

SOIL MICROBES DIFFERENCE AND THE INFLUENCING FACTORS IN RICE PLANTING AREAS IN JILIN PROVINCE, CHINA

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Abstract. Soil microorganisms are an essential part of soil ecosystems. With the intensification of the global greenhouse effect, the impact of climate change on rice soil is receiving increasing attention. To elucidate environment effect on the structure and diversity of rice soil microorganisms in different planting areas of Jilin province, China, 60 soil samples from three rice planting areas (Eastern (E), Central (C), and Western (W)) of Jilin province were collected, soil chemical properties, soil enzyme activities, and soil microbial structure and diversity were determined in this study. The results showed that soil pH increased gradually from E (5.5) to W (8.3); OM content in C area (14.9 g/kg) was significantly lower than in E (26.3 g/kg) and W (17.0 g/kg). The soil urease content in E (16.6 mg/g per d) and W (21.0 mg/g per d) was significantly higher than in C (9.8 mg/g per d). pH, accumulation temperature, annual average temperature, and altitude were the main influencing factors for soil fungi; however, pH, AN, and rainfall were the main influencing factors for soil bacteria. Climate factors (accumulation temperature, annual average temperature and rainfall) have important effects on soil microorganisms. Moreover, there is a significant positive correlation between soil fungi and rice yield. Therefore, for the quality of soil microorganisms and rice yield, while paying attention to the impact of human factors on soil microorganisms, we should also pay attention to the effects of climate factors on soil microorganisms.

Keywords: *pH, enzyme, climate, fungus, bacteria, yield*

Introduction

Soil microbes account for many soil organisms, which play essential roles in energy flow, nutrient cycling, and organic matter turnover in soil [1]. As a critical part of the soil, soil microorganisms are affected by the surrounding environment and soil properties [19] et al., 2016; [73]. They can predict changes in the soil environment and are an essential indicator for evaluating soil quality and soil restoration performance [43]. In recent years, due to the threat of climate warming, more and more studies have found that climatic factors can affect soil microbial communities, especially in agriculture [51] et al., 2019; [17]. So, the impact of climatic factors on soil microbes has become a problem that most countries have to deal with in agriculture [16] et al., 2021; Naher et al., 2021[59].

Soil chemistry and soil enzyme activity affect soil microbial community composition [35] et al., 2020; [1]. Too high or too low soil pH will directly affect the digestion and absorption of nutrients by microorganisms [30], and the differences in soil organic matter (“OM”), alkali-hydrolyzed nitrogen (“AN”), available phosphorus (“AP”), and available potassium (“AK”) content and the C:N ratio in soil will also lead to differences in

microbial community structure and distribution [74] et al., 2012, 2020; Sattar et al., 2019; [23] et al., 2020[45]. Soil enzymes are a class of bioactive substances with catalytic ability released into the soil by decomposing animal and plant residues and remains. Hydrolysing activity of urease soil microbial quantity, organic matter content, total nitrogen, and available nitrogen content and plays a crucial role in agro-ecosystems [60]. Sucrase can directly participate in transforming soil organic matter and soil microorganisms' metabolism and plays a vital role in increasing soluble nutrients in the soil, a characteristic enzyme in soil [61]. Phosphatase is an enzyme that catalyzes phosphorus cycling and transformation in soil ecosystems and can ensure the nutrient supply of phosphorus to soil microorganisms [8].

Soil fungi and bacteria are part of soil microorganisms. The response of bacterial and fungal communities to climate change may be closely related to soil chemical properties and soil enzyme activities. Numerous studies have assessed the impact of climate change on soil microbial communities [47] et al., 2016; Zhu et al., 2019). However, these findings are not consistent. Some studies emphasize that climate change does not significantly affect soil microbial activity [49], while others find that climate change significantly affects soil microbial activity [14]. With the increasing impact of climate warming on soil biological properties, more and more studies have focused on global warming-sensitive factors such as rainfall, average temperature, and accumulated temperature on soil microbial communities [31] et al., 2021[12].

At present, the research on soil microbes is mainly based on maize research [32] et al., 2022; [81], some studies have shown that chemical factors can affect maize soil microorganisms (Dai et al., 2012), some studies have shown that enzyme activity can affect maize soil microorganisms (Xu et al., 2024), and some studies have shown that climate factors can affect soil microorganisms (Zhou et al., 2024). but there is not much comprehensive research on rice soil microbes. And some research results show that soil microorganisms are affected by soil chemical properties, soil enzyme activities, and surrounding climatic factors [42] et al., 2013; [58]. So does this conclusion hold in the rice ecosystem? And most of the studies are based on a single field study [20], so does this conclusion hold in different regions? Suppose soil chemical properties, soil enzyme activities, and climate factors can affect the diversity of rice soil microorganisms in different regions. Will the diversity of soil microorganisms in different regions affect rice yield in different zones? Therefore, this study proposed the following hypotheses: (1) In rice ecosystems in different zones, soil chemical properties, soil enzyme activities, and climatic factors would affect soil microbial community structure. (2) Differences in soil microbial diversity in different regions will affect rice yield in different regions.

Jilin Province is located in the central part of Northeast China and is an important grain production base as well as a major high-quality japonica rice production base. It occupies a pivotal position in China's agricultural landscape and has high quality and large yield of rice, ranking among the top in the country in terms of output (Ma et al., 2021). But here, the terrain is complex, based on differences in climate conditions, environmental factors, and topography, Jilin Province is divided into three ecological zones: the eastern humid mountainous area (E), the central semi humid plain area (C), and the western semi-arid plain area (W), where there are significant differences in soil microorganisms and rice yields. Previous studies have mostly focused on the relationship between small-scale crop yields and soil microorganisms, but there is relatively little research exploring the relationship between regional scale climate factors, soil fertility characteristics, and soil microbial structure from the perspective of biogeography. This study aims to clarify the

effects of different climatic conditions and soil physicochemical properties on the soil structure and yield of rice, in order to provide scientific basis and practical guidance for high-yield and efficient management of rice.

Materials and methods

Study sites and soil sampling

The research was conducted in Jilin Province. Jilin Province is located in northeast China. The terrain is high in the southeast and low in the northwest. Bounded by the middle of the Dahei Mountains, it is divided into two significant landforms: the eastern mountains and the central and western plains. The eastern mountains are divided into the Changbai Mountains, the middle and low mountains, and the low hilly areas. The west and central plains are divided into the central plateau plains and the western meadows, lakes, wetlands, and sandy areas. Jilin Province is located on the east side of the Eurasian continent at mid-latitudes. It has a temperate continental monsoon climate with four seasons and average annual precipitation of about 400-600 mm.

This research collected 60 rice soil samples from six prefecture-level Changchun, Siping, Jilin, Tonghua, Liaoyuan, and Baicheng in Jilin province at the end of September 2018 (*Fig. 1*). The rice varieties in the sampling area are mainly Jijing, Nongda, super rice, and Changbai series. The fertilization methods of rice in the sampling area included basal fertilizer, tiller fertilizer, ear fertilizer, and grain fertilizer [76], and the irrigation method was mostly water-saving irrigation [62].

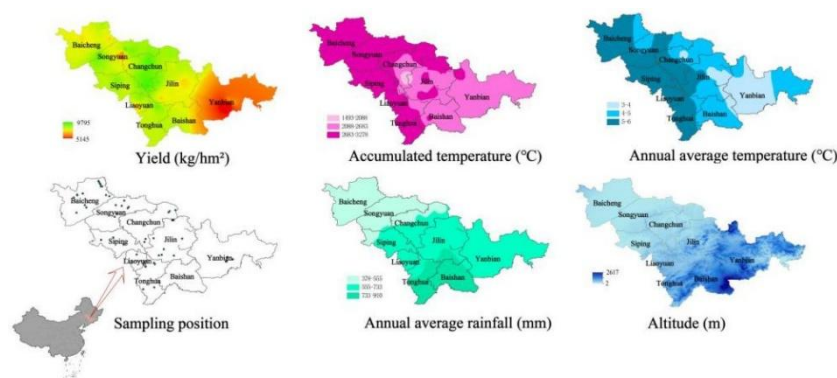


Figure 1. Sampling location, rice yield, and climate distribution in Jilin province

To represent the study, the method of collecting paddy soil in this study was the five-point sampling method. The five-point sampling method is an efficient soil sampling method. Its principle is to randomly select five points on the sample plot, take soil samples of a certain depth at each point, mix these samples, and analyze them. The five-point sampling method can reduce sampling bias caused by local environmental changes and improve sampling accuracy. And the operation is simple, just determine the midpoint of the diagonal as the center sampling point, and then select four points on the diagonal that are equidistant from the center sampling point as sampling points (Li et al., 2024). the paddy soil collected was non-rhizosphere soil, the reason why we use non-rhizosphere soil is that, on the one hand, we believe that the non-rhizosphere microbial community can explain the climate effect well, as it is stronger in the microbial structure of non-

rhizosphere soil (Li et al., 2022). On the other hand, current research on soil microorganisms in Jilin province mostly focuses on the study of rhizosphere soil, and the study of non-rhizosphere soil is still unclear. And the soil collection depth was 0-20 cm. After collecting soil samples, they were filtered through a 2 mm sieve and divided into three portions. One part is air-dried, one factor is stored in the regular refrigerator, and one is stored in the ultra-low freezer.

Methods for the determination of soil chemical properties and enzymatic activities

Soil microorganisms play a positive role in degrading organic matter and promoting nutrient cycling. Soil pH are comprehensive reactions of various chemical properties of soil, moreover, soil fertility characteristics, synthesis and decomposition of soil organic matter, transformation and release of various nutrients have important impacts on the activity of soil microorganisms. Soil chemical properties were determined using air-dried soil. The potassium dichromate volumetric method was used to measure soil organic matter content [5], the Kjeldahl distillation method was used to measure soil alkaline hydrolyzable nitrogen content [48], the Mo-Sb colorimetric method was used to measure soil available phosphorus content **Hiba! A hivatkozási forrás nem található..** The flame photometric method was used to measure the range of available potassium in the bottom soil [21], and the potentiometric method was used to measure soil pH [2].

Urease and sucrase are both important hydrolytic enzymes in soil, which can directly or indirectly reflect the intensity of soil biological activity. The activity of soil phosphatase directly affects the decomposition, transformation, and bioavailability of organic phosphorus in soil, and has a significant impact on the absorption utilization of phosphorus fertilizer and yield. Soil enzyme activities were determined using soil samples stored in a conventional refrigerator. Soil urease was measured by the sodium phenate-sodium hypochlorite colorimetric method [53], soil sucrase was measured by the 3,5 - dinitrosalicylic acid colorimetric method [55], soil phosphatase content was determined by the phenyl disodium phosphate colorimetric method (use borate buffer to measure alkaline phosphatase content, use citrate buffer to measure neutral phosphatase content, and use acetate solution to measure acid phosphate Enzyme content) [54].

High-throughput sequencing of soil microbes

High-throughput sequencing was performed using soil samples stored in an ultra-low temperature freezer. Soil samples were first extracted using the FAST DNA SPIN extraction kit (MP Biomedicals, Santa Ama, CA, United States). Then, a UV spectrophotometer quantitatively analyzed the DNA, and the DNA quality was detected by electrophoresis. After electrophoresis detection, qualified soils were screened out, and the soil samples with capable quality were sent to Shanghai Parsenor Company for sequencing using Illumina Mi Seq's high-throughput technology. The amplification method used the ITS amplification method, the amplification sequence before primer was ACGCGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGCGCCTCAGTGT-CAGTTAC, and the latter amplification sequence was ABABADBBDDFFFGGGFG-GGFGGHGBGHGGHGGGGGGH-GGGGGGGHHGGFBGEGGEG. The enzyme for PCR amplification was NEB's Q5 high-fidelity DNA polymerase. At the same time as amplification, the number of amplification cycles should be strictly controlled, and the number of amplification cycles should be minimized while ensuring the same amplification conditions. Libraries were prepared and screened using Illumina's TruSeq Nano DNA LT Library Prep Kit. After screening out qualified libraries, denatured with

sodium hydroxide, 2×250 bp double-stranded sequencing [7]. The classification operation unit (OUT) first uses the QIIME software to classify and divide the obtained sequences with 97% sequence similarity and then selects the most abundant sequence in each OTU as the representative sequence of the OTU. Finally, get all OUT information by the number of sequences covered by each OTU in each sample.

Data analysis

Using ArcGIS software to generate sampling point distribution map and meteorological distribution map, using R software to generate soil microbial abundance map and redundancy analysis (CCA) map. The Simpson index, ACE index, Shannon index, and Chao1 index in taxa were calculated using OTU results. Use Excel software to process soil chemical properties, enzymes, fungi, and bacteria data. Use the processed data to generate chemical properties, enzyme activities, and microbial diversity index tables. Use SPSS20.0 software to analyze various indicators in paddy soil. The difference is significant.

Results

Chemical properties of soil

The soil chemical properties of different rice-growing areas in Jilin province are shown in *Figure 2*. There were significant differences ($P < 0.05$) in soil pH, AN, and OM contents in the three planting areas but not in AP and AK contents. Soil pH increased gradually from east (5.5) to west (8.3). The soil AN content in the central part was significantly higher than that in the eastern and western portions. There was no significant difference in soil OM content between the western and eastern regions. Still, the soil OM content in the central area (14.9 g/kg) was significantly lower than in the eastern (26.3 g/kg) and western regions (17.0 g/kg). The content of AP and AN in the middle soil was the highest, and the range of AK was the lowest. The eastern soils had the lowest AP and AN contents. Western soils have the highest levels of AK.

Enzyme activity of soil

The soil enzyme content of different rice-growing areas in Jilin province is shown in *Figure 3*. According to this figure, there were significant differences in soil urease, alkaline phosphatase, and neutral phosphatase among the three planting areas ($P < 0.05$). The soil urease content in the eastern (16.6 mg/g per d) and western regions (21.0 mg/g per d) was significantly higher than in the central part (9.8 mg/g per d). Soil alkaline phosphatase in the west was considerably higher than in the east and center. Neutral phosphatase levels were markedly higher in the central and east regions than in the western areas. There were no significant differences in soil invertase and acid phosphatase contents among the three planting areas. Invertase was the highest in the center, and acid phosphatase was the highest in the east. The diversity index can reflect the stability and resistance of ecosystems, with ecosystems with high diversity indices typically having higher stability and resistance, The higher the biodiversity, the stronger the anti-interference ability of the ecosystem, which can better cope with external disturbances and pressures (Mukhtar et al., 2021). The diversity index can also reflect the restoration capacity of ecosystems, and ecosystems with high diversity can recover faster after being disturbed. For example, when species diversity is high in agricultural

ecosystems, the resistance to invasive species is strong, which can prevent biological invasion, reduce ecological damage, and thus increase crop yields (Chen et al., 2022).

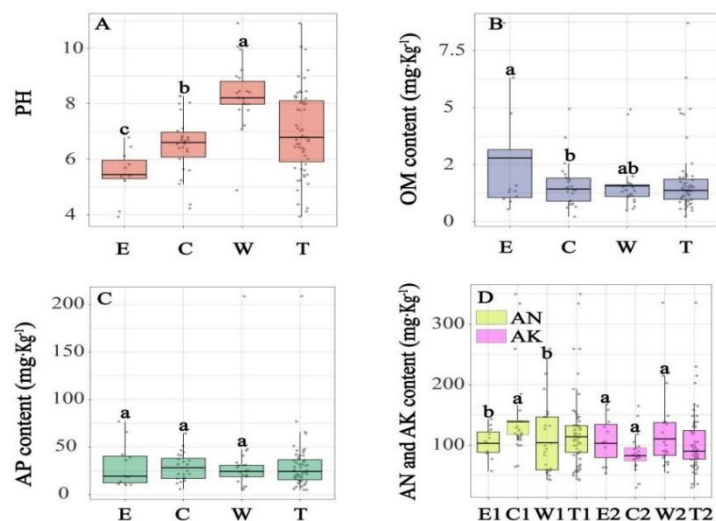


Figure 2. Soil chemical properties in different rice planting areas of Jilin province. (A) means pH, (B) means OM, (C) means AP, (D) means AN and AK; E means eastern, C means central, W means western, T means total

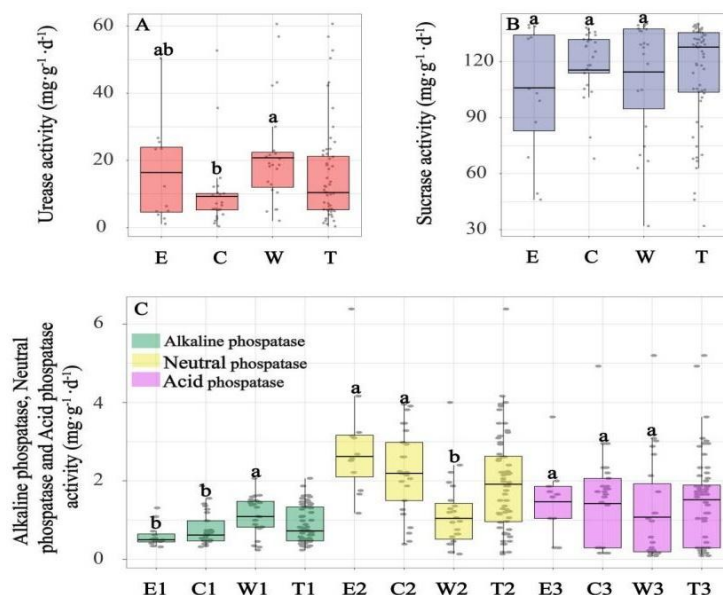


Figure 3. Soil enzymatic activity in different rice planting areas of Jilin province. (A) means urease, (B) means sucrase, (C) means phosphatase; 1 means alkaline phosphatase, 2 means neutral phosphatase, 3 means acid phosphatase; E means eastern, C means central, W means western, T means total

Index of soil microbes

Approximately 2,600,604 and 2,188,644 sequences were obtained for fungal and bacterial communities. A total of 26,735 fungal and 397,147 bacterial OTUs at the 97% similarity level were obtained based on these sequences.

The Alpha Diversity Index reflects the diversity and richness of soil microorganisms. Chao1 and ACE reflect the microbial richness, and the higher the Chao1 and ACE values, the higher the soil microbial richness. Shannon and Simpson are indicators of soil microbial diversity. The higher the Shannon and Simpson scores, the more diverse the microbial community.

The Alpha diversity index of the fungal community is shown in *Table 1*. The Chao1 and ACE indices in the eastern and central regions were significantly higher than those in the western areas, indicating that the fungal diversity in the west and the central areas was considerably higher than in the west regions. The Alpha diversity index of the bacterial community is shown in *Table 2*. The Chao1 and ACE indices in the eastern and central areas were significantly higher than those in the western areas, indicating that the bacterial diversity in the west and central regions was considerably higher than in the western areas.

Table 1. Fungal diversity index of different rice planting areas in Jilin province

Ecotope	Statistics project	Simpson	Chao1	ACE	Shannon
East	Luffing	0.68-0.99	327.37-677.51	321.98-683.21	3.88-7.51
	Arithmetic mean	0.91a	503.05a	502.70a	5.79a
	Standard deviation	0.09	116.21	114.33	1.22
	Coefficient of Variation (%)	11.01	24.18	23.77	0.22
Center	Luffing	0.88-0.97	282.61-746.59	283.77-727.87	4.81-7.11
	Arithmetic mean	0.94a	495.43a	493.55a	6.08a
	Standard deviation	0.06	109.45	106.22	0.83
	Coefficient of Variation (%)	6.62	22.28	21.71	13.76
West	Luffing	0.84-0.99	267.24-779.31	269.90-789.77	4.42-6.88
	Arithmetic mean	0.92a	478.03b	477.52b	5.57a
	Standard deviation	0.06	113.17	112.85	0.82
	Coefficient of Variation (%)	6.73	24.28	24.27	15.21

Table 2. Bacterial diversity index in different rice planting areas in Jilin province

Ecotope	Statistics project	Simpson	Chao1	ACE	Shannon
East	Luffing	0.98-0.99	1002.00-1836.53	1002.00-1961.59	8.47-9.97
	Arithmetic mean	0.99a	1416.07ab	1472.20ab	9.44a
	Standard deviation	0.003	274.32	310.70	0.35
	Coefficient of Variation (%)	0.39	20.96	22.86	4.10
Center	Luffing	0.98-0.99	977.00-1948.85	977.34-2040.82	8.62-10.07
	Arithmetic mean	0.99a	1543.06a	1598.07a	9.43a
	Standard deviation	0.003	273.76	296.08	0.33
	Coefficient of Variation (%)	0.32	18.30	19.15	3.64
West	Luffing	0.98-0.99	830.00-1846.57	632.82-1922.01	7.00-9.77
	Arithmetic mean	0.99a	1274.69b	1316.11b	9.09a
	Standard deviation	0.007	299.29	311.21	0.71
	Coefficient of Variation (%)	0.81	24.35	24.53	8.21

Community structure of soil microorganisms

Community structure of soil fungal

In this study, the top 10 fungi at the phylum and class level and the top 20 fungi at the genus level were selected to analyze the composition of microbial communities in the three planting areas (*Fig. 4* and *Fig. 5*). In all regions, the predominant phylum of fungi were Ascomycota (58.8%-63.1%), Basidiomycota (19.2%-20.1%) and Zygomycota (3.4%-5.2%), the predominant class of fungi were Sordariomycetes (20.9%-30.8%), Agaricomycetes (2.8%-7.6%) and Tremellomycetes (2.0%-3.2%), the predominant genus of fungi were Ascomycota (6.9%-10.5%), Podospira (1.9%-3.6%) and Mortierella (2.3%-5.1%).

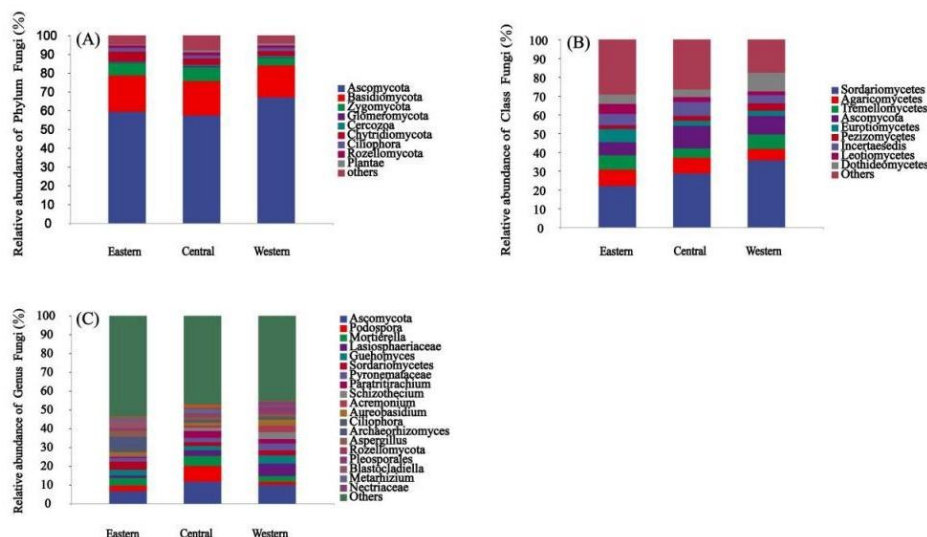


Figure 4. Relative abundance of fungi in different rice planting areas at the phylum level (A), class (B), and genus (C) level

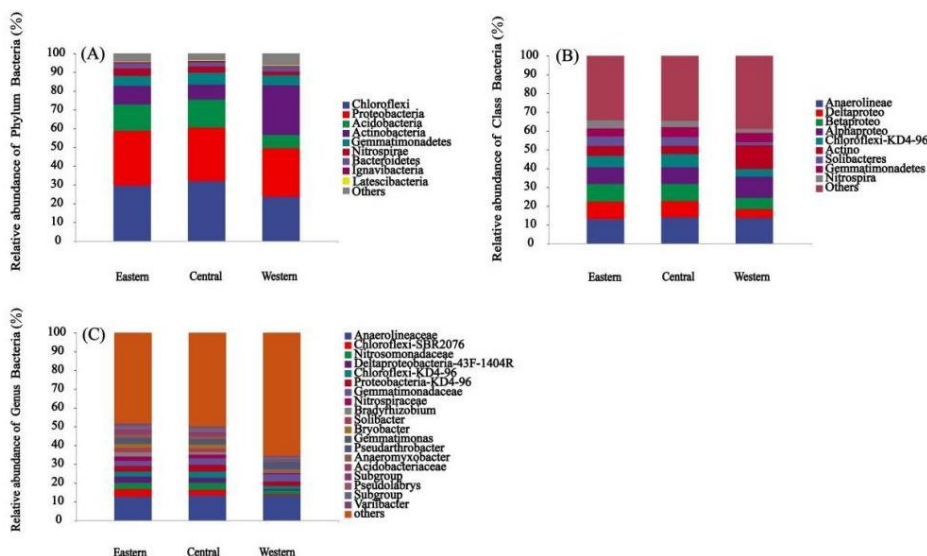


Figure 5. Relative abundance of bacteria in different rice planting areas at the phylum level (A), class (B), and genus (C) level

Community structure of soil bacterial

In all regions, the predominant phylum of bacteria were Chloroflexi (22.5%-30.9%), Proteobacteria (20.9%-30.8%) and Acidobacteria (5.9%-12.3%), the predominant class of bacteria were Anaerolineae (11.8%-12.3%) and Deltaproteo (5.3%-9.8%), Betaproteo (6.4%-8.8%), the predominant genus of bacteria were Anaerolineaceae (6.9%-10.5%), Chloroflexi (1.9%-3.7%) and Nitrosomonadaceae (2.4%-3.7%).

Influence factors of microbial community

In this study, the influence factors of soil microorganisms distributed were analyzed by CCA. It can be seen that the pH in the soil's chemical properties and the accumulation temperature, annual average temperature, and altitude in the environmental factors have the most significant effects on the soil fungal microbial colony structure (Fig. 6A). The soil samples in the eastern region are mainly distributed in the positive direction of the horizontal axis of CCA. In contrast, the soil samples in the western part are distributed primarily in the negative direction of the horizontal axis. It indicated that the soil fungal community structure in the two ecoregions had different characteristics.

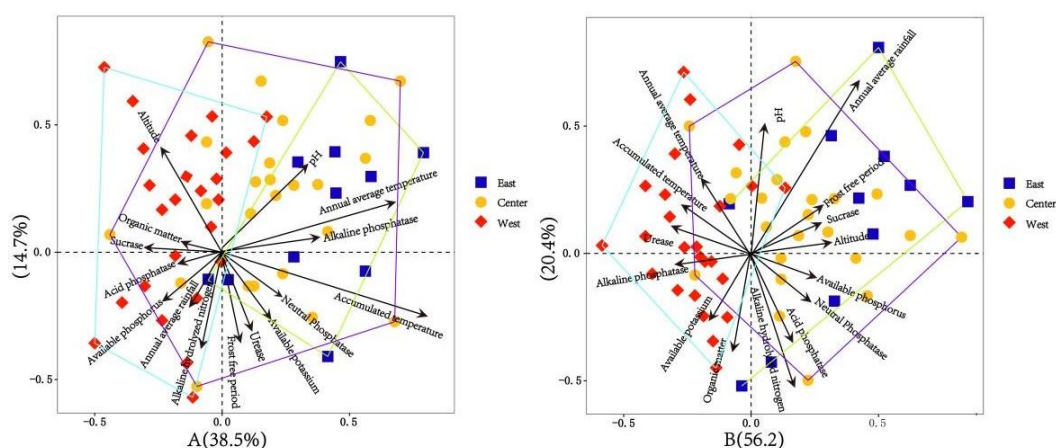


Figure 6. CCA analysis of different impact factors. (A) means fungi, (B) means bacteria; E means Eastern, C means Central, and W means Western; the acute angle between the lines is a positive correlation, the right angle is irrelevant, and the obtuse angle is a negative correlation

According to Figure 6B, among the chemical properties, pH and alkaline hydrolyzable nitrogen had the most significant impact on soil bacterial community structure and diversity. Among environmental factors, rainfall had the most significant effect on soil bacteria. From the perspective of bacterial distribution, the soil samples in the east are distributed in the positive direction of the CCA axis. Most of the soil samples in the western region are distributed in the negative direction of the CCA axis. The bacteria in the east and west have overlapping parts. It shows that the bacterial community structure of the two ecoregions has unique characteristics and similar structures.

Correlation between impact factors and microbial diversity

Figure 7 shows the correlation between different influencing factors and soil microbial diversity. According to this figure, fungal diversity was positively correlated with a frost-free period, organic matter, and rice yield. Among the positively correlated factors, the highest correlation was with rice yield. Fungal diversity was negatively correlated with

annual average temperature, average yearly rainfall, accumulated temperature, altitude, pH, hydrolyzable nitrogen, available phosphorus, available potassium, and sucrase, and among the negatively correlated factors, the correlation with altitude was the greatest.

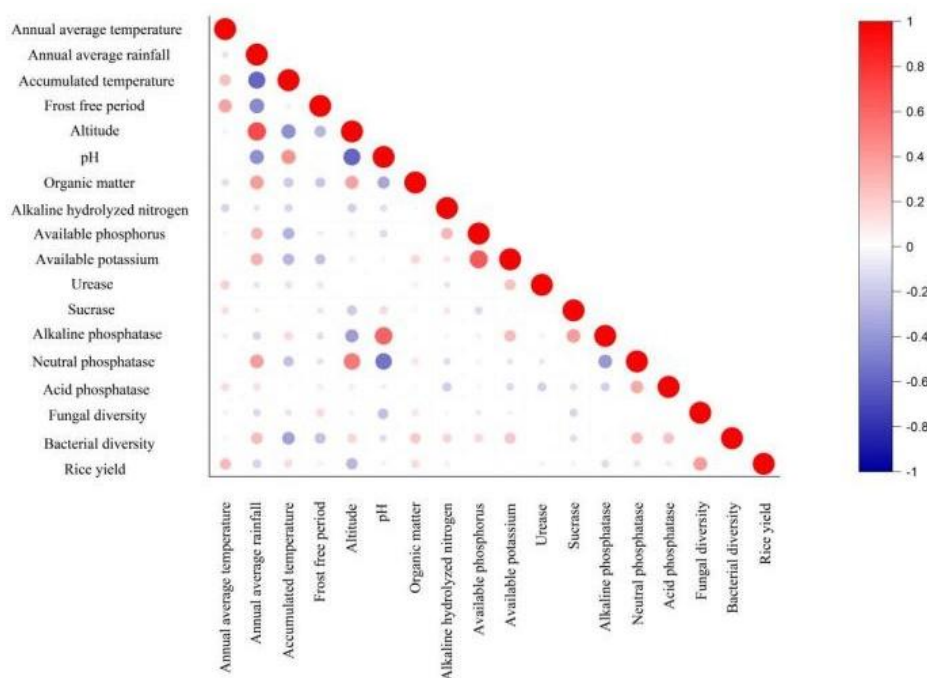


Figure 7. Correlation heatmap

According to *Figure 7*, bacterial diversity was positively correlated with annual average temperature, annual average rainfall, altitude, organic matter, alkaline hydrolyzable nitrogen, available phosphorus, available potassium, neutral phosphatase, and acid phosphatase and, among the positively correlated factors, with mean annual rainfall Quantity is most relevant. Bacterial diversity was negatively correlated with annual accumulated temperature, frost-free period, pH, sucrase, and alkaline phosphatase. The highest correlation was annual mean temperature among the negatively correlated factors.

Discussion

Analysis of soil chemical properties

There were significant differences in soil pH, AN, and organic matter content among the three rice-growing areas in Jilin province, indicating that the soil fertility of the three rice-growing areas was significantly different, and this difference was mainly affected by human and natural factors [18][71]. Human factors mainly include factors such as rice irrigation patterns, types of fertilization, and amount of fertilization [64], while natural factors mainly include factors such as temperature, rainfall, soil moisture, geology, and landforms in the planting area [29]. The western soil has the highest pH value among the three planting areas and is alkaline. This is mainly due to the low rainfall and high temperature in the western part of Jilin province, resulting in a soft soil moisture content

[50], leading to the accumulation of salts in the soil. The soil surface layer thus causes the soil pH to be high and alkaline. At the same time, due to the lower terrain in the western part of Jilin province, water-soluble salts moved from the central and eastern parts of the higher landscape to the west [72] which further led to the increase of soil pH. And due to the rise in soil pH in the west, some fungi and bacteria will decompose and transform [66], resulting in the lowest soil microbial diversity. The eastern soil has the highest OM content because the eastern part of Jilin province used to have more forests, and now some paddy fields are based on forest soil, resulting in high OM content [69][4], indicated that soil pH was the main influencing factor of soil microorganisms. Soil pH mainly affects the diversity of microorganisms by influencing their absorption of nutrients and their activity. In this study, soil pH is the main chemical influencing factor for soil fungi and bacteria (Liang et al., 2023). In this study, soil pH was the primary chemical influencing factor of soil fungi and bacteria. This further confirms the importance of soil pH for soil microorganisms.

Analysis of soil enzyme activity

Soil microbial and soil enzyme activities are the main driving forces affecting soil ecosystems' material cycle and energy flow [15]. Soil urease is one of the most active hydrolytic enzymes in soil, which can catalyze the hydrolysis of urea in the soil to generate ammonia and CO₂ [57]; its activity can reflect the nitrogen supply capacity of the soil and plays a vital role in soil nitrogen cycle [56]. Soil invertase is widely present in the soil, and its activity reflects the metabolic status of the soil biome and the conversion efficiency of carbon, the main soil nutrient element [13]. Soil phosphatase content is an important indicator reflecting soil organophosphate mineralization potential [63]. There were significant differences in soil urease and phosphatase activities among the three rice-growing regions in Jilin province, and the content of urease in the west was the highest, which may be due to the relatively low annual temperature in the west, which is more suitable for the survival of urease [9]. There are also significant differences in soil phosphatase in the three planting areas. Some studies have found that phosphatase content is mainly affected by soil pH and phosphorus content [40], while there is no difference in phosphorus content in the three planting areas. This may be due to the fact that besides phosphorus, there are other factors that can affect phosphatase activity in this study. The effect is small, and the impact of pH on the phosphatase content is the largest. According to *Figure 6*, soil enzyme content affects soil microbes, but lesser. Enzymes mainly affect microorganisms by participating in microbial metabolism [67]. Still, this process is very complicated. This process is also interfered with by the surrounding environment [36], so enzymes have little effect on soil microorganisms than chemical and climatic factors.

Long term conservation tillage, rational fertilization, balanced fertilization, and accurate nitrogen phosphorus potassium ratio can significantly increase soil organic carbon content and soil fertility, and improve soil microbial structure (Li et al., 2024). Deep tillage of straw returning to the field can increase soil enzyme activity (Rok et al., 2024).

Analysis of influence factors of soil microorganisms

According to *Figure 4*, *Figure 5*, *Table 1*, and *Table 2*, there were significant differences in the structure and diversity of fungi and bacteria among the three rice-growing regions in Jilin province. Meanwhile, according to *Figure 6*, pH, AN among

chemical factors, and temperature and rainfall among climatic factors are the main influencing factors of soil microorganisms. This conclusion is consistent with the findings of [68] and [28]. pH affects microbial structure and diversity by affecting soil matrix composition, soil chemistry, and microbial utilization efficiency of organic matter [46][38]. Bacteria are less tolerant to pH, and bacterial diversity is significantly reduced when the soil is alkaline [6]. The differences in nitrogen content in different regions were mainly due to the differences in nitrogen application rates in the different areas, which affected the structure and diversity of microorganisms. Some studies have found that the microorganisms will continue to grow and reproduce when the nitrogen application rate increases, thus affecting the microbial structure [70]. Among the climatic factors, temperature and rainfall are the main influencing factors of soil microorganisms, and temperature mainly affects the respiration and metabolism of microorganisms to affect the activity of microorganisms [33]. According to *Figure 1*, *Figure 4*, and *Figure 5*, Ascomycota and Sordariomycetes are more suitable for high temperatures. Differences in rainfall can lead to differences in soil moisture content in different regions. The activities of microorganisms are inseparable from water [3], especially soil microorganisms in rice-growing areas. Therefore, the irrigation pattern of rice also affects soil microbial structure and diversity [41]. According to *Figure 7*, there is also a correlation between microbial diversity and rice yield. Fungal diversity is positively correlated with rice yield, which is significant. Still, bacterial diversity has little correlation with rice yield, but this conclusion needs further Experimental analysis, which is also the next research plan.

Study's limitation

This study provides a new perspective on the differential impact of environmental factors on regional soil microorganism, but there are still some limitations. The study only explored the short-term effects of various environmental factors on soil microorganism in the region, and failed to fully reveal the long-term dynamic relationship between soil microorganisms and the environment, therefore, the impact of environmental factors on soil microorganisms may be uncertain and requires further verification.

Conclusions

There were significant differences in soil chemical properties, enzyme activities, microbial structures, and diversity among the three rice-growing regions in Jilin province. Soil pH increased gradually from (5.5) to west (8.3); OM content in the central area (14.9 g/kg) was significantly lower than in the eastern (26.3 g/kg) and western regions (17.0 g/kg). The soil urease content in the eastern (16.6 mg/g per d) and western regions (21.0 mg/g per d) was significantly higher than in the central part (9.8 mg/g per d). Climate factors have important effects on soil microorganisms, which is consistent with the initial assumption. We have further clarified that soil pH, accumulation temperature, annual average temperature, and altitude are the main influencing factors of soil fungi; and Soil pH, AN, and rainfall are the main influencing factors of soil bacteria. Moreover, differences in soil microbial diversity in different regions affect rice yield in different regions, especially soil fungi and rice yield were positively and strongly correlated, which further confirms our hypothesis. Here we suggest that for soil microbial quality and rice yield, while paying attention to the influence of human factors on soil microorganisms,

we should also pay attention to the effect of climatic conditions on soil microorganisms in the future.

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