


RESEARCH ARTICLE

Effects of organic amendments on soil bacterial community structure and yield in a saline-sodic soil cropped with rice

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Abstract

Organic improvement measures play a crucial role in the reclamation of saline-sodic soil. However, there is still a limited understanding regarding the relationships between soil microbes and soil properties and crop yield in response to the application of these organic materials to saline-sodic soils. In a field trial, the following treatments were carried out: no modifier input (CK) and compound lignite organic modifier 30 t/ha (LOM) with 2 years of rice cultivation, no modifier input (RF) with 5 years of rice cultivation, and the full amount of straw was returned to the field with rice-duck farming (SW). Compared with RF and CK, the SOM content in the 0–20 cm soil layer of SW and LOM was significantly increased by 4.600 and 5.020 g kg⁻¹, respectively, while the total alkalinity and pH were significantly decreased. In the 20–40 cm soil layer, the LOM treatment resulted in decreased pH and total alkalinity compared with other treatments. Overall, changes in soil microbial structure changes were significantly associated with SOM and pH levels. In the 0–20 cm soil layer, the LOM treatment significantly increased the relative abundance of Proteobacteria, while SW treatment significantly increased the relative abundance of Bacteroidetes and Firmicutes compared with CK. Moreover, the relative abundances of Longobacteriaceae of Bacteroidetes, Hydrogenaceae, and Xanthomonas of Proteobacteria were positively correlated with crop yield. The yields of SW and LOM were 6985.587 and 7879.910 kg ha⁻¹, respectively. These results demonstrate that implementing comprehensive organic improvement measures can enhance the properties of saline-sodic soil and increase crop yield, with lignite composite organic amendments may be more suitable for sustainable agricultural development.

KEYWORDS

bacterial community structure, lignite, rice yield, rice-duck farming, saline-sodic soil, straw return

1 | INTRODUCTION

Soil salinization has emerged as a major agricultural problem worldwide, affecting an area of approximately 1×10^9 ha of global saline-sodic land (Singh, 2016), which is primarily found in arid and semiarid regions. Due to the progress of urbanization and population growth, there is a shortage of food and a decline in arable land. Consequently,

poor salt-affected soil must be cultivated to meet the challenges of global food security (Kopittke et al., 2019). With an area of more than 5×10^6 ha, Songnen Plain in Northeast China represents one of the most problematic lands in the world, having experienced, rapid development in recent decades (Yang et al., 2016). The dominant salts in this region are sodium carbonate (Na₂CO₃) and sodium bicarbonate (NaHCO₃) (Ye et al., 2017). Excess sodium ions (Na⁺) in soil colloids

contribute to clay dispersion and pore clogging, leading to reduced soil permeability and nutrient availability (Adeli et al., 2017). To reclaim saline-sodic land, it is necessary to remove the excess exchangeable sodium from the cation exchange sites by replacing it with other cations, such as calcium (Ca^{2+}), followed by leaching of the replaced sodium from the soil profile using good-quality water. Although the above strategies may work well, the SOM content remains low under the condition of solely inorganic improvement, while the soil physico-chemical properties and the ability to supply nutrient continuously are relatively poor compared with high-yield fields (Bai et al., 2018), resulting in lower yields and incomes after improvement. This phenomenon dampens farmers' enthusiasm for reclaiming saline-sodic land (Seenivasan et al., 2015). Therefore, the goal of improving saline-sodic land is not only to improve soil quality but also, more importantly, to achieve higher yields within a shorter time frame, requiring cost-effective and time-effective solutions (Shrivastava & Kumar, 2015).

The rice-duck farming technology represents an ecological agricultural innovation that has been inherited and developed based on duck farming in rice fields with hundreds of years of history in China (Zhang, 2013). In recent years, it has been adapted and applied to rice fields in saline-sodic land management. Operating as a relatively closed system in rice-duck farming, the use of duck manure as a nutrient source to maintain rice growth promotes the accumulation of SOM and nitrogen (Ebissa et al., 2018). Simultaneously, the activities of duck flocks alter soil structure, improve soil permeability and redox potential (Xu et al., 2017), and facilitate the growth and development of rice roots (Teng et al., 2016). Furthermore, straw returning has been extensively studied as a method to increase SOM (Tian et al., 2015; Yan et al., 2020). In the process of straw returning in saline-sodic land, it can enhance soil porosity and directly improve soil physical properties (Ebrahim Yahya et al., 2022). Additionally, straw decomposition contributes organic acids and other substances that aid the dissolution and release of calcium ions in the soil, thus improving the properties of saline-sodic soils (Zhao, Zhu, et al., 2019). Liu et al. (2017) demonstrated the beneficial impact of rice-duck farming and organic matter return on rice yield in the Yangtze River Basin. However, limited research has focused on combined effects of these two practices on soil improvement in saline-sodic soils. Therefore, the integration of straw returning to the field and rice-duck farming holds significant importance for comprehensive research on saline-sodic land improvement.

Nonetheless, it is worth noting that the long-term or repeated field application of conventional organic inputs may be problematic due to the high turnover of conventional organic materials (Gregorich et al., 2017). Therefore, highly processed organic materials with high soil stability are increasingly being alternative soil amendments to offset the limitations of traditional organic amendments (Amoah-Antwi et al., 2020). In the context of global warming and under the pressure of carbon emissions, natural gas and renewable energy have been prioritized in national policies, and the use of coal derivatives in energy production has been greatly reduced. Lignite possesses several advantages as the main material for soil amendments: (1) it is abundant in

reserves and economical to mine (Qi et al., 2011); (2) it contains a large number of organic compounds and is an acidic material (Amoah-Antwi et al., 2022); (3) it is rich in calcium and magnesium substances (Chassapis & Roulia, 2008). Therefore, lignite is an obvious choice for improving saline-sodic soil. Unfortunately, most humic substances in lignite are bound to calcium and magnesium, which are poorly soluble in water and cannot be directly utilized by soil or crops (Klučáková & Pekař, 2005). Therefore, activation processes are often required to convert these humic substances into water-soluble forms for agricultural applications. Compared with raw lignite, the molecular composition of humic acid in activated lignite has a less aromatic structure but a higher content of lipids, proteins, amino sugars, and carbohydrates (Tang et al., 2020). The abundant functional groups with enhanced activity ensure nutrient retention, thereby improving soil aggregate stability and related structures (Fatima et al., 2021). Tang et al. (2019) developed a novel large-particle activated lignite slow-release fertilizer with good water retention by mechanically extruding activated lignite and conventional fertilizers, which can enhance nutrient absorption capacity and good water retention, thereby promoting plant growth. However, in order to improve saline-sodic soil, activated lignite cannot provide sufficient calcium for the replacement of exchangeable sodium on soil colloids. Exogenous calcium needs to be added to enhance the improvement (Li et al., 2020). Therefore, we combined calcium source materials (mineral elements such as gypsum) with activated acidic lignite to produce lignite composite soil conditioners, which theoretically have the potential to replace exchangeable sodium on the soil surface, reduce soil pH, and improve soil structure and quality to promote plant growth. Hence, it is of great significance to study the improvement of lignite compound modifier on saline-sodic soil.

There are numerous microbial groups in the soil, which play a vital role in facilitating the energy flow and nutrient cycling of the soil ecosystem (Pandey et al., 2014). Recent studies have revealed an inevitable relationship between soil microorganisms and crop yield (Li et al., 2021; Yang et al., 2021). Soil microbial communities are recognized as significant contributors to soil carbon sequestration and stabilization (Zhu et al., 2020). They serve as sensitive indicators, reflecting changes in the quality and quantity of organic material inputs to soil amendment, soil disturbance, and changes in soil physicochemical environment (Zhou, Wang, et al., 2022; Zhou, Xu, et al., 2022). Organic inputs and soil tillage practices impact the structure of soil microbial community by modifying the availability and accessibility of soil nutrients, thereby governing the decomposition and stabilization of SOM decomposition processes (Zhao, Qiu, et al., 2019). Numerous studies have shown that the application of gypsum or farmyard manure alone can increase the SOM content of saline-sodic soil and change the abundance of soil microbial communities (Luo et al., 2018; Shi et al., 2019). However, addressing the more severe challenges associated with saline-sodic land generally requires the implementation of comprehensive measures. In the process of saline-sodic land improvement, the relative contribution of comprehensive measures to the soil microbial community was studied to further determine them. The intrinsic relationship with SOM can

provide valuable information for a better understanding of the underlying mechanisms of SOM sequestration and soil productivity enhancement during saline-sodic soil improvement.

Studies have indicated that straw returning to the field requires a certain period of time to exhibit its effectiveness (Wang et al., 2018; Wang et al., 2021; Yan et al., 2019). Therefore, in this study, we conducted a 5-year conventional organic effects of materials (straw returning to the field and rice-duck farming) and a 2-year lignite compound organic amendment field experiment on saline-sodic soil chemical properties, bacterial communities, and rice yield. Therefore, we aimed to (i) evaluate changes in the soil chemistry and rice yield component treatments under organic material, and (ii) identify the dominant environmental factors that control these relationships across biomes. We hypothesized that (1) the addition of organic materials can increase soil organic matter and improve soil quality and crop yield; (2) soil pH and organic matter content may be the factors driving changes in soil microbial community structure; and (3) yield changes could be associated with specific bacterial microorganisms.

2 | MATERIALS AND METHODS

2.1 | Study area

The field experiment was carried out at the Niuxintaobao Reed Field (123°21' E, 45°14' N), in the western part of the Songnen Plain, Northeast China. The region is characterized by a temperate continental monsoon climate, that is, with dry and cold winter, and arid and windy spring. The average annual rainfall is <400 mm, and the average annual evapotranspiration is more than 1800 mm. This is a typical sodic saline-salt soil, its pH value is generally above 9.5, and its EC is generally above 2 dS·m⁻¹. Na⁺ ions accounted for more than 70% of the total soil cations, and CO₃²⁻ and HCO₃⁻ ions dominated the anions (Zhang et al., 2013). And rice cultivation is popular to use and improves the saline-sodic land.

2.2 | Experiment design and field management

Each test plot covers an area of 10,000 m², and a ridge (width 0.8, height 0.5) is set to block water flow. The pH of the soil used is 9.45, the electrical conductivity of 1:5 soil-water extract (EC) is 3.382 mS cm⁻¹, the exchangeable sodium percentage (ESP) is 38.530%, and SOM content is 2.022 g kg⁻¹. The four treatments are as follows, with three replicates per treatment using a randomized block design, resulting in a total of 12 experimental units.

CK: No amendment input, rice planting started in spring, 2020. Straw removed from the paddy fields after rice harvesting.

LOM: Compound lignite organic modifier (activated lignite and calcium-based substances at a ratio of 1:5) 30 t ha⁻¹, evenly sprayed on the soil surface, and mixed by rotary tillage into 15 cm; it was added only once, rice planting started in spring, 2020. Straw removed from the paddy fields after rice harvesting.

RF: No amendment input, rice planting started in spring, 2017. Straw removed from the paddy fields after rice harvesting.

SW: The full amount of straw (6 t·ha⁻¹) is returned to the field every year with the addition of duck manure (0.75 t·ha⁻¹) through duck stocking, rice planting started in spring, 2017.

The rice variety Jihong 6 was planted, and all seeds were soaked at room temperature for 48 h and germinated under room conditions. Every year on April 10, the germinated seeds are sown in the nursery plastic house. On May 15–May 25 each year, the seedlings were transplanted to the experimental field at a spacing of 13 cm × 30 cm. Before transplanting, nitrogen (N) >28%, phosphorus pentoxide (P₂O₅) >7%, potassium oxide (K₂O) >10% compound fertilizer (Hebei Silicon Valley Fertilizer Co. Ltd.) 500 kg ha⁻¹, ammonium sulfate 300 kg ha⁻¹, and bacterial fertilizer (Microbial Inoculants, Weinan Sunshine High-Tech Co. Ltd.) 300 kg ha⁻¹ were applied in each plot. Only in the SW treatment, ducklings were released to the treated plots at a density of 75 ducklings per plot 25 days after rice seedling transplantation. Each plot was fenced with 50 cm high nylon netting to prevent ducks from escaping. Ducks are raised in the field until October 14. After the rice is harvested, use the rice straw returning machine (Qilifor roller leveler, Qilifor Agricultural Machinery, Changchun, China) to return all the rice straws to the field. All plots were kept flooded to a depth of 3–7 cm, and irrigation was stopped 1 week before the rice harvest.

2.3 | Soil collection and measurement

Soil samples were taken after the rice harvest on 25 October 2021. Three soil samples were taken from each plot of 0–20 cm and 20–40 cm in each layer, and three soil samples from the same layer were mixed to make composite samples. Twelve soil samples were taken from each layer, totaling 24 soil samples. All soil samples were divided into two groups: one group (200 g) was air-dried for soil chemical analysis; another (20 g) was stored at –80°C for DNA extraction.

Soil pH was determined using a pH meter (PHSJ-3F, Shanghai), and soil conductivity was determined using a conductivity meter (DDS-120 W, Shanghai) in a soil-to-water ratio of 1:5, respectively (Rayment & Lyons, 2011). The concentration of soluble Na⁺ was determined by flame photometer (FP6410, Shanghai), and Ca²⁺, Mg²⁺, and SO₄²⁻ were determined by EDTA titration. Soluble CO₃²⁻ and HCO₃⁻ were analyzed by dilute acid titration. Cl⁻ was determined by titration of silver nitrate solution. Sodium adsorption ratio (SAR) and the total alkalinity are calculated using the following equations, where the cation concentration is expressed in mmol_c·L⁻¹ (same as milliequivalents per liter) (Zhang et al., 2021). Soil organic matter was measured both by oxidation with potassium dichromate and by titration with ferrous ammonium sulfate (Nelson & Sommers, 1996).

$$SAR = \frac{[Na^+]}{\sqrt{\frac{Ca^{2+} + Mg^{2+}}{2}}} \text{ (mmol}_c\text{L}^{-1}\text{)}$$

$$\text{Alkalinity} = \text{CO}_3^{2-} + \text{HCO}_3^- \text{ (mmol}_c \text{ L}^{-1}\text{)}$$

After rice harvest, undisturbed soil samples (5-cm long \times 5-cm diameter) were collected from each plot at 0- to 20- and 20- to 40-cm depths on October 25, 2021. Each treatment was replicated three times, and soil cores were used to measure bulk density, which is the mass of dried soil per volume of core (Black & Hartge, 1986).

2.4 | Rice harvest and yield measurement

In early October, the rice was harvested from each plot. After natural drying, we measured the number of grains per panicle, thousand-grain weight, number of holes per square meter, unfilled grains per panicle, number of panicles per hole, and rice yield. Ammonium sulfate solution with a specific gravity of 1.06 was used to separate the number of real grains per panicle and the number of unfilled grains per panicle.

2.5 | DNA extraction, Illumina sequencing, and sequence data processing

According to the manufacturer's instructions, the total DNA of soil microorganisms was extracted using the OMEGA Soil DNA Kit (D5625 01) (Omega Bio-Tek, Norcross, GA, USA), and the molecular size was determined by 0.8% agarose gel electrophoresis. A luminometer quantifies DNA. In this experiment, the highly variable V3V4 region of bacterial 16S rRNA gene with a length of about 468 bp was selected for sequencing. PCR amplification selects bacterial 16S rDNAV3V4 region-specific primers, 338F (5' barcode+ACTCC-TACGGGAGGCAGCA 3') and 806R (GGACTACHVGGGTWTCTAAT 3'). After PCR, the products are further purified and pooled in equimolar concentrations to use the sequencing program on the platform. For eligible libraries, we performed 2×250 bp paired-end sequencing on an Illumina NovaSeq machine using the NovaSeq 6000 SP Reagent Kit (500 cycles). Microbiome bioinformatics were performed with QIIME 2.2019.4 (Bolyen et al., 2019) with slight modification according to the official tutorials (<https://docs.qiime2.org/2019.4/tutorials/>). Taxonomy was assigned to ASVs using the classify-sklearn naïve Bayes taxonomy classifier in feature-classifier plugin (Bokulich et al., 2018) against the silva_132 99% OTUs reference sequences. Sequences were deposited in the NCBI Sequence Read Archive under BioProject accession number PRJNA825351.

2.6 | Random forest regression model

Random forest regression was used to identify significant predictors of microbial composition on rice yield and use the randomForest package on the R platform (<http://cran.r-project.org>). We calculated the significance of predictors and the overall variance explained using 1000 trees with 500 replications. During the process of constructing

random forest models at the OTU level, rare OTUs with relative abundances of <0.05% were removed. A ranking is performed for each OTU, and the OTU whose cross-validation error rate is lowest is selected as an OTU predictor through random forest.

2.7 | Statistical analysis

All statistical analyses were performed in R software. We performed the Levene test on raw data or log-transformed data before performing ANOVA and LSD test to satisfy the premise of homoscedasticity. Linear discriminant analysis (LDA) effect size (LEfSe) was used to calculate the microbial biomarkers, with log LDA scores >3.3 and Kruskal–Wallis test $p < 0.05$. In addition, nonparametric multivariate analysis of variance (ANOSIM) and NMDS analysis were performed using the “vegan” package in the R environment to reveal the effects of different levels of disturbance on bacterial community structure. Correlations between bacterial communities and soil chemistry were performed by the Mantel test and distance-based redundancy analysis (db-RDA) in the R environment using the “vegan” package. Soil chemical properties significantly associated with bacterial communities are marked with an asterisk ($p < 0.05$ for “*”, $p < 0.01$ for “**”).

3 | RESULTS

3.1 | Soil physical and chemical properties

In 0–20 cm soil layer, compared with CK, LOM treatment significantly decreased soil pH, EC, total alkalinity, and SAR ($p < 0.05$). The treatment of SW significantly decreased soil pH and total alkalinity as compared with RF. Compared with CK, RF significantly decreased SAR, pH, and total alkalinity; the pH in LOM was significantly reduced by 1.29 compared with SW. Soil bulk density varied significantly among treatments, with the largest CK and the smallest SW. In 20–40 cm soil layer, compared with other treatments, LOM treatment decreased pH and total alkalinity; RF treatment increased soil total alkalinity. The bulk density was opposite to that of 0–20 cm soil layer. With the increase in planting years, the lower soil bulk density showed an increasing trend (Figure 1).

In 0–20 cm soil layer, compared with CK, LOM treatment significantly increased SOM content by 5.02 g kg^{-1} , and compared with RF, SW treatment significantly increased SOM content by 4.2 g kg^{-1} .

3.2 | Soil bacterial community composition characteristics

In this study, major bacterial phylums/classes (average relative abundance higher than 5%) were Proteobacteria (36.46%), Chloroflexi (14.55%), Bacteroidetes (11.10%), Actinomycetes (10.81%), Firmicutes, and the phylum Acidobacteria (10.74%), and Acidobacteria (6.18%) were present in all soil samples. In 0–20 cm soil layer, LOM

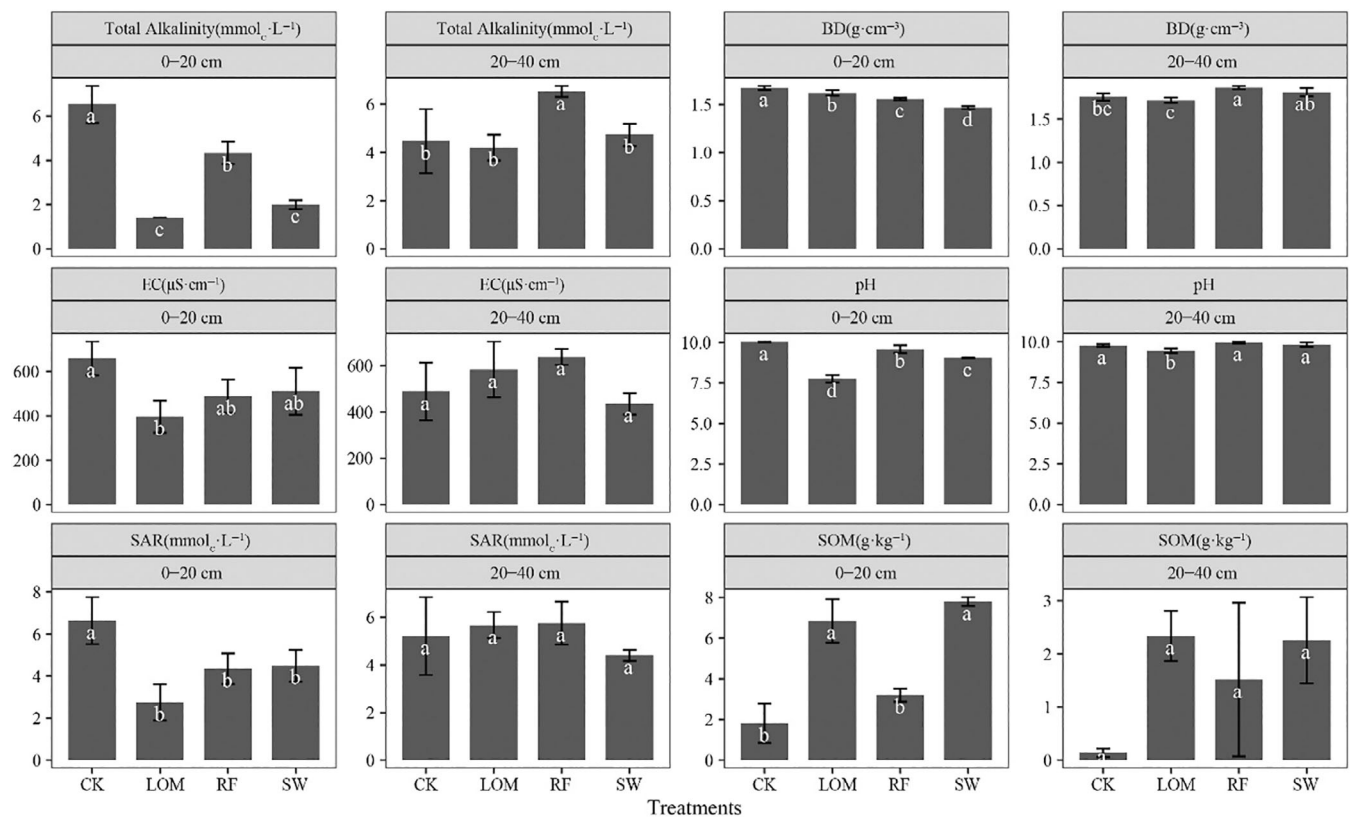


FIGURE 1 Effects of different improvement treatments on soil physical and chemical properties, mean \pm standard error is provided for each treatment ($n = 3$), and different letters indicate significant differences by the LSD test ($p < 0.05$).

treatment significantly increased the relative abundance of Proteobacteria and decreased the relative abundance of Chloroflexibacteria as compared with CK, and SW treatment significantly increased the relative abundance of Bacteroidetes and Firmicutes ($p < 0.05$) (Figure 2a). At 20–40 cm, the relative abundance of Bacteroidetes increased in SW compared with CK, and the relative abundances of Chloroflexi and Actinobacteria decreased significantly (Figure 2b). LEfSe analysis revealed differentially processed microbial biomarkers from phylum to genus level. It can be seen from the data that Bacteroidetes and Firmicutes are the dominant biomarkers after straw returning; Epsilonbacteraeota is the main biomarker of LOM in the soil of 0–40 cm as compared with CK; and RF did not have major landmark organisms at the phylum level (Figure 2c).

3.3 | Soil bacterial diversity and correlations with soil chemical properties

Soil bacterial alpha diversity was calculated, including Chao1, Shannon, Observed_species, and Pielou_e, etc. In 0–20 cm soil layer, the Shannon index and Pielou_e index were significantly reduced compared with CK and RF, in SW and LOM treatments (Table 1). In 20–40 cm soil layer, the Observed_species index in LOM treatment was significantly higher than that in RF and SW, while the Goods_coverage index was significantly lower. The Pielou_e index in SW treatment

was significantly lower than that of the other treatments (Table 2). This indicated that the diversity and uniformity of soil microbial community decreased to a certain extent after adding organic matter amendments or returning straw to the saline-sodic soil.

The ANOMIS test and NMDS analysis based on the Weighted_unifrac algorithm for soil bacterial communities showed that different treatments affected soil bacterial communities. Different treatments had their own unique community structure (Figure 3a–c). The microorganisms treated with SW and LOM were significantly different from CK ($R > 0.5$, $p < 0.05$) (Table 3). Compared with RF, SW and LOM tended to be different ($0.3 < R < 0.5$, $p < 0.05$). This showed that the bacterial community of rice soil in saline-sodic soil could be changed with the extension of rice planting time, the return of straw, and the addition of organic matter improver. However, planting rice alone without organic matter input for 3 years did not significantly change the microbial structure.

Mantel analysis showed that soil pH, CO_3^{2-} , HCO_3^- , SO_4^{2-} , SOM, and BD were significantly correlated with bacterial community structure ($p < 0.05$) (Figure 4). After screening by variance inflation factor (VIF), the 0–40 cm db-RDA (Figure 3d) showed that soil pH, HCO_3^- , CO_3^{2-} , Mg^{2+} , and SOM had the most important regulatory effects on bacterial community structure under the input of improved materials ($p < 0.05$). In addition, the db-RDA (Figure 3e) at 0–20 cm soil layer showed that the regulation of pH, EC, HCO_3^- , CO_3^{2-} , Na^+ , and SOM on bacterial community structure was the most important

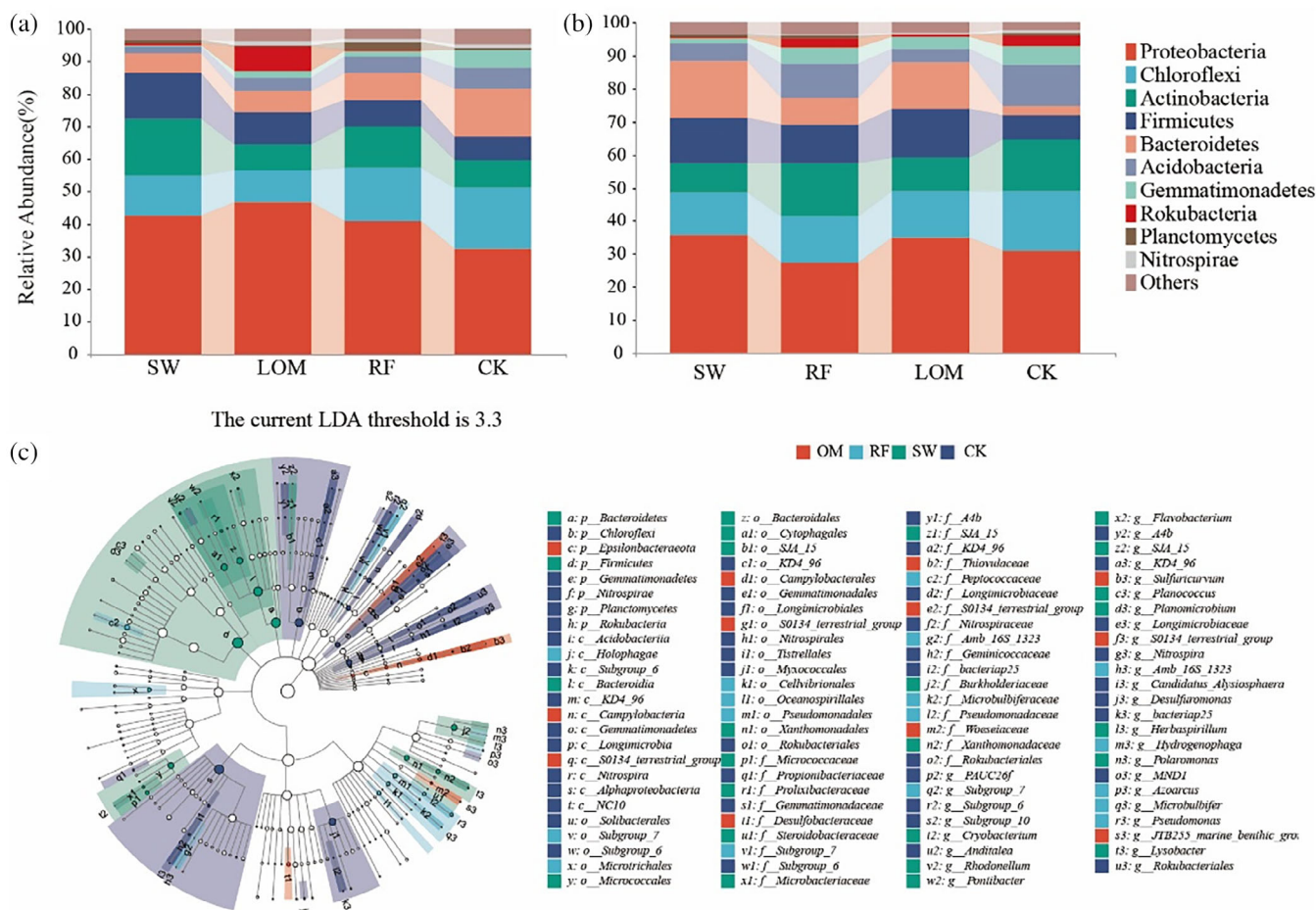


FIGURE 2 The composition of the soil bacterial community and the effect of treatment on the community in two soil depths. Biomarkers in different treatments from phylum level to genus level (c) are based on LDA effect size (LEfSe) analysis with log-linear discriminant analysis (LDA) score >3.3 and Kruskal–Wallis test $p < 0.05$. [Colour figure can be viewed at wileyonlinelibrary.com]

TABLE 1 Alpha diversity index of 0–20 cm soil layer soil bacteria.

0–20	CK	LOM	RF	SW
Chao1	4486.327 ± 195.821a	3861.927 ± 143.327a	4364.843 ± 486.189a	3565.327 ± 630.821a
Shannon	10.293 ± 0.149a	9.22 ± 0.459b	9.988 ± 0.105a	9.159 ± 0.498b
Observed_species	4010.133 ± 167.252a	3541.133 ± 171.588a	3871.933 ± 400.268a	3253.433 ± 493.614a
Faith_pd	427.697 ± 8.314a	396.810 ± 14.055a	429.235 ± 43.137a	370.384 ± 46.694a
Goods_coverage	0.982 ± 0.001a	0.986 ± 0.001a	0.982 ± 0.004a	0.987 ± 0.004a
Simpson	0.998 ± 0a	0.985 ± 0.014a	0.996 ± 0.001a	0.990 ± 0.004a
Pielou_e	0.860 ± 0.008a	0.782 ± 0.036b	0.838 ± 0.013ab	0.786 ± 0.036b

Note: Mean ± standard error is provided for each treatment ($n = 3$), and different letters indicate significant differences by the LSD test ($p < 0.05$).

($p < 0.05$); however, the db-RDA (Figure 3f) at 20–40 cm soil layer showed that pH, K^+ , Mg^{2+} , and SOM had the most important regulatory effect on bacterial community structure ($p < 0.05$).

3.4 | Rice grain yield and yield components

After harvest, total grain yield, 1000-grain weight, number of full grains per panicle, seed-setting rate, number of panicles per hole, and

number of holes per square meter for rice were measured to determine planting year and improvement effect of different organic material applications (Table 4). The results showed that different treatments significantly affected rice grain yield and yield components, specifically, LOM > SW > RF > CK ($p < 0.05$). The maximum yield 7879.910 kg ha⁻¹ was recorded in LOM treatment, while that in CK was only 184.330 kg ha⁻¹, and the yield components except 1000-grain weight were significantly higher than that in CK. The grain yield of SW was significantly higher than that of RF, and the grain

TABLE 2 Alpha diversity index of 20–40 cm soil layer soil bacteria.

20–40	CK	LOM	RF	SW
Chao1	3620.96 ± 300.234a	4449.133 ± 409.493a	3365.673 ± 517.013a	3288.363 ± 531.552a
Shannon	9.76 ± 0.244a	9.722 ± 0.061a	9.73 ± 0.286a	9.035 ± 0.5a
Observed_species	3220.267 ± 256.939ab	3911.833 ± 208.753a	3032.4 ± 448.484b	2965.1 ± 418.872b
Faith_pd	362.801 ± 29.974a	418.926 ± 9.063a	346.926 ± 42.597a	342.369 ± 63.772a
Goods_coverage	0.986 ± 0.001ab	0.981 ± 0.003b	0.988 ± 0.003a	0.988 ± 0.004a
Simpson	0.997 ± 0.001a	0.994 ± 0.001a	0.997 ± 0.001a	0.99 ± 0.007a
Pielou_e	0.838 ± 0.013a	0.815 ± 0.002ab	0.842 ± 0.009a	0.784 ± 0.03b

Note: Mean ± standard error is provided for each treatment (n = 3), and different letters indicate significant differences by the LSD test (p < 0.05).

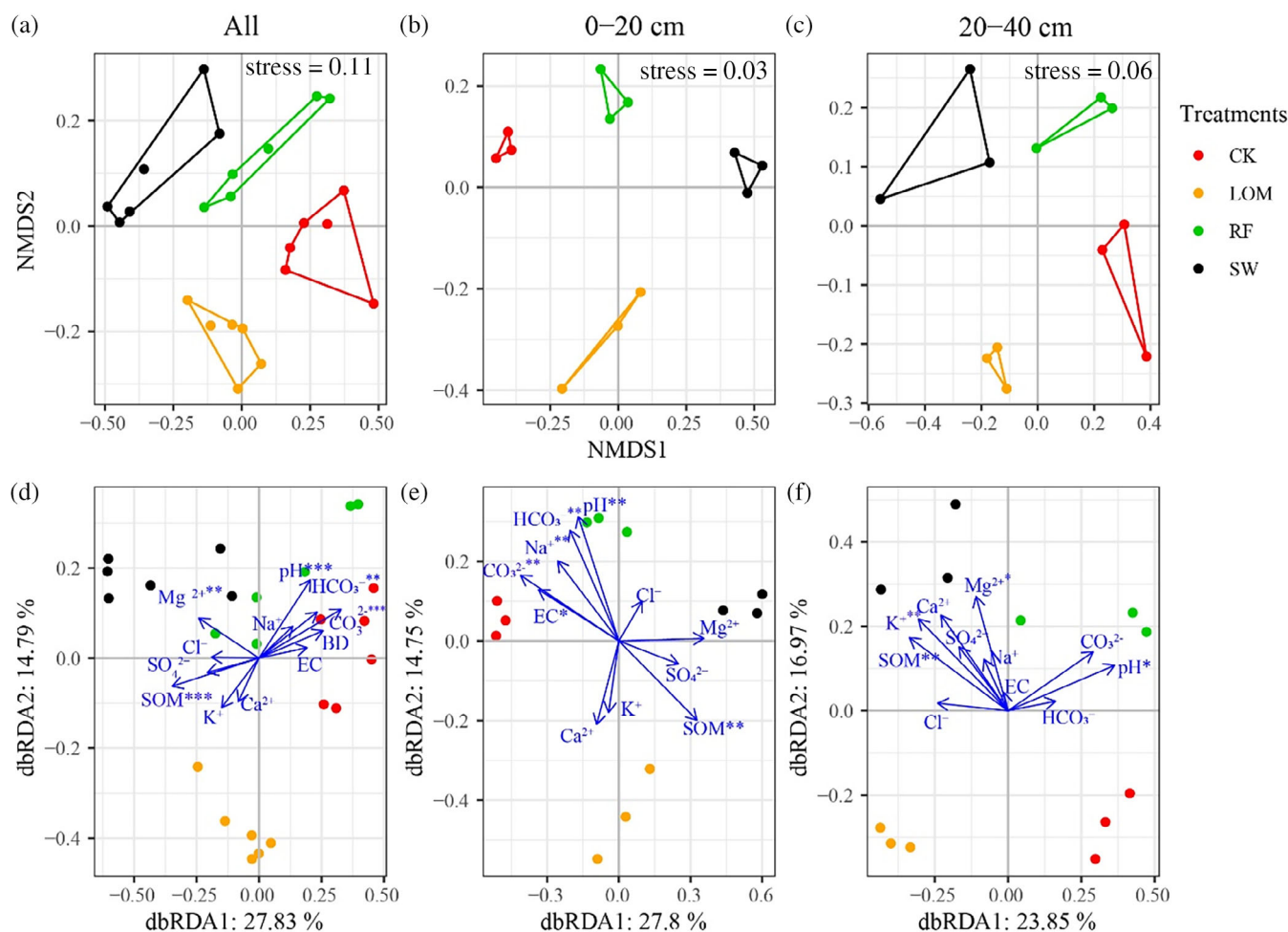


FIGURE 3 Beta diversity of soil bacteria in different treatments (a–c) and the redundant analysis (db-RDA) of the bacterial community and soil properties (d–f). NMDS analysis was applied to visualize soil bacterial diversity using weighted_unifrac distances. There was significant environmental factor involvement in db-RDA when tested by Envfit (*p < 0.05; **p < 0.01; ***p < 0.001). [Colour figure can be viewed at wileyonlinelibrary.com]

number per panicle and panicle number per hole in SW were significantly increased (p < 0.05). In addition, the yield in LOM was significantly higher than that in SW by 11.35% (p < 0.05), and the number of real grains per panicle in LOM was significantly higher than that in SW.

3.5 | Random forest regression model to analyze the effect of flora on rice grain yield

The consortium of 22 OTUs from 0 to 20 cm soil layer with low cross-validation error rates were selected to predict rice yield, and the

result was 58.25% explained variance (Figure 5). These OTUs include Actinobacteria (2 OTUs), Bacteroidetes (4 OTUs), Firmicutes (1 OTU), and Proteobacteria (9 OTUs), Chloroflexi (4 OTUs), Epsilonbacteraeota (1 OTU), and Deinococcus-Thermus (1 OTU). Heat map analysis showed that after the organic material application, the bacterial species with yield relevance changed significantly, and each had its unique flora. Paenisporosarcina in Firmicutes and Sulfurimonas in Epsilonbacteraeota were abundant in high-yielding samples. At the same time, there are also populations with different roles in the same phylum. After the correlation analysis between the relative abundance of selected OTUs and rice yield, the three OUT showed a significant

positive correlation with rice yield. Longobacteriaceae of Bacteroidetes, Hydrogenaceae, and Xanthomonas of Proteobacteria ($p < 0.05$, Figure 6).

4 | DISCUSSION

4.1 | Soil physical and chemical properties

In this study, SOM significantly increased in both SW and LOM of 0–20 cm soil layer, leading to a substantial reduction in soil salt content, total alkalinity, and soil pH. This can be attributed to the continuous input of organic material, which are decomposed by microorganisms to produce organic acids. These organic acids can dissolve and release calcium ions from the soil, leading to a calcium-sodium replacement process (Qadir et al., 2003). Additionally, the application of straw and manure promotes soil aggregation and gradually restored soil structure (Benbi & Senapati, 2010). This process accelerates the leaching of salts, ultimately improving the saline-sodic land. Similarly, the compound lignite organic modifier also exhibited a comparable effect on soil improvement. This is because the compound modifier provides inorganic calcium and magnesium ions, and the activated lignite humic acid activity is enhanced. Consequently, this further facilitated the release of soil calcium ions (Chassapis & Roulia, 2008), promoting the replacement of exchangeable sodium in the soil exchange complex. As a result, the soil alkalinity decreased, and pH significantly declined, creating favorable conditions for organic matter accumulation and nutrient release. Sodic soils with high exchangeable Na^+ on colloidal surfaces tend to have reduced capacity to retain decomposition products since organic mineral interactions are primarily dependent on

TABLE 3 Statistical test of Anomist to analyze the effects of different improved treatments on soil bacterial community compositions.

Samples	Anomist ^a	
	R	p-Value
All	0.516	0.001
OM vs RF	0.394	0.013
OM vs SW	0.411	0.02
OM vs CK	0.683	0.005
RF vs SW	0.493	0.019
RF vs CK	0.231	0.06
SW vs CK	0.894	0.002

^aThe significance of differences between groups was tested by similarity analysis (Anosim). At $0.5 < R < 0.75$, $p < 0.05$ indicates a significant difference; at $0.3 < R < 0.5$, $p < 0.05$ indicates a trend, and at $R < 0.3$, there is no difference.

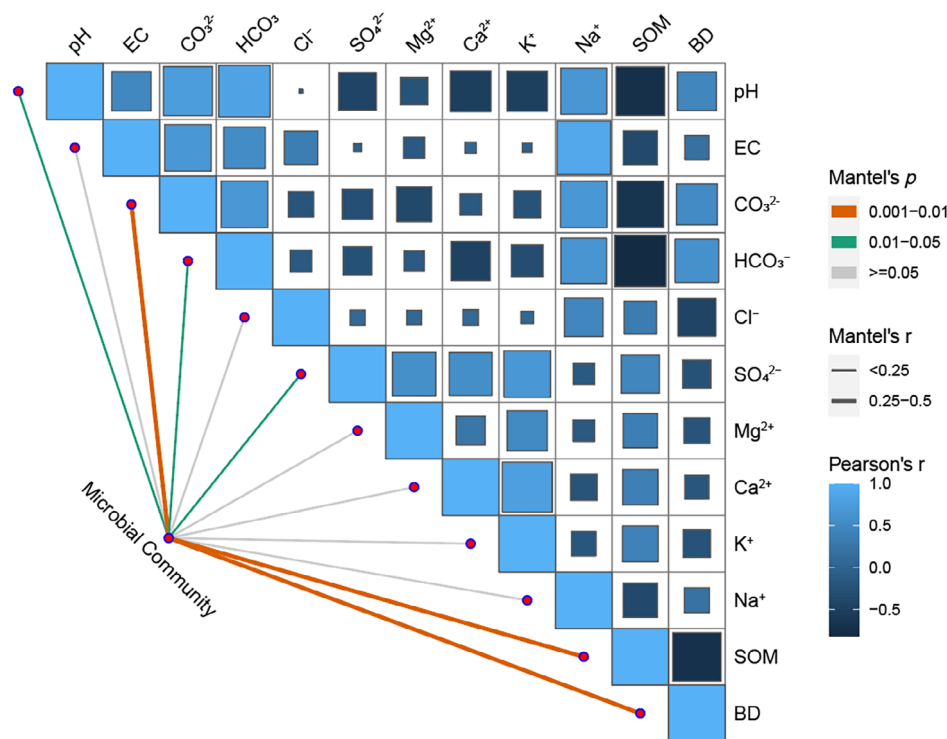


FIGURE 4 Mantel analysis in soil microbial community and soil physicochemical properties. [Colour figure can be viewed at wileyonlinelibrary.com]

TABLE 4 Rice yield and yield components in 2021.

Treatments	Yield	1000-grain weight	Seed-setting rate	Real grains per ear	Holes per square meter	Ears per hole
CK	184.330 ± 45.563d	15.767 ± 3.436b	0.683 ± 0.114b	36.750 ± 4.548d	8.000 ± 1.000b	4.000 ± 0d
RF	2553.587 ± 142.426c	18.000 ± 1.000ab	0.813 ± 0.015ab	58.040 ± 2.646c	22.333 ± 1.155a	11.000 ± 1.000c
LOM	7879.910 ± 625.252a	20.467 ± 1.021ab	0.923 ± 0.032a	110.537 ± 11.806a	23.333 ± 1.155a	15.000 ± 1.000b
SW	6985.587 ± 628.535b	22.167 ± 1.457a	0.870 ± 0.104ab	80.880 ± 4.190b	20.667 ± 3.055a	19.000 ± 1.000a

Note: Mean ± standard error is provided for each treatment ($n = 3$), and different letters indicate significant differences by the LSD test ($p < 0.05$).

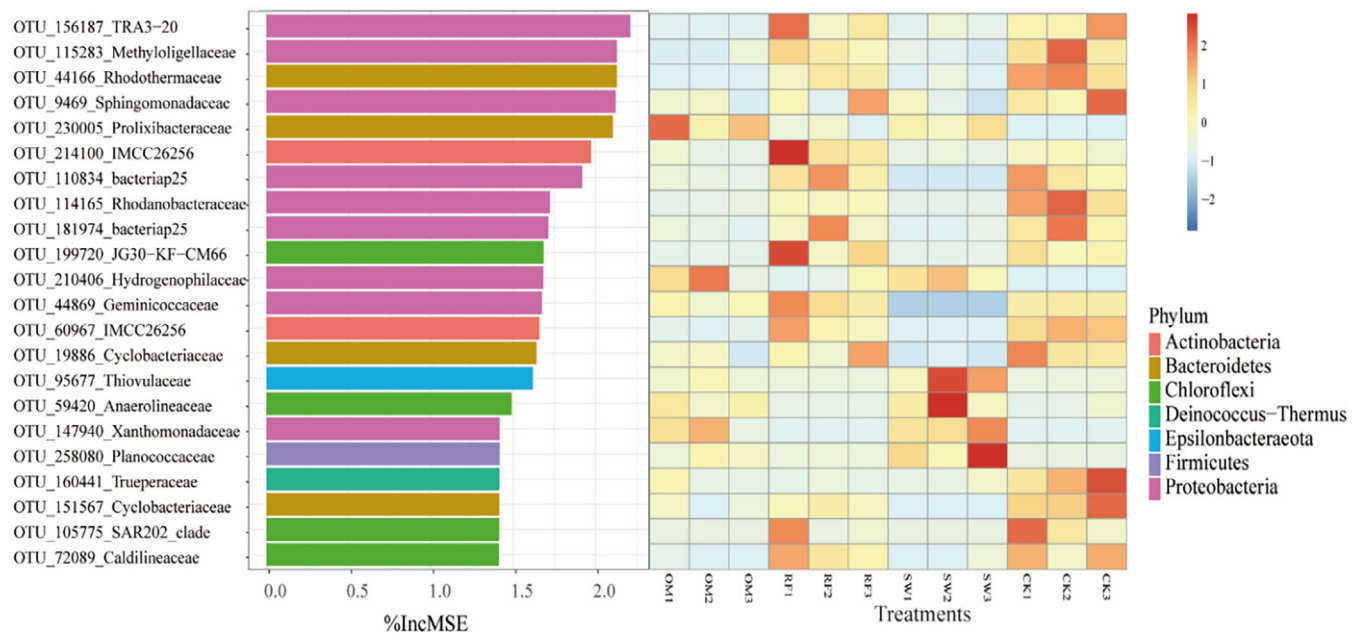


FIGURE 5 Prediction of the rice grain yield through the bacterial community in the soil depth of 0–20 cm at operational taxonomic unit (OTU) level based on the random forest regression model. [Colour figure can be viewed at wileyonlinelibrary.com]

cation bridges involving Ca^{2+} rather than Na^+ (Naidu & Rengasamy, 1993). The replacement of sodium with calcium promotes the formation of stable connections between clay particles and organic matter (Feng et al., 2021), thereby reducing the loss of soil organic matter. This process enhances the efficiency of calcium and sodium replacement (Cubillos-Hinojosa et al., 2017), effectively washing out excess salt ions and improving soil physical and chemical properties, such as soil pH, salinity, organic matter, and soil structure.

At the 20–40 cm soil layer, only the LOM treatment resulted in reduced pH and total alkalinity of the soil, while the RF treatment led to a significant increase in total alkalinity. This difference may be due to the high ionic strength in the leaching compound modifier. However, under the RF treatment, the total alkalinity increased, indicating that soluble ions were leaching into the subsoil, potentially creating a barrier layer that could impact later yield increase. These results demonstrate that LOM rapidly improves saline-sodic soil and increases SOM content compared with traditional straw returning and farmyard manure for a long time.

Additionally, the results revealed that the soil BD decreased gradually over time, attributed to continuous disturbance of cultivation and of organic matter input (Schjøning et al., 1994). However, in deeper soil layers, mechanical disturbance and compaction led to increased soil BD, while the input of organic matter helped alleviate this increase (Osunbitan et al., 2005).

4.2 | Soil microbial composition and structure

Bacteria are the predominant microorganisms in saline-sodic soils. Excessive salinity-sodicity and poor physical soil stability are dispersive characteristics that have negative impacts on microbial processes (Yuan et al., 2007). Therefore, improvements in soil physicochemical properties resulting from reduced salinity-sodicity can have positive effects on microbial growth and activity (Setia et al., 2011). Organic matter degradation can enhance the soil microbiome involved in nutrient cycling. Our findings revealed that the addition of straw and duck

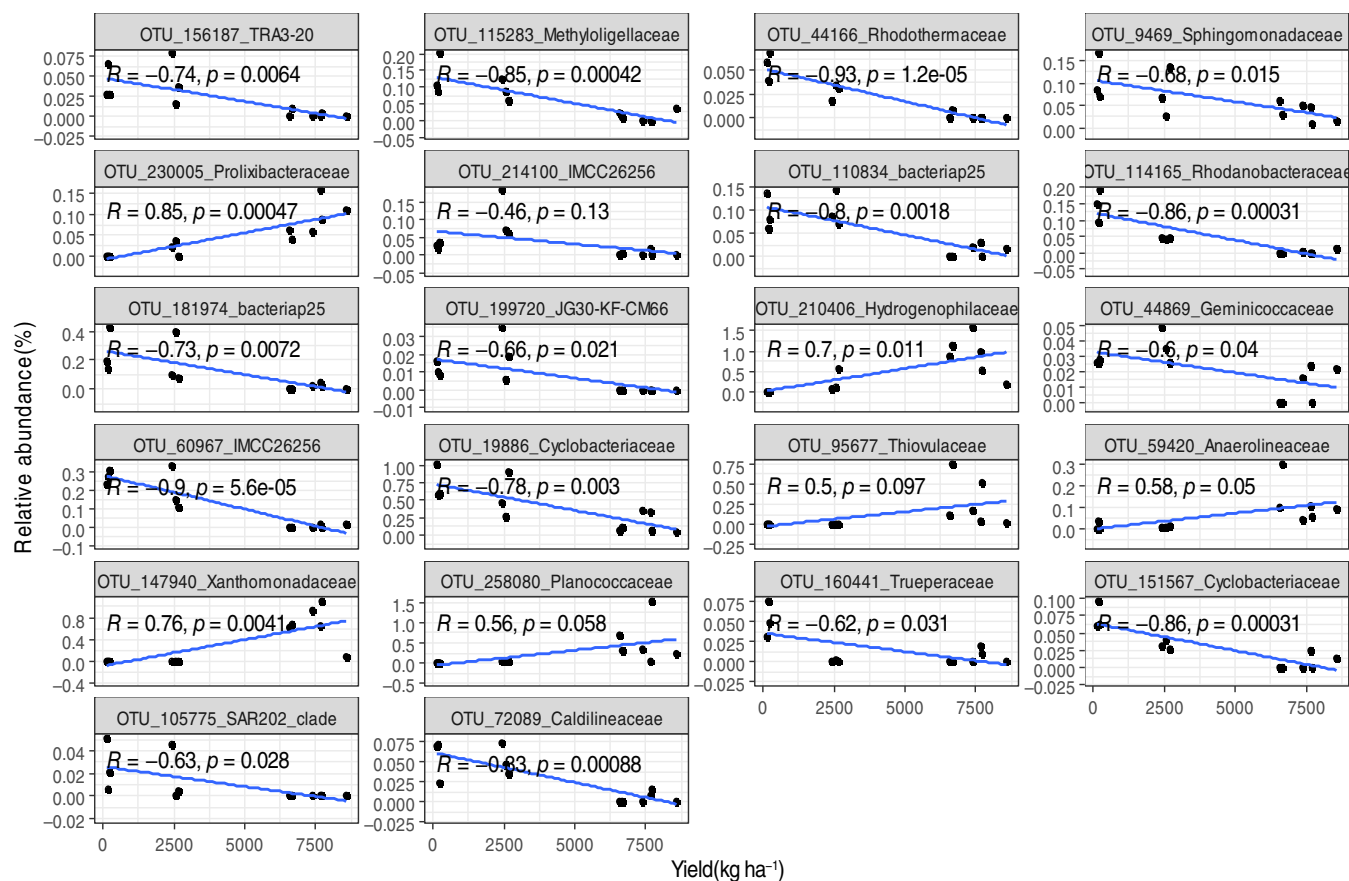


FIGURE 6 Pearson correlation coefficients between selected OTUs and rice yield based on the random forest regression model. [Colour figure can be viewed at wileyonlinelibrary.com]

manure increased the abundance of Bacteroidetes and Firmicutes in 0–20 cm soil layer, while the compound lignite modifier treatment significantly increased the relative abundance of Proteobacteria. These observations may be attributed to the specific species of soil organic matter, as microbial species' relative abundances can be influenced by carbon availability (Eilers et al., 2010). Manure, for instance, may harbor a high number of Bacteroidetes, while Bacteroidetes and Firmicutes play an important role in rice straw decomposition (Gavande et al., 2021; Ji et al., 2018), Proteobacteria usually considered to be an eutrophic microorganism with an R-type growth strategy, it is abundant in nutrient-rich soils (Zhou et al., 2017); Singh et al. (2022) found that Proteobacteria also occupied during the ecological restoration of lignite mines important role. Epsilonbacteraeota, an iconic microorganism in lignite, is an autotrophic, motile, thermophilic chemoautotroph that may assimilate nitrogen, through the use of various functional ammonium or environmental nitrates and metabolites. This is supported by the nutrient-retaining properties of lignite (Waite et al., 2017).

In this study, the bacterial communities were significantly influenced by the different treatments. The results demonstrated that the Shannon index decreased after improvement and cultivation, which is consistent with the findings of Zhao et al. (2018). This decline could be attributed to the altered soil structure after cultivation and the

decreased diversity and uniformity of microorganisms. A significant relationship was observed between soil chemical properties and bacterial community structure. This relationship could be attributed to the variations in soil properties resulting from different amelioration methods. SOM and carbonates played a dominant role in driving the differentiation of soil samples in 0- to 40-cm depth. SOM serves as the primary source of energy and nutrients for soil microorganisms, and changes in the microbial community are strongly influenced by it (Moreau et al., 2019). The decrease in carbonate content reduces soil alkalinity and improves soil structure, which, in turn, affects the structure and growth of soil microorganisms.

4.3 | Rice yield

Due to high Na^+ content and low organic matter content, saline-sodic soils typically result in low crop yields (Qadir et al., 1996). In this study, we compared the effect of 5 years of duck manure application combined with straw returning to the field to 2 years of lignite compound modifiers for reclaiming severely saline-sodic soil under rice cultivation. The results demonstrate that rice cultivation alone is also an effective measure to improve saline-sodic land (Huang et al., 2022; Xu et al., 2020). In the RF treatment, as the planting years increased,

the soil was continuously flushed with fresh water, leading to a certain decrease in soil salinity. However, the SOM did not increase, which was affected by the soil properties and the harsh soil environment, resulting in the survival of rice seedlings after transplantation. This significantly reduced the yield, which corresponds to the number of holes per square meter in the yield component, a significant factor contributing to the yield challenge (Hakim et al., 2014). Under the SW treatment, the long-term rice with the addition of straw and duck manure improved soil structure, enhanced the flushing effect, and provided nutrients (Yan et al., 2019). Importantly, the rice yield in the LOM treatment was significantly higher than that in SW treatment. Further analysis shows that the number of seeds per panicle and the seed-setting rate of LOM treatment are significantly higher than that of SW treatment. This may be attributed to the lignite compound organic amendment, which not only contributes to soil structure and enhances the survival and tillering of rice seedlings but also decompose to provide nutrients and absorbs soil nutrients, preventing nutrient loss and improving nutrient utilization efficiency, thereby enhancing crop yield in saline-sodic soil (Tran et al., 2015).

Both soil properties and certain bacterial phyla may contribute to yield variability (Song et al., 2022). We selected specific bacterial communities that were used to predict rice yield, explaining 58.25% of the variance, illustrating the importance of key species in maintaining soil function. According to the correlation analysis, the abundance and diversity of bacterial community were positively correlated with yield, indicating that the stability and balance of bacterial community play an important role in improving yield. Meanwhile, we found that some bacterial genera were significantly positively correlated with yield, the relative abundances of the family Longobacteriaceae of Bacteroidetes, Hydrogenaceae, and Xanthomonas of Proteobacteria were positively correlated with yield, which may increase yield by promoting plant growth or inhibiting pathogens. Similarly, it has been reported that OTUs belonging to Firmicutes in the modified rice soil after gypsum and brackish water freezing application were aggregated in low-yielding samples to predict rice yield, while high-yielding samples were enriched in Proteobacteria and Bacteroidetes OTUs (Zhang et al., 2021).

5 | CONCLUSION

The physicochemical properties and bacterial communities of saline-sodic paddy soil were characterized under different organic materials applications and varying planting durations. The results demonstrated that the rice yield in saline-sodic soil increased with the increase in planting time. The addition of organic materials can better improve the yield of rice, and the addition of organic materials can significantly increase the content of SOM, leading to a reduction in total alkalinity and pH of the saline-sodic soil paddy. The changes in soil properties also influenced the composition of the soil microbial community. The relative abundances of Longobacteriaceae in Bacteroidetes, Hydrogenaceae, and Xanthomonas in Proteobacteria were positively correlated with yield. Additionally, the lignite organic compound modifier

results in the highest yield and reduces the reclamation period. This demonstrates that the lignite compound organic modifier offers an alternative for economically and environmentally sustainable development for improving saline-sodic soils.

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CONFLICT OF INTEREST STATEMENT

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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