Agriculture Group (ORG): Fully apply organic fertilizers and use physical/biological methods to control pests and diseases, which have been implemented for at least 5 years.

③ Ecological Enhancement Group (ECO): Integrating and applying efficiency enhancing measures on the basis of conventional management, such as applying microbial agents, planting green manure, and crop rotation.

④ Natural Recovery Team (NAT): Select adjacent land parcels that have been naturally restored for more than 5 years as a reference for evaluating the potential of farmland ecosystem restoration.

⑤ Each processing group shall have no less than 3 duplicate plots, with each plot covering an area of no less than 1 acre, randomly arranged.

2.2. Sample Collection and Processing

Sampling is carried out in the critical growth period of crops to capture the dynamic changes of microbial communities. Sampling continuously for 2-3 growing seasons to obtain interannual variation data. In each plot, 0-20 cm topsoil was collected by S-shaped or plum blossom-shaped distribution method. Use sterile soil to drill more than 10 sub-samples and mix them into a representative sample, about 1kg. Sterile gloves is used throughout the operation to avoid cross-contamination. The soil samples were screened by 2mm sieve to remove impurities such as plant roots and stones. Then it was divided into two parts: one part was put into a sterile centrifuge tube, immediately put into liquid nitrogen for quick freezing, and then transferred to an ultra-low temperature refrigerator at -80℃ for microbial DNA extraction; The other one was stored at 4℃ for the determination of soil physical and chemical properties.

2.3. Microbial Diversity Analysis

Total DNA was extracted from 0.25g soil by using commercially available soil genomic DNA extraction kit. The V4-V5 region of bacterial 16S rRNA gene and ITS1 region of fungi were amplified by PCR with primers with specific barcodes. The amplified products of each sample were purified, quantified and homogenized to construct a sequencing library. Double-ended sequencing was performed using Illumina NovaSeq.

Use QIIME2 to perform quality control on raw sequencing data, remove primers, filter low-quality sequences, and merge them into optimized sequences based on overlapping relationships. Using the DADA2 method to generate more accurate Amplitude Sequence Variants (ASVs). Species taxonomic annotation of representative sequences based on Silva (bacteria) and UNITE (fungi) databases. Calculate the alpha diversity index and beta diversity of each sample using QIIME2, and visualize them through principal coordinate analysis (PCoA).

2.4. Ecosystem Stability Assessment

Comprehensively evaluate ecosystem stability from two dimensions: resistance and resilience. Measure resistance by calculating the coefficient of variation (CV) of crop yield in the year of extreme climate events (the lower the CV, the stronger the resistance), and evaluate the rate and degree of yield recovery to its original level after extreme events to reflect resilience; The ratio (μ/σ) of the average and standard deviation of crop yield in multiple growing seasons is used as the index of time stability. The higher the ratio, the more stable the system is in time series. At the same time, the stability of the ecological process driven by soil microorganisms was evaluated by measuring the activities of key soil enzymes related to nutrient cycling, such as urease, phosphatase and sucrase, so as to comprehensively reflect the functional stability of the ecosystem.

2.5. Data Analysis Method

Using one-way analysis of variance (ANOVA) and post hoc multiple comparisons to test the differences in soil physicochemical properties, microbial alpha diversity, and ecosystem stability among different treatment groups, and using Adonis analysis to test the inter group differences in microbial beta diversity; Exploring the impact of environmental factors on microbial community structure through redundancy analysis, constructing a co-occurrence network to evaluate the complexity and stability of the community, and using a random forest model to identify key microbial groups and soil factors that affect ecosystem stability; Finally, a structural equation model (SEM) was constructed to integrate the path of "management measures → soil properties → microbial diversity → ecosystem stability" and quantitatively analyze the direct and mediating roles of microbial diversity in it.

3. Result

3.1. Soil Physical and Chemical Properties and Microbial α Diversity under Different Management Measures

Different agricultural management measures have significantly changed the physical and chemical properties of soil (Table 1). Compared with CON, ORG and ECO significantly increased the contents of soil organic matter (SOM), total nitrogen (TN) and pH value ($p < 0.05$).

Table 1. Basic physical and chemical properties of soil under different agricultural management measures

Processing group	pH	Organic matter (g/kg)	Total nitrogen (g/kg)	Available phosphorus (mg/kg)
CON	6.20 ± 0.15b	15.32 ± 1.05c	0.87 ± 0.08b	45.62 ± 5.33a
ORG	6.85 ± 0.10a	28.75 ± 2.11a	1.45 ± 0.12a	32.18 ± 4.07b
ECO	6.70 ± 0.12a	23.41 ± 1.87b	1.32 ± 0.10a	38.24 ± 3.56ab
NAT	6.90 ± 0.18a	31.02 ± 2.54a	1.51 ± 0.15a	15.76 ± 2.89c

Note: Different lowercase letters in the same trade indicate significant differences between treatments ($p < 0.05$).

At the same time, the α diversity of soil microorganisms is sensitive to management measures (Figure 1). Shannon-Wiener index of soil bacteria and fungi under the treatment of ORG and ECO were significantly higher than that under the treatment of CON ($p < 0.05$), among which the diversity index of bacteria under the treatment of ECO was the highest, while the diversity of fungi under the treatment of ORG was the highest.

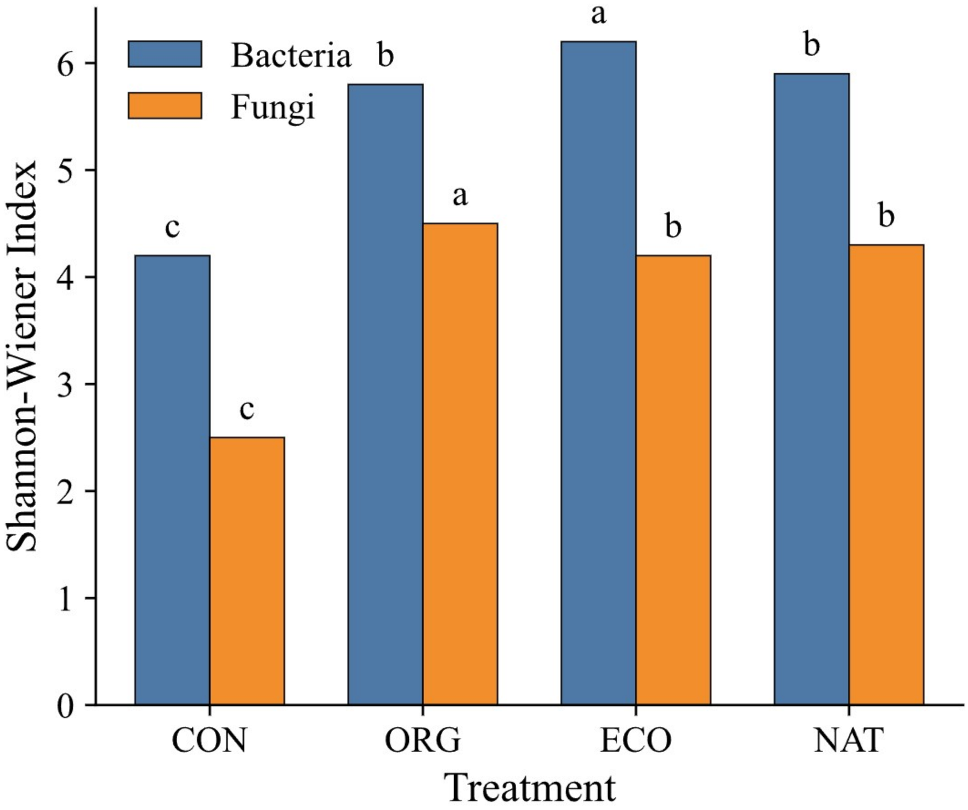

Figure 1. Shannon-Wiener index of soil microorganisms under different treatments

3.2. The Structure of Soil Microbial Community Has Changed Significantly

PCoA showed significant segregation of soil microbial community structures among different treatment groups (Bray Curtis distance, PERMANOVA: $R^2= 0.35$, $p = 0.001$). The community structure of the CON treatment group was significantly different from other groups, while the ORG and ECO groups partially overlapped and were closer to the NAT group (Figure 2), indicating that ecological and organic management help restore soil microbial communities to a more natural state.

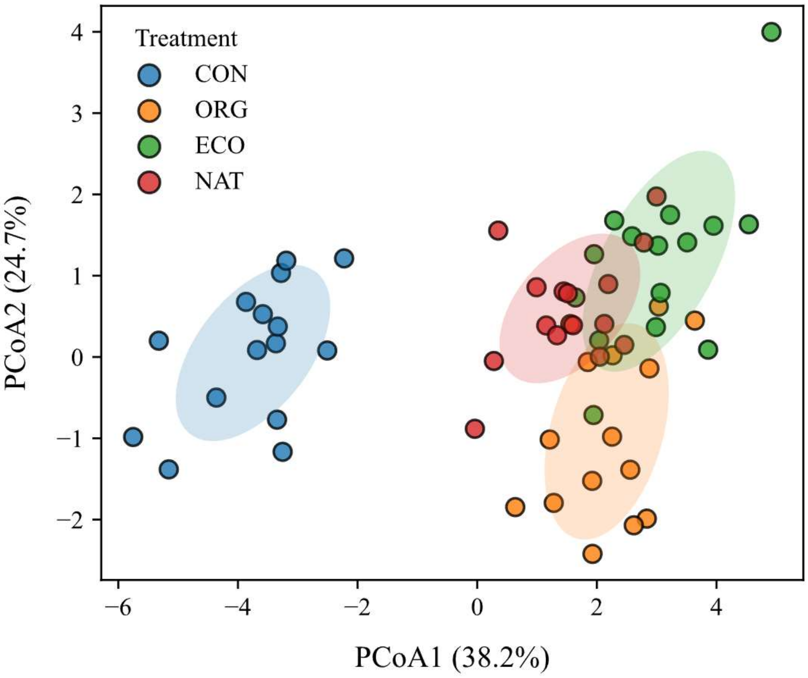

Figure 2. Principal coordinate analysis of soil bacterial community based on Bray-Curtis distance

3.3. The Complexity of Microbial Network is Significantly Related to the Stability of Ecosystem.

The co-occurrence network analysis shows that the microbial network under ECO treatment has the highest number of nodes, connections, and average degree, while its modularity coefficient is the lowest, indicating a more complex network structure and tighter connections (Table 2). Random forest regression analysis further identified 15 key taxa, including Proteobacteria and arbuscular mycorrhizal fungi (AMF), whose relative abundance was significantly correlated with the ecosystem stability index.

Table 2. Topological characteristics of soil microbial co-occurrence network under different treatments

Processing group	Number of nodes	Connection number	Average degree	Modular coefficient
CON	385	855	4.44	0.72
ORG	451	1252	5.55	0.65
ECO	512	1688	6.59	0.58

3.4. Microbial Diversity Regulates Ecosystem Stability through Multiple Paths.

SEM fitted the data well (χ^2/df=1.25, CFI=0.98, RMSEA=0.04), revealing the regulatory pathway. The model indicates that management measures not only directly and positively affect ecosystem stability (path coefficient=0.25), but more importantly, enhance stability through two indirect pathways: improving soil organic matter and increasing microbial diversity. Among them, microbial diversity is the most core direct driving factor affecting stability (path coefficient=0.55).

4. Discussion

By comparing the effects of different agricultural management measures on soil microbial diversity and farmland ecosystem stability, this study revealed the core role of soil microorganisms in maintaining farmland ecological health. It was found that the management of ORG and ECO significantly increased the content of soil organic matter and total nitrogen, and at the same time enhanced the α diversity of soil microorganisms, especially the Shannon-Wiener index of bacteria and fungi, which indicated that the management strategy of reducing the dependence on chemical fertilizers and pesticides and increasing the input of organic matter had a positive impact on soil biological community [6].

PCoA further confirmed that the soil microbial community structure under the ecological and organic management mode is closer to NAT, which highlights the potential of sustainable agricultural practices for soil ecological restoration [7]. Co-occurrence network analysis revealed that the complexity of microbial network treated by ECO was the highest, and key groups such as Proteus and arbuscular mycorrhizal fungi were significantly correlated with the stability index of ecosystem, which emphasized the importance of microbial community interaction network in ecosystem function.

SEM quantitatively analyzed the path of management measures indirectly enhancing ecosystem stability by improving soil organic matter and microbial diversity, among which microbial diversity was identified as the core direct driving factor. This discovery provides a scientific basis for optimizing agricultural management strategies, that is, by promoting soil microbial diversity, the resistance and resilience of farmland ecosystems can be effectively improved, and food security and ecological sustainability can be guaranteed [8]. Future research needs to further explore the mechanism of specific microbial functional groups and their responses under different environmental conditions.

5. Conclusion

By comparing the effects of different agricultural management measures on soil microbial diversity and farmland ecosystem stability, this study revealed the core role of soil microorganisms in maintaining farmland ecological health. The study found that:

(1) ORG and ECO management significantly increased the content of soil organic matter and total nitrogen, and at the same time enhanced the α diversity of soil microorganisms, especially the Shannon-Wiener index of bacteria and fungi, which indicated that the management strategy of reducing the dependence on chemical fertilizers and pesticides and increasing the input of organic matter had a positive impact on soil biological community.

(2) PCoA further confirmed that the soil microbial community structure under the ecological and organic management mode was closer to NAT, which highlighted the potential of sustainable agricultural practices for soil ecological restoration. Co-occurrence network analysis revealed that the complexity of microbial network treated by ECO was the highest.

(3) SEM quantitatively analyzed the path of management measures indirectly enhancing ecosystem stability by improving soil organic matter and microbial diversity, among which microbial diversity was identified as the core direct driving factor.

References

[1] Volodin V V ,Gladysh S N ,Piskunov K A , et al.Evaluation of Gut Microbial Diversity of the Domestic Goat Capra hircus[J] .Biology Bulletin Reviews,2025,15(4):461-466.

[2] Kassogué A ,Traore S ,Dao S , et al.Assessment of the Diversity of Endophytic, Rhizospheric and Soil Bacteria Using a Targeted Metagenomic Approach in Mali[J] .Annual Research & Review in Biology,2024,39(12):158-170.

[3] Priya ,Agrawal S ,Solanki V , et al.Microbial Diversity of Bacterial Species (Rhizobium and Azospirillum) under Different Agroforestry Land Use Systems[J] .Archives of Current Research International,2024,24(12):300-306.

[4] Tang H ,Shi L ,Wen L , et al.Effects of different long-term fertilization on rhizosphere soil nitrogen mineralization and microbial community composition under the double-cropping rice field[J] .Archives of Agronomy and Soil Science,2024,70(1):1-16.

[5] Korneykova V M ,Soshina S A ,Fokina V N , et al.Number and Taxonomic Diversity of Microorganisms in the Profiles of Urban Soils in the Arctic (Murmansk)[J] .Eurasian Soil Science,2024,57(12):2108-2121.

[6] Zhou T ,Liang G ,Reich B P , et al.Promoting effect of plant diversity on soil microbial functionality is amplified over time[J] .One Earth,2024,7(12):2139-2148.

[7] Vasudevan P ,Jaybhaye G R ,Panicker S .Effect of Shifting Cultivation on Soil health and Microbial Diversity in Junnar Taluka of Pune District[J] .Asian Journal of Soil Science and Plant Nutrition,2023,9(4):180-189.

[8] Zhou J ,Qin W ,Lu X , et al.The diversity and ecological significance of microbial traits potentially involved in B12 biosynthesis in the global ocean[J] .mLife,2023,2(4):416-427.