IMPACT OF DIFFERENT FERTILIZER MANAGEMENT STRATEGIES ON RICE YIELD AND SOIL BACTERIAL COMMUNITY STRUCTURE

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Abstract. This study examines the effects of various fertilizer practices on rice yield and soil bacterial communities through field experiments. Treatments included no fertilization, single nutrient deficiencies (nitrogen, phosphorus, or potassium), and compound fertilizer application. Results showed that compound fertilization significantly boosted rice yield to 8740.5 kg/ha, a 62.3% increase compared to the no-fertilizer control (5385.0 kg/ha). It also enhanced nutrient levels in rice grains, straw, and soil. Nitrogen deficiency treatment did not significantly increase rice yield (5463.0 kg/ha) by only 1.4%, and nitrogen deficiency had a similarly large effect on the accumulation of nutrients in seeds and straw and on soil TN and effective phosphorus. Microbial analysis revealed that compound fertilization increased nitrogen-fixing (e.g., Anaeromyxobacter spp.) and phosphorus-solubilizing bacteria (e.g., Bradyrhizobium spp.) by 20.8% and 31.6%, respectively. Under nitrogen deficiency, Acidobacteriota abundance increased, indicating nitrogen's role in microbial activity and soil acidification. Phosphorus deficiency promoted Anaeromyxobacter and nitrifying Nitrospira, enhancing anaerobic decomposition and nitrification. Potassium deficiency elevated Thiobacillus, suggesting a microbial response to potassium scarcity. These findings highlight the importance of balanced fertilization with proper N, P, and K ratios to improve rice productivity, enhance soil health, and support sustainable agricultural practices.

Keywords: *fertilization strategies, soil microorganisms, rice cultivation, microbial community, soil health, microbial diversity*

Introduction

Rice, as one of the world's most essential food crops, directly influences the food security of over half of the global population. However, rice production faces the challenge of excessive chemical fertilizer use, which not only reduces fertilizer efficiency but also contributes to environmental degradation, threatening the sustainability of agriculture (Tayefeh et al., 2018; Sun et al., 2020). According to the Food and Agriculture Organization of the United Nations (FAO), global fertilizer use has steadily increased in recent years, however, this rise has not been accompanied by corresponding improvements in fertilizer efficiency. This issue is particularly acute in Asia, the largest riceing gree-producing region (FAO, 2019). Consequently, reducing fertilizer input while enhancing fertilizer efficiency, without reducing yields, has emerged as a critical concern in agricultural research (Tilman et al., 2002). In this context, optimizing fertilizer management and exploring the impact of innovative fertilizers on rice growth and soil microbial communities are not only of academic interest but also have significant economic value in promoting agricultural development and mitigating environmental pollution (Ji et al., 2020; Wang et al., 2019).

Extensive studies have shown that fertilizer management significantly influences rice yield and soil health. Although the long-term application of nitrogen, phosphorus, and potassium fertilizers can boost rice yields, it may also lead to soil acidification, nutrient imbalances, and alterations in microbial community structure (Li et al., 2023; Dai et al., 2018; Ma et al., 2022). For instance, Lee (2021) demonstrated that rational nitrogen fertilizer management improves nitrogen use efficiency, reduces nitrogen loss, and mitigates its environmental impact. Similarly, Wang et al. (2021) highlighted that the rational use of compound fertilizers not only maintains soil nutrient balance and enhances crop yields but also optimizes microbial community structure. They emphasized that balanced N, P, and K fertilization is crucial for crop growth and soil health. Furthermore, Qin et al. (2020) warned that excessive phosphorus application may initially boost yields but eventually leads to phosphorus accumulation in soil, increasing the risk of environmental pollution. In addition, the composition of bacterial communities is closely related to crop yield. Zhang et al. (2018) further underscored that adjusting fertilizer combinations can significantly reshape microbial community structure, improving soil fertility and crop health.

While numerous studies have explored the effects of fertilization on rice yield and soil microbial communities, most have focused on individual fertilizer components. There remains a lack of comprehensive research on the effects of various fertilizer combinations on rice yield and soil microbial communities (Zhang et al., 2022). Additionally, little is known about the dynamic changes in soil bacterial communities and their ecological functions in response to fertilizer application, particularly in key rice-growing regions. Addressing this gap, this study systematically investigates the effects of different fertilization regimes—including no fertilization, single nutrient deficiencies, and compound fertilizer treatments—on rice yield and soil bacterial community structure through field experiments. Relevant data was presented in the form of charts, and the correlations among the various data points were analyzed.

This study primarily evaluates three aspects: the effects of different fertilization regimes on the growth characteristics and yield of rice, their impact on soil and rice nutrient content, and the dynamic changes in soil bacterial communities and their ecological functions under different fertilization treatments. The findings will provide a scientific basis for optimizing fertilizer management, improving fertilizer efficiency, reducing agricultural pollution, and supporting sustainable agricultural development.

Materials and methods

Study area description

The experiment was conducted in Pan’an County, Jinhua City, located in central Zhejiang Province, China, which experiences a subtropical monsoon climate characterized by distinct seasonal variations and alternating winter and summer monsoons. The complex topography of the area results insignificant temperature fluctuations between day and night, as well as geographical variations across the county. The average annual temperature ranges from 13.9°C to 17.4°C, with January being the coldest month (average: 2.0-4.3°C) and July the warmest (average: 25.6-28.8°C), reaching an extreme high of 40.6°C. Prior to the experiment, the basal soil conditions were as follows: pH 5.25, Organic matter (OM) 25.58 g/kg, total nitrogen

(TN) 2.119 g/kg, Available Nitrogen (AN) 134.64 mg/kg, Available Phosphorus (AP) 7.25 mg/kg, and Available Potassium (AK) 69.43 mg/kg. Sowing period: April to May (avoiding the inverted spring cold and stabilizing the temperature above 15℃). Tillering period: June to July (temperature 25-30℃, with rainfall in the rainy season to promote tillering). Tapering and flowering: August (avoid high temperature or heavy rain to affect pollination). Ripening and harvesting: October (sunny and less rain in fall, conducive to seed filling).

Test materials

The rice variety used for the experiment was *Zhongzheyou No.8*. The fertilizers applied included urea (46% N), calcium superphosphate (12% PO), potassium chloride (60% KCL), and a compound fertilizer (20-10-15, N + PO + KCL 45%, provided by Jiangsu Compound Fertilizer Chemical Co.).

Processing method

A total of five treatments were set up in the experiment, namely: blank control, no nitrogen, no phosphorus, no potassium and compound fertilizer (20-10-15), with three replications for each treatment and a total of 15 plots, with a plot area of 20 m^2. Rice seeds were soaked at 25° C for 48 h, broken at 35° C for germination, and planting density was set at row spacing × hole spacing: 30 cm × 16 cm, and mechanically transplanted, with 3 seedlings planted in each hole to reach a basic seedling number of 198,000 plants/ha. Thiamethoxam granules were used to treat the soil prior to transplanting, and the mixture of chlorothalonil and tricyclonazole was sprayed once at the tillering stage and once during the spike stage to prevent and control insect pests and rice blast disease. Shallow water layer management was implemented during the whole life cycle: 3-5 cm of water layer was maintained between transplanting and tillering, the tillers were controlled by sunshine for 7 days at the end of tillering stage, and the water was rewatered to 5 cm at the stage of spiking. ridges were constructed to segregate the small zones, and the ridges were covered with black film (with a thickness of 0.1 mm) buried 50 cm deep and equipped with a single irrigation and single drainage system, and the irrigation outlet was set up with a 60-mesh nylon filter to prevent the entry of sundry materials. The detailed fertilization treatments for each treatment are shown in *Table 1*.

Sampling and analysis

Prior to the experiment, large-area soil samples were collected for laboratory analysis to guide fertilizer application. Field management practices and fertility periods were recorded. Basic seedling characteristics were measured post-transplanting, with the tallest seedlings assessed at the end of the tillering stage. During the harvesting period, soil samples from 0-20 cm depth were collected from each experimental plot using the S-sampling method, and three replicates of the samples were mixed to form a single sample. Fresh soil samples were partly stored at -80°C, while the remainder was air-dried, sieved through a 0.25 mm mesh, and thoroughly mixed for the determination of soil pH, OM, TN, AP, and AK.

In each plot, avoiding the marginal rows and the two ends of the rice to reduce edge effects, two 1 m sections of rice rows were randomly selected. The above-ground parts of the plants were collected at the root-stem interface as composite samples. Each sample was labelled with its plot number and the sampling date. These samples were first analyzed for key economic traits (e.g., effective panicles, panicle length, total grains per panicle, filled grains, unfilled grains, grain-filling rate, 1000-grain weight). The rice plants were then rinsed with deionized water and divided into straw and seed portions. These were initially heated at 105°C for 30 min to stop enzyme activity and then dried at 65°C to a constant weight. The dry weight of each part was recorded, pulverized with a stainless steel plant pulverizer, and stored for the determination of nitrogen, phosphorus, and potassium content in each part of the rice plants. Rice yield for each plot was also recorded at harvest.

Table 1. *Fertilizer and nutrient inputs for each treatment in the experiment (kg/ha)*

Treatment ID	**Treatment**	**Basal fertilizer**	**Topdressing**	**Input**	**Input**	**Input**
				(N) (kg/ha)	**(P_2O_5) (kg/ha)**	**(KCL) (kg/ha)**
1	No fertilizer	/	/	0	0	0
2	No nitrogen	Superphosphate ($Ca(H_2PO_4)_2 \cdot H_2O$) 500, Potassium chloride (KCl) 150	/	0	60	90
3	No phosphorus	Urea ($CO(NH_2)_2$) 411, Potassium chloride (KCl) 150	Urea ($CO(NH_2)_2$) 150	189	0	90
4	No potassium	Urea ($CO(NH_2)_2$) 411, SuPerphosphate ($Ca(H_2PO_4)_2 \cdot H_2O$) 500	Urea ($CO(NH_2)_2$) 150	189	60	0
5	Compound fertilizer (20-10-15)	(20-10-15) 600	Urea ($CO(NH_2)_2$) 150	189	60	90

Physicochemical analysis

The determination of soil and plant physicochemical properties followed the procedures outlined in "Soil Agrochemical Analysis" (Bao, 2000). Soil pH was measured in a 2.5:1 water-to-soil ratio suspension using a pH meter (FE28). OM was determined using the potassium dichromate oxidation method, AP by the molybdenum-blue colorimetric method, and AK using a flame photometer (FP640). Plant nitrogen, phosphorus, and potassium were measured after digestion with hydrogen peroxide and sulfuric acid, using the alkaline diffusion method for nitrogen, the molybdenum-blue colorimetric method for phosphorus, and a flame photometer for potassium (*Fig. 1*).

Macrogenome sequencing

The process of soil DNA extraction begins with the homogenization of soil samples, which can be performed using a vortex or bead mill, with the addition of Buffer SOL, Reagent DX, and Buffer SDS to ensure thorough lysis. After centrifugation to remove cellular debris, the supernatant is collected and treated with Buffer PS for further processing. Absorber Solution is then added to remove humic acids and inhibitory factors, ensuring the high quality of the purified DNA. Following centrifugation, Buffer GDP is used for washing the DNA, which is then further purified using the HiPure DNA Mini Column. After multiple wash steps, DNA is eluted using Buffer AE and stored at -20°C.

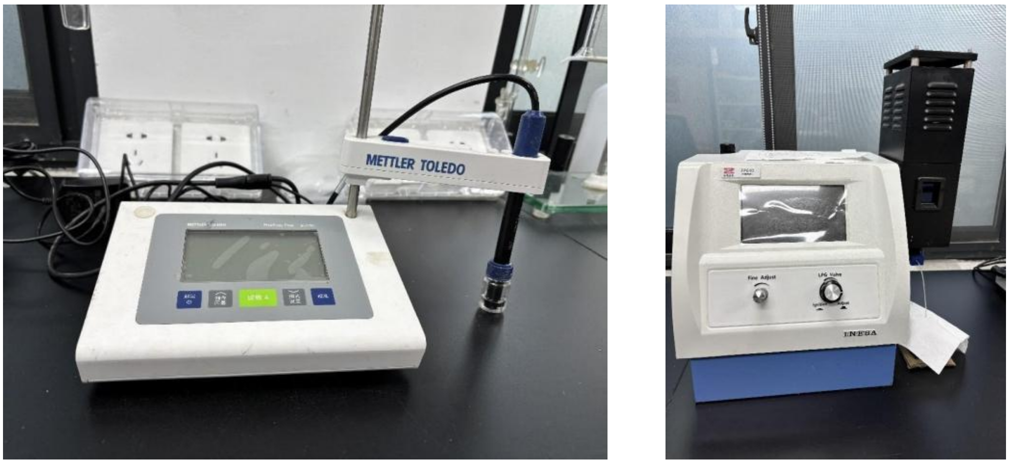

Figure 1. *pH meter (FE28) (left), flame photometer (FP640) (right)*

Raw data were processed using bcl2fastq (v2.17.1.14) for base calling and quality control, generating FASTQ format files. Sequences containing junctions, low-quality reads, or over 10% N-base content were filtered out using cutadapt (v1.9.1), with a minimum read length of 75 bp retained. Host genome sequences were removed using BWA (v0.7.12), and assembly analysis was performed using MEGAHIT (v1.1.3), selecting the optimal assembly results. Gene prediction was carried out with Prodigal (v3.02), and gene function and taxonomic annotation were done using Diamond (v0.8.15.77) against several databases.

Data processing

Raw data were organized using Excel 2007. Graphs were plotted using Origin 2019. Species that differed significantly at the phylum and genus level were analyzed using the Kruskal-Wallis test. Redundancy analysis (RDA) was performed using Canoco software.

Results

Rice yield for each treatment

As shown in *Table 2*, the compound fertilizer treatment (20-10-15) resulted in the best performance across all rice growth parameters, with a plant height of 130.0 cm, 3,255,000 effective spikelets/ha, 231.2 grains per spikelet, and a 1000-grain weight of 25.7 g. The final yield was 8740.5 kg/ha, representing a 62.3% increase compared to the blank control (5385.0 kg/ha). The potassium-deficient treatment yielded 7392.0 kg/ha, 37.3% higher than the blank control, while the phosphorus-deficient treatment yielded 7042.5 kg/ha, a 30.8% increase. In contrast, the nitrogen-deficient treatment showed only a slight increase of 1.4%, with a yield of 5463.0 kg/ha.

Table 2. *Growth characteristics and yield of rice in each treatment of the experiment*

Treatment	Plant height (cm)	Effective panicles (spikelets/ha)	Grains per panicle (quantities)	Thousand-grain weight (kg)	Yield (kg/ha)
No fertilizer	120.3	2370000	178.4	22.9	5385.0
No nitrogen	121.0	2325000	170.2	22.1	5463.0
No phosphorus	124.0	2760000	200.2	24.5	7042.5
No potassium	126.3	3105000	190.2	23.9	7392.0
Compound fertilizer (20-10-15)	130.0	3255000	231.2	25.7	8740.5

Overall, the compound fertilizer significantly promoted rice growth and increased yield, followed by the potassium- and phosphorus-deficient treatments. The nitrogen-deficient treatment, however, did not show a substantial yield improvement over the blank control, which underscores the critical role of nitrogen in rice growth.

Rice nutrient content

As shown in *Table 3*, the compound fertilizer treatment resulted in the highest nutrient content in rice seeds, with nitrogen, phosphorus, and potassium levels of 101.40 kg/ha, 58.20 kg/ha, and 30.75 kg/ha, respectively. These values represent increases of 110.6%, 68.7%, and 64.0%, respectively, compared to the blank control group. The potassium-free and phosphorus-free treatment groups also exhibited higher nitrogen, phosphorus, and potassium contents than the blank control, though to varying extents. Notably, the potassium-free treatment group saw a greater increase in nitrogen content, at 71.3%. In contrast, the nitrogen-deficient treatment group had slightly lower nitrogen content compared to the control, while phosphorus and potassium contents showed modest increases, indicating that nitrogen deficiency had a more pronounced impact on nutrient accumulation in rice seeds.

In the straw, the compound fertilizer treatment also yielded the highest nutrient content, with nitrogen, phosphorus, and potassium levels of 42.45 kg/ha, 15.75 kg/ha, and 223.65 kg/ha, respectively, representing increases of 126.4%, 54.4%, and 78.8% compared to the blank control group. Both the phosphorus-free and potassium-free treatment groups also showed higher nutrient contents than the control. The phosphorus-free treatment led to a particularly notable increase in nitrogen content, up to 84.0%. Conversely, the nitrogen-deficient treatment group exhibited reduced nitrogen and phosphorus levels compared to the control, while potassium content showed a slight increase. These results suggest that nitrogen deficiency significantly inhibits nutrient accumulation in rice straw.

Table 3. *Nutrient content of rice in each treatment of the experiment*

Treatment	Seeds kg/ha			Stalk kg/ha		
	N	P_2O_5	K_2O	N	P_2O_5	K_2O
No fertilizer	48.15	34.50	18.75	18.75	10.20	125.10
No nitrogen	46.05	36.90	20.10	17.25	8.7	150.90
No phosphorus	69.00	44.10	27.15	34.50	12.15	186.90
No potassium	82.50	46.65	23.25	30.30	11.40	199.95
Compound fertilizer (20-10-15)	101.40	58.20	30.75	42.45	15.75	223.65

Soil nutrient content

As shown in *Table 4*, the different fertilizer treatments had significant effects on soil pH, OM, TN, AP and AK. The differences in soil pH between the treatment groups were small, and the compound fertilizer treatment group had a pH of 5.54, which was basically the same as the blank control group (5.55). The OM content of the combined fertilizer treatment group was the highest at 24.97 g/kg, an increase of 6.1% compared to the blank control group, and the OM content of the phosphorus-free treatment group was the lowest at 22.53 g/kg. The TN content reached the highest in the combined fertilizer treatment group, which was 2.24 g/kg, an increase of 14.3% compared to the blank control group, and the nitrogen-deficient treatment group had the low TN content of 2.00 g/kg, which was close to the blank control group (1.96 g/kg). Effective phosphorus was significantly higher in the combined fertilizer and potassium-free treatment groups at 8.36 mg/kg and 8.37 mg/kg respectively, both an increase of 28.0% compared with the blank control. Quick potassium content varied less between treatments and was slightly higher in all groups than the blank control (61.65 mg/kg).

Table 4. *Soil nutrient content of each treatment in the experiment*

Treatment	pH	Organic matter (g/kg)	Total nitrogen (g/kg)	Available phosphorus (mg/kg)	Available potassium (mg/kg)
No fertilizer	5.55	23.54	1.96	6.53	61.65
No nitrogen	5.53	24.18	2.00	6.10	64.01
No phosphorus	5.36	22.53	2.15	7.07	62.28
No potassium	5.57	24.76	2.10	8.37	61.70
Compound fertilizer (20-10-15)	5.54	24.97	2.24	8.36	62.82

Changes in soil bacterial community structure in rice under different fertilization treatments

As shown in *Figure 2*, the four Venn diagrams illustrate that the number of shared operational taxonomic units (OTUs) in the soil bacterial community was relatively high across the different fertilization treatments (WN, WP, WK, NPK) and the blank control group (CK). This suggests that the overall structure of the soil bacterial community remained largely similar despite the different treatments. Both the WN and NPK treatments shared 3190 OTUs with the control group, while the WP and WK treatments shared 3181 and 3153 OTUs, respectively, indicating slight variations in the degree of influence of each treatment on the bacterial community.

In terms of unique OTUs, the WK treatment had the most significant effect on the bacterial community, with only 121 unique OTUs in the WK group, compared to 200 unique OTUs in the blank control group, highlighting a substantial difference. By contrast, the NPK, WN, and WP treatments showed relatively similar numbers of unique OTUs, with 148, 153, and 135, respectively, indicating a less pronounced effect on soil bacterial community structure.

Overall, while there were observable differences in the effects of the fertilization treatments on the soil bacterial community, the general community structure remained highly similar across treatments.

Based on the analysis of species composition at both the bacterial phylum and genus levels in soil samples, different fertilization treatments had a significant impact on the structural distribution of soil bacterial communities. As illustrated in *Figure 2a*, at the bacterial phylum level, the dominant groups were Pseudomonadota, Acidobacteriota, Chloroflexota, and unclassified_Bacteria, with relative abundances ranging from 19.31% to 24.53%, 11.53% to 18.32%, 10.66% to 15.71%, and 8.93% to 12.52%, respectively. At the bacterial genus level, the dominant groups included Anaeromyxobacter, Nitrospira, Sphingomonas, and Geobacter, with relative abundances of 14.44% to 22.11%, 4.24% to 4.93%, 2.51% to 3.15%, and 2.31% to 3.73%, respectively.

Different fertilization treatments significantly altered the relative abundance of these dominant taxa, reflecting distinct functional characteristics. Under the nitrogen deficiency treatment (WN), the abundance of Acidobacteriota was 12.17%, slightly higher than in the control (CK) (11.53%), but lower than in the other treatments. This suggests that nitrogen may play a crucial role in microbial activities related to OM decomposition and soil acidification. In contrast, the abundance of Anaeromyxobacter spp. increased to 19.79% compared to 18.28% in the control, indicating enhanced OM decomposition in anaerobic environments.

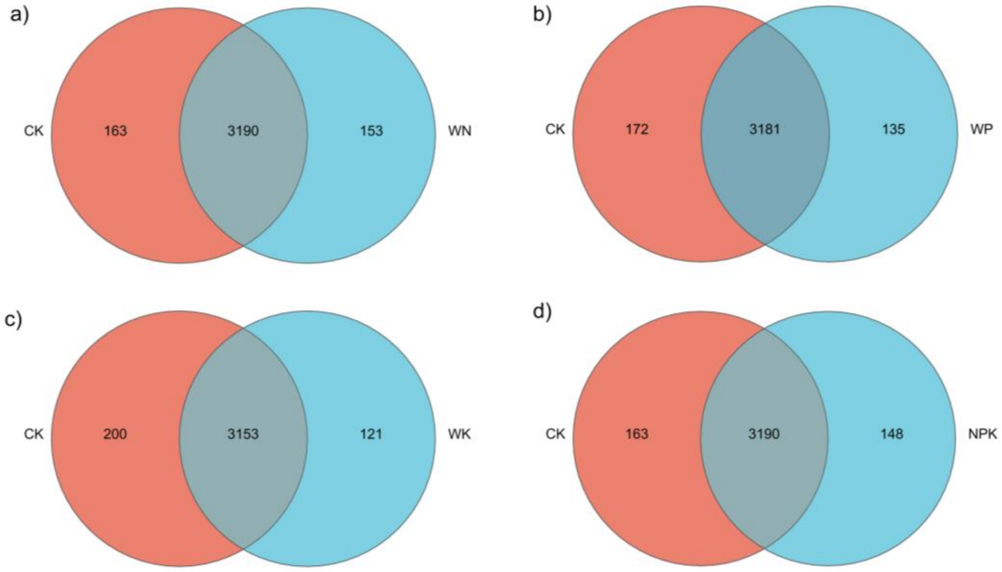

Figure 2. *Wayne's plot of all detectable species of Bacteria spp. between each treatment group and the control group: (a) Nitrogen deficient treatment group and control (CK-WN), (b) Phosphorus deficient treatment group and control (CK-WP), (c) Potassium deficient treatment group and control (CK-WK), (d) Compound fertilizer treatment group and control (CK-NPK)*

As shown in *Figure 3*, in the phosphorus deficiency treatment (WP), Anaeromyxobacter spp. reached its highest abundance at 22.11%, suggesting that microorganisms adapted to phosphorus deficiency by enhancing anaerobic OM degradation. Additionally, Nitrospira abundance was significantly higher in the WP treatment (4.93%) than in the other treatments, indicating enhanced nitrification processes. However, the abundance of Pseudomonadota decreased significantly to 19.31% compared to 24.53% in the control, implying that phosphorus deficiency suppressed microbial activities related to phosphorus metabolism, weakening phosphorus solubilization and nitrogen cycling efficiency in the soil. The abundance of Chloroflexota also decreased to 12.99% compared to 15.71% in the control, suggesting a suppression of microbial functions related to OM decomposition.

Under potassium deficiency (WK), Thiobacillus spp. increased significantly to 3.04%, compared to 2.18% in the control, indicating that sulphur oxidation functions were enhanced under potassium deficiency, possibly as a microbial compensatory mechanism for potassium scarcity. Additionally, the highest abundance of Bradyrhizobium was observed in the compound fertilizer (NPK) treatment at 2.95%, reflecting that compound fertilizer application significantly promoted nitrogen fixation and improved nitrogen availability in the soil. The abundance of Acidobacteriota also increased significantly in the NPK treatment to 18.23%, compared to 11.53% in the control, suggesting that compound fertilizer may have enhanced the efficiency of OM decomposition in the soil.

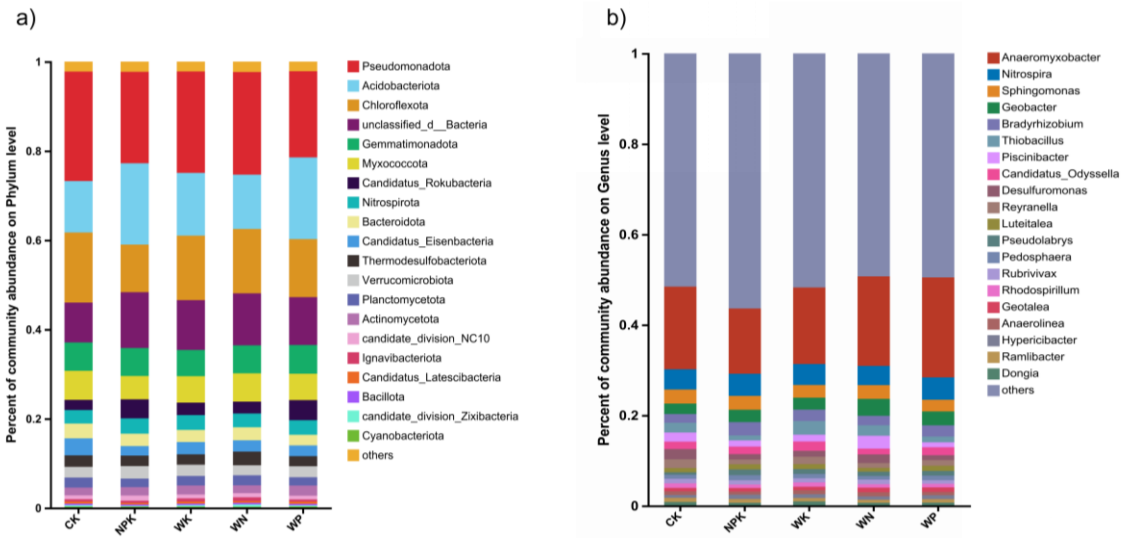

Figure 3. *Dominant bacterial phylum (a), abundance map of bacterial genera (b)*

Figure 4 illustrates that different fertilization treatments significantly influenced the abundance of several bacterial genera in the soil, with statistically significant differences observed across all treatment groups. *Candidatus_Odyssella* (candidate Odysseyella spp.) was the dominant bacterial genus in all treatments, with particularly higher abundances in the WK, WP, and NPK groups.

The abundance of *Aromatoleum* and *Candidatus_Sulfobium* was significantly higher in the NPK treatment group compared to other treatments, indicating that the NPK fertilization strongly promoted the growth of these genera. In contrast, *Candidatus_Binatus* showed the highest abundance in the NPK-treated group but was barely detectable in other treatments, suggesting a specific response to NPK fertilization.

Additionally, *Azospirillum* (a genus of nitrogen-fixing spirochetes), *Paraburkholderia* (a genus related to *Burkholderia pasteurianum*), and *Cupriavidus* (a genus related to *Pseudomonas aeruginosa*) had relatively similar abundances across all treatment groups, with the NPK group showing a slight increase compared to the others.

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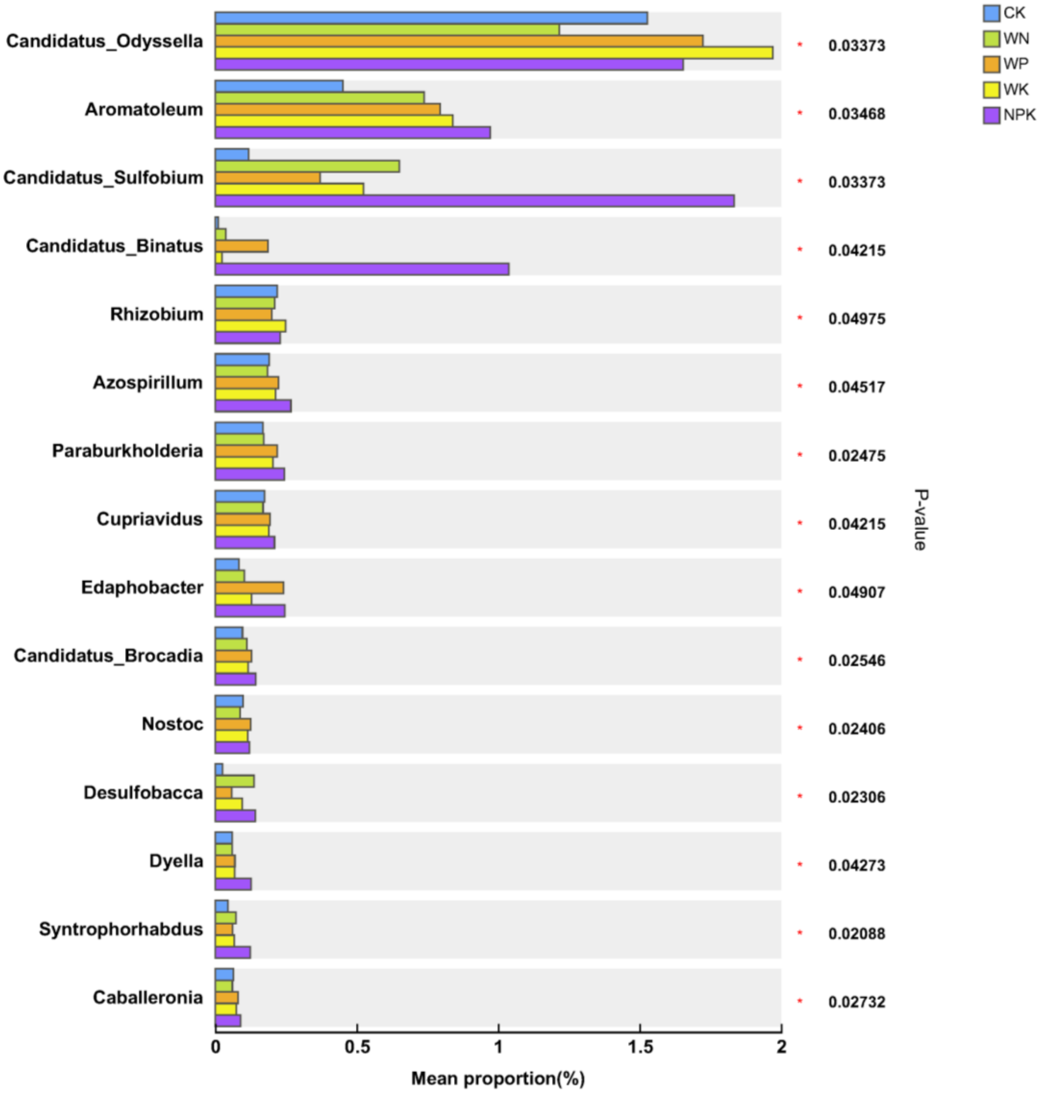

Figure 4. *Bar chart of species differences at the genus level*

Overall, the NPK treatment led to a significant rise in the abundance of several key genera, highlighting its crucial role in shaping the structure of soil bacterial communities.

Analysis of factors influencing changes in the composition of the rice soil bacterial community

RDA analysis plot showing that the variation in the composition of the rice soil bacterial community was significantly influenced by soil nutrient factors, specifically AP, TN, and soil organic matter (SOM) (*Fig. 5*). RDA1 and RDA2 explained 59.93% and 11.14% of the total variation, respectively, indicating that these factors play critical roles in shaping the bacterial community structure.

The bacterial community in the NPK treatment group showed a strong, significant positive correlation with the soil nutrient factors AP, TN, and SOM. This suggests that phosphorus and nitrogen fertilization in the NPK treatment strongly promoted bacterial communities that thrive in high phosphorus and nitrogen environments. Conversely,

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SOM and soil pH were significantly positively correlated with the bacterial communities in the WP and CK groups, indicating that OM content and pH were more critical factors in shaping the bacterial communities in these treatment groups.

Interestingly, AK exhibited a negative correlation with the other factors, suggesting that high potassium levels uniquely influence the abundance of specific bacterial groups. These findings suggest that fertilization treatments significantly impacted the structure of rice soil bacterial communities by altering key soil nutrient levels, particularly AP, TN, and SOM.

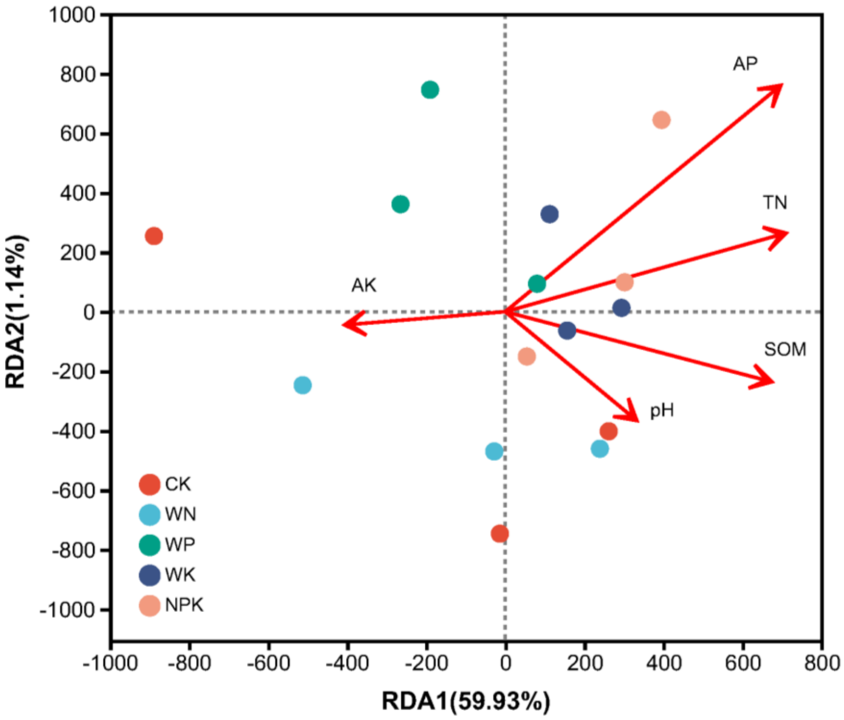

Figure 5. *RDA plots of species abundance versus soil nutrient content at the genus level of the bacterial communities*

Discussion

This study investigated the effects of different fertilizer management strategies on rice yield and soil bacterial community structure. The results demonstrated that fertilizer treatments significantly influenced both rice yield and the composition of soil microbial communities.

Effects of treatments on growth characteristics and yield of rice

The application of compound fertilizers markedly improved rice growth characteristics and yield, aligning with findings from previous studies. For instance, Istiqomah et al. (2020) demonstrated that an optimal balance of nitrogen, phosphorus, and potassium could significantly enhance rice plant height and the number of effective spikes, thus increasing total yield. In the present study, the compound fertilizer treatment group recorded significantly higher plant height (130 cm), effective spike count (217,000 spikes/acre), and grains per spike (231.2), consistent with the improvement in crop yield observed by Pachauri et al. (2021). Single nutrient

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deficiencies also had observable effects on rice growth and yield. The nitrogen-deficient treatment resulted insignificantly lower yield (5463.0 kg/ha) compared to other treatments, corroborating findings by Fageria (2014), who identified nitrogen as crucial for plant biomass accumulation. Xiong et al. (2018) further highlighted that nitrogen deficiency can severely impact grain weight and total yield, which was also observed in this study.

In contrast, the relatively higher yields in phosphorus- (7042.5 kg/ha) and potassium-deficient (7392 kg/ha) groups suggest that rice can tolerate moderate deficiencies in phosphorus and potassium, findings consistent with Du et al. (2021). Overall, compound fertilizers greatly enhanced rice yield and growth characteristics, while nitrogen deficiency had the most pronounced negative impact, further highlighting the importance of balanced fertilization in improving crop yield.

Effects of treatments on nutrient content of rice and rice soil biomass

The present study also revealed that compound fertilizers significantly increased the nutrient content of rice, with nitrogen, phosphorus, and potassium levels in seeds rising by 110.6%, 68.7%, and 64.0%, respectively. Moreover, compound fertilizer application improved soil OM and AP levels, indicating enhanced nutrient uptake efficiency by crops and better soil nutrient supply (Mao et al., 2021). In contrast, treatments deficient in key nutrients, particularly nitrogen and phosphorus, significantly reduced soil fertility and rice yield (Wen et al., 2016). This is consistent with other research underscoring the importance of balanced N, P, and K fertilization in sustaining soil fertility and achieving high crop yields (Chen et al., 2021). Furthermore, compound fertilizers contribute to nutrient sustainability by reducing nutrient loss, providing a solid basis for optimizing fertilizer use in agriculture (Liu et al., 2024; Taj et al., 2023).

Effects of treatments on changes in the structure of rice soil bacterial communities

The Venn diagram analysis showed that compound fertilizer treatments shared many operational taxonomic units (OTUs) with the control group, but also significantly increased the presence of unique OTUs. This suggests that fertilization not only preserves the core bacterial community structure but also promotes the colonization of specific microbial groups (Yang et al., 2019). Conversely, potassium deficiency notably reduced the number of unique OTUs, reflecting a negative impact on microbial diversity. At both the phylum and genus levels, compound fertilizers increased the abundance of key bacterial groups, such as Ascomycetes and Acidobacteria, which are critical for OM decomposition and nutrient cycling (Gao et al., 2022). Phosphorus deficiency, on the other hand, reduced the presence of anaerobic bacteria, impairing OM decomposition (Fang et al., 2019). Compound fertilizer treatments also promoted the growth of nitrogen-fixing bacteria like Bradyrhizobium, while phosphorus and potassium deficiencies hindered the growth of functional bacteria, weakening soil nutrient cycling (Qiu et al., 2023; Borges et al., 2021). Redundancy analysis (RDA) revealed that TN, AP, and soil OM were the main drivers of bacterial community shifts. These nutrient levels increased significantly under compound fertilizer treatments and were positively correlated with bacterial diversity and functional activity (Chen et al., 2024), consistent with other findings highlighting nutrient availability as a key determinant of microbial activity and ecological balance (Yin et al., 2022).

Conclusions

This study highlights the substantial impact of different fertilizer management strategies on rice yield and soil bacterial community structure, underscoring the importance of optimizing fertilizer application to achieve high yields while protecting the environment. The compound fertilizer treatment not only maximized rice yield (8740.5 kg/ha) but also microorganisms are key factors driving the nutrient cycling in soil, thereby promoting plant growth, that improved the structure of the soil microbial community by promoting the colonization of beneficial bacteria, such as nitrogen-fixing and phosphorus-solubilizing species. This offers a practical framework for reducing chemical fertilizer use while enhancing fertilizer efficiency. However, the mechanisms by which microbial diversity and abundance affect rice yield are still not well understood.

Conversely, single nutrient deficiency treatments, especially nitrogen and phosphorus deficiencies, had detrimental effects on both rice yield and soil health. This underscores the critical role of nitrogen and phosphorus in maintaining crop productivity and facilitating soil nutrient cycling. In conclusion, a well-balanced fertilization strategy that optimally combines nitrogen, phosphorus, and potassium can significantly enhance rice productivity, promote soil ecosystem health, and support the sustainability of agricultural production. This study provides a scientific basis for reducing chemical fertilizer inputs and improving fertilizer efficiency while ensuring high yields, making it a valuable contribution to future agricultural practices.

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REFERENCES

[1] Bao, S. D., (2000): Soil and Agricultural Chemistry Analysis. – China Agriculture Press, Beijing.

[2] Borges, W. L., Ferreira, N. d. S., Rios, R. d. M., Rumjanek, N. G. (2021): Liming, fertilization, and rhizobia inoculation on cowpea yield in a Brazilian Amazon upland forest environment. – Pesquisa Agropecuária Brasileira 56: e02191.

[3] Chen, A., Zhang, W., Sheng, R., Liu, Y., Hou, H., Liu, F., Ma, G., Wei, W., Qin, H. (2021): Long-term partial replacement of mineral fertilizer within situ crop residues ensures continued rice yields and soil fertility: a case study of a 27-year field experiment in subtropical China. – Science of the Total Environment 787: 147523.

[4] Chen, Z., Li, S., Sun, X., He, L., Zhou, W., Zhao, G., Yu, J., Bai, X., Zhang, J. (2024): Characteristics of bacterial communities under different tree species and their response to soil physicochemical properties. – Forests 15: 740.

[5] Dai, Z., Su, W., Chen, H., Barberán, A., Zhao, H., Yu, M., Yu, L., Brookes, P. C., Schadt, C. W., Chang, S. X., Xu, J. (2018): Long-term nitrogen fertilization decreases bacterial diversity and favors the growth of Actinobacteria and Proteobacteria in agro-ecosystems across the globe. – Global Change Biology 24: 3452-3461.

[6] Du, M., Zhang, W., Gao, J., Liu, M., Zhou, Y., He, D., Zhao, Y., Liu, S. (2021): Improvement of root characteristics due to nitrogen, phosphorus, and potassium

interactions increases rice (Oryza sativa L.) yield and nitrogen use efficiency. – Agronomy 12: 23.

[7] Fageria, N. (2014): Nitrogen harvest index and its association with crop yields. – Journal of Plant Nutrition 37: 795-810.

[8] Fang, X. M., Zhang, X. L., Chen, F. S., Zong, Y. Y., Bu, W. S., Wan, S. Z., Luo, Y., Wang, H. (2019): Phosphorus addition alters the response of soil organic carbon decomposition to nitrogen deposition in a subtropical forest. – Soil Biology and Biochemistry 133: 119-128.

[9] FAO (2019): National assessment of nitrogen fertilizers fate and related environmental impacts of multiple pathways in China. – FAO, Rome 277: 1-25.

[10] Gao, D., Sheng, R., Moreira-Grez, B., Liu, S., Xu, R., Li, K., Wei, W. (2022): Influences of phosphorus and potassium deficiencies on the methanotrophic communities in rice rhizosphere. – Applied Soil Ecology 170: 104265.

[11] Istiqomah, N., Tafakresnanto, C. (2020): The increased yield of rice due application of high-potassium-NPK fertilizer to low-potassium-soil content. – In: Proceedings of the IOP Conference Series: Earth and Environmental Science. IOP Publishing 456: 012059.

[12] Ji, Y., Conrad, R., Xu, H. (2020): Responses of archaeal, bacterial, and functional microbial communities to growth season and nitrogen fertilization in rice fields. – Biology and Fertility of Soils 56: 81-95.

[13] Lee, S. (2021): Recent advances on nitrogen use efficiency in rice. – Agronomy 11: 753.

[14] Li, J., Liu, K. L., Chen, J., Xie, J., Jiang, Y., Deng, G. Q., Li, D. M., Guan, X. J., Liang, X. H., Chen, X. M., Qiu, C. F., Qian, Y. F., Xia, W. J., Liu, J., Peng, C. R., Bell, S. M., Chen, J. (2023): New insights from soil microorganisms for sustainable double rice-cropping system with 37-year manure fertilization. – Agronomy 13: 261.

[15] Liu, J., Wang, D., Yan, X., Jia, L., Chen, N., Liu, J., Zhao, P., Zhou, L., Cao, Q. (2024): Effect of nitrogen, phosphorus and potassium fertilization management on soil properties and leaf traits and yield of Sapindus mukorossi. – Frontiers in Plant Science 15: 1300683.

[16] Ma, T., He, X., Chen, S., Li, Y., Huang, Q., Xue, C., Shen, Q. (2022): Long-term organic–inorganic fertilization regimes alter bacterial and fungal communities and rice yields in paddy soil. – Frontiers in Microbiology 13: 890712.

[17] Mao, L., Zha, R., Chen, S., Zhang, J., Jie, L., Zha, X. (2021): Mixture compound fertilizer and super absorbent polymer application significantly promoted growth and increased nutrient levels in Pinus massoniana seedlings and soil in seriously eroded degradation region of southern China. – Frontiers in Plant Science 12: 763175.

[18] Pachauri, S., Srivastava, P., Rawat, D., Mathpal, B., Sankhyadhar, S., Pandey, P., Shukla, A. (2021): Effect of fertilizer management practices on grain yields, concentrations of micronutrient cations and phytic acid in rice and wheat grains under a long term fertility trial. – Int. J. Curr. Microbiol. App. Sci 10: 1718-1724.

[19] Qin, X., Guo, S., Zhai, L., Pan, J., Khoshnevisan, B., Wu, S., Wang, H., Yang, B., Ji, J., Liu, H. (2020): How long-term excessive manure application affects soil phosphorous species and risk of phosphorous loss in fluvo-aquic soil. – Environmental Pollution 266: 115304.

[20] Qiu, T., Yu, J., He, L., Liu, J., Cui, Q., Cui, Y., Duan, C., Zhao, S., Wang, Y., Fang, L. (2023): Slope position mediates the co-utilization of phosphorus by plants and microbes through rhizosphere processes in a phosphorus-limited forest. – Catena 222: 106808.

[21] Sun, C., Chen, L., Zhai, L., Liu, H., Wang, K., Jiao, C., Shen, Z. (2020): National assessment of nitrogen fertilizers fate and related environmental impacts of multiple pathways in China. – Journal of Cleaner Production 277: 123519.

[22] Taj, A., Bibi, H., Akbar, W. A., Rahim, H. U., Iqbal, M., Ullah, S. (2023): Effect of poultry manure and NPK compound fertilizer on soil physicochemical parameters, NPK availability, and uptake by spring maize (Zea mays L.) in alkaline-calcareous soil. – Gesunde Pflanzen 75: 393-403.

[23] Tayefeh, M., Sadeghi, S. M., Noorhosseini, S. A., Bacenetti, J., Damalas, C. A. (2018): Environmental impact of rice production based on nitrogen fertilizer use. – Environmental Science and Pollution Research 25: 15885-15895.

[24] Tilman, D., Cassman, K. G., Matson, P. A., Naylor, R., Polasky, S. (2002): Agricultural sustainability and intensive production practices. – Nature 418: 671-677.

[25] Wang, J. L., Liu, K. L., Zhao, X. Q., Zhang, H. Q., Li, D., Li, J. J., Shen, R. F. (2021): Balanced fertilization over four decades has sustained soil microbial communities and improved soil fertility and rice productivity in red paddy soil. – Science of the Total Environment 793: 148664.

[26] Wang, W., Luo, X., Chen, Y., Ye, X., Wang, H., Cao, Z., Ran, W., Cui, Z. (2019): Succession of composition and function of soil bacterial communities during key rice growth stages. – Frontiers in Microbiology 10: 421.

[27] Wen, Z. H., Shen, J. B., Martin, B., Li, H. G., Zhao, B. Q., Yuan, H. M. (2016): Combined applications of nitrogen and phosphorus fertilizers with manure increase maize yield and nutrient uptake via stimulating root growth in a long-term experiment. – Pedosphere 26: 62-73.

[28] Xiong, Q., Tang, G., Zhong, L., He, H., Chen, X. (2018): Response to nitrogen deficiency and compensation on physiological characteristics, yield formation, and nitrogen utilization of rice. – Frontiers in Plant Science 9: 1075.

[29] Yang, Y., Wang, P., Zeng, Z. (2019): Dynamics of bacterial communities in a 30-year fertilized paddy field under different organic–inorganic fertilization strategies. – Agronomy 9: 14.

[30] Yin, S., Suo, F., Zheng, Y., You, X., Li, H., Wang, J., Zhang, C., Li, Y., Cheng, Y. (2022): Biochar-compost amendment enhanced sorghum growth and yield by improving soil physicochemical properties and shifting soil bacterial community in a coastal soil. – Frontiers in Environmental Science 10: 1036837.

[31] Zhang, J., Zheng, C., Zhang, L., Zhang, C., Lv, Y., Nie, L., Zhang, X., Li, B., Cao, W., Li, M., Liu, C., Zhang, Y. (2022): Effects of Chinese milk vetch returning on soil properties, microbial community, and rice yield in paddy soil. – Sustainability 14: 16065.

[32] Zhang, M., Yao, Y., Tian, Y., Ceng, K., Zhao, M., Zhao, M., Yin, B. (2018): Increasing yield and N use efficiency with organic fertilizer in Chinese intensive rice cropping systems. – Field Crops Research 227: 102-109.