agronomy

Article

Response of Soil Fungal Community in Coastal Saline Soil to Short-Term Water Management Combined with Bio-Organic Fertilizer

Meng Xiao [1,2], Cheng Chen [1], Rongjiang Yao [2], Xiuping Wang [3] and Guangming Liu [2,*]

[1] Henan Small Watershed Ecological Water Conservancy Engineering Technology Research Center, Yellow River Water Conservancy Vocational and Technical College, Kaifeng 475000, China; xiaomeng@yrcti.edu.cn (M.X.)
[2] State Key Laboratory of Soil and Sustainable Agriculture, Institute of Soil Science, Chinese Academy of Sciences, Nanjing 210018, China
[3] Institutes of Coastal Agriculture, Hebei Academy of Agriculture and Forestry Sciences, Tangshan 063299, China
* Correspondence: gmliu@issas.edu.cn

Abstract: This study aimed to elucidate the response of soil microbial communities to saline soil amelioration via biological organic fertilizer. A year-long experiment was conducted on coastal saline soil, employing water and fertilizer strategies. Three treatments were compared: dry field (control, CK), paddy field (W), and combined dry and irrigated fields with biological organic fertilizer (BW). Soil DNA was extracted and sequenced using high-throughput methods, revealing significant reductions in soil electrical conductivity (EC) and pH with W and BW treatments. Moreover, the BW treatment notably increased soil organic carbon content by 17.2%, as well as soil urease and alkaline phosphatase activity. Fungal community richness increased, with the BW treatment showing a 36% rise in the ACE index and a 24% increase in the Shannon index, while the Simpson index decreased by 59%. Dominant fungal phyla were Ascomycota, Mortierellomycota, and Basidiomycota, with Basidiomycota prevailing at the genus level. Redundancy analysis (RDA) indicated that soil pH, EC, and organic carbon were key determinants of fungal community distribution, with the BW treatment correlating negatively with pH and salt and positively with soil organic carbon (SOC). Fungal functional groups varied among treatments, with saprophytic fungi predominating, but the BW treatment showed a higher relative abundance of animal pathogenic fungi. In summary, the integration of biological organic fertilizer with flooding ameliorates soil properties and influences the changes in soil fungal community structure and function in the short term. These results could enhance the scientific basis for the efficient utilization and development of saline soil resources in coastal areas.

Keywords: dry land to water field; biological organic fertilizer; coastal saline soil; soil fungal community structure; functional gene prediction

check for updates

Citation: Xiao, M.; Chen, C.; Yao, R.; Wang, X.; Liu, G. Response of Soil Fungal Community in Coastal Saline Soil to Short-Term Water Management Combined with Bio-Organic Fertilizer. *Agronomy* **2024**, *14*, 1441. https://doi.org/10.3390/agronomy14071441

Academic Editor: Nikolaos Monokrousos

Received: 25 May 2024
Revised: 14 June 2024
Accepted: 25 June 2024
Published: 2 July 2024

Copyright: © 2024 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https://creativecommons.org/licenses/by/4.0/).

1. Introduction

Soil salinization has become a global constraint affecting land production, food security, and the healthy development of the ecological environment [1]. The remediation process of saline soil becomes complex and variable due to typical characteristics such as poor aggregate structure, poor water and air permeability, and poor fertilizer retention caused by soil salinization [2,3]. China, for instance, is the third-largest saline–alkali land distribution country in the world [4]. According to the statistics of the World Food and Agriculture Organization, China has approximately 2×10^8 hm^2 of contiguous saline–alkali wasteland, accounting for more than 6% of the country's cultivated land area, with the salinized farmland area distributed in coastal and North China Plain being about 6×10^4 hm^2 [5,6].

Saline soil in this region has typical soil compaction, high soil pH and salt content, and low nutrient availability saline–alkali barriers, which seriously affect local agricultural production and sustainable economic development [7,8]. Therefore, the development of efficient and sustainable saline–alkali soil improvement measures and models is of great practical significance to improve the utilization rate of land resources and cultivated land productivity in coastal areas.

Soil microorganisms, as the core driving force of soil nutrient mineralization and decomposition, play a positive role in promoting nutrient cycling, compound degradation, plant growth, and disease control [9,10]. In addition, the distribution and composition of soil microbial species determine soil nutrient storage, structural stability, and land productivity, and are also highly susceptible to various environmental factors [11]. Soil salinity is a key factor affecting the stability of soil microbial community structure and species diversity [12]. Studies have pointed out that soil salinization enhances the competitiveness of soil-specialized microbial communities and reduces the richness and diversity of soil microbial communities [13,14]. In heavily saline–alkali soil, fungal communities are reported to be more saline–alkali tolerant than bacterial communities, and their composition is not easily affected by the external environment [15,16]. However, some studies have pointed out that fungal communities contribute greatly to disease or drought resistance [17]. Particularly in lightly or moderately saline soils, changes in the external environment may lead to changes in fungal communities, such as irrigation affecting the activities of microorganisms, resulting in increased metabolism and increased abundance of anaerobic methanogenic communities [18,19]. Moreover, the increase in exogenous organic nutrients will also trigger the instant response of soil microbial flora. For example, fertilization can promote the decomposition and denitrification of organic matter, directly increase microbial growth nutrients, and stimulate microbial activities [20,21]. However, under the combined regulation of multiple measures, the response characteristics and potential mechanisms of microbial communities, especially bacterial communities, are still unclear.

Studies have shown that water leaching and the addition of exogenous organic materials are both effective measures to rapidly reduce salinity and restore soil fertility in the topsoil [22,23]. Among them, irrigation measures have achieved wide recognition and effect in the practice of agricultural production activities [8,24]. Leaching plays a role in leaching salt and pressing alkali quickly and also indirectly affects the physical properties, chemical properties, and biological processes of regional farmland soil [25]. In addition, bio-organic fertilizer, as a common organic material, can increase the nutrient storage capacity in the topsoil layer and regulate soil structure, and many studies have reported the improvement effect of its application in saline soil [26,27]. Studies have shown that the addition of bio-organic fertilizer not only increases soil organic matter and the total amount of cation exchange content in the topsoil layer but also reduces soil pH value and salt content and displaces toxic saline–alkali ions such as Na^+ and K^+ [8,28]. However, existing studies mostly focus on the soil effect under a single measure and take the change in the soil's basic physical and chemical properties as the main measure, ignoring the response characteristics and driving mechanism of microorganisms under multiple control measures. Therefore, we hypothesized that (1) the addition of bio-organic fertilizer and irrigation alleviated the saline–alkali characteristics of coastal saline soil and improved the physical and chemical properties of soil and (2) fungal communities responded to soil environmental changes under fertilizer addition and irrigation practices. At the same time, this study aimed at (1) analyzing the changes in soil environment under fertilizer addition and irrigation measures, (2) revealing the response characteristics of soil fungal community to organic fertilizer and irrigation in coastal saline soil, and (3) exploring the driving factors and mechanism of community structure change in the sanitary area after adding exogenous materials. This study will help us understand the effects of new, improved materials and their combined organic fertilizer applications on soil properties and microbial communities.

2. Materials and Methods

2.1. Site Description

The study area was situated on a farm in Ninghe District, Tianjin, China (117°30′4″ E, 39°25′54″ N). It lies at the confluence of the alluvial plain, characterized by low and flat terrain sloping from the Middle East to the south. The area experiences a warm temperate monsoon continental climate marked by significant monsoons, distinct seasons, and ample sunlight. The average annual precipitation is 590 mm, occurring mainly in summer, with an average of 65 precipitation days annually. The mean annual temperature is 11.1 °C, with ground temperatures ranging from 2.7 °C to 4.9 °C. Sunshine duration averages 2801.7 h annually, with sunlight accounting for 63% of the year [29]. The soil type in the area is saline–alkali tidal soil.

2.2. Experimental Design

The field experiment commenced in September 2021. Three treatments were established: a control treatment (CK) with a dry field and no bio-organic fertilizer application, a paddy field treatment (W), and a paddy field combined with bio-organic fertilizer treatment (BW). The biological organic fertilizer was jointly developed by Nanjing Ningliang Biological Fertilizer Co., Ltd., Nanjing Agricultural University, and Jiangsu Academy of Agricultural Sciences. It is made from high-quality chicken manure, medicinal residue, and other materials that have been fully fermented and matured by adding efficient composite strains and then processed. The total nutrient content ($N+P_2O_5+K_2O$) is $\geq$6%, and the organic matter is $\geq$45%. The effective live bacteria count (CFU) is $\geq 2 \times 10^8$ per gram, the moisture content is $\leq$10%, and the pH value ranges from 5.5 to 8.0. The application rate of the biological organic fertilizer in the treatment is 6000 kg hm^{-2}. Each treatment consisted of three replicates randomly distributed across different plots, resulting in nine experimental plots, each covering an area of 1320 m^2 (24 m × 55 m). The trial field is planted with the rice variety "Jinyuan 89". Throughout the rice growing period, except for allowing the water to dry out at maturity, the water level in the field should be maintained at 3–5 cm during all other stages of growth. Before the experiment's onset (June 2021), soil samples were collected from the 0–20 cm depth. The soil properties were as follows: pH 8.8, EC 634 μs·cm^{-1}, bulk density 1.45 g·cm^{-3}, organic carbon 4.22 g·kg^{-1}, alkaline-hydrolyzable nitrogen 26.20 mg·kg^{-1}, available phosphorus 6.05 mg·kg^{-1}, and available potassium 110.67 mg·kg^{-1}.

2.3. Soil Example Collection and Analysis

At the experiment's conclusion (October 2022), soil samples were collected using a small soil drill with a 5 cm diameter. Five random points were selected within each plot, and soil samples from the 0–20 cm depth were collected from the surface at each point. After thorough mixing, samples were packed into self-sealed bags labeled accordingly and transported to the laboratory in insulated containers. Plant residues and stones were removed, and half of each sample was stored at 4 °C for biological analysis, while the other half was air-dried, crushed, and sieved through 1mm and 0.15 mm meshes for basic soil physical and chemical analysis.

Soil pH and EC were measured using a pH meter (LE703, Mettler Toledo, Shanghai, China) and an EC meter (LE438, Mettler Toledo, Shanghai, China) at a 1:5 ratio (soil:water), respectively. Water-soluble salt content was determined by the mass method [30]. Organic carbon (SOC) was measured using the potassium dichromate oxidation method [30]. Soil-available potassium (AK) was analyzed by flame photometry (FP6410, Shanghai Yi electric Analytical Instrument Co., Ltd., Shanghai, China) [30]. Soil-available nitrogen (AN) was determined by the alkaline hydrolysis diffusion method, and soil-available phosphorus (AP) by the molybdenum antimony colorimetric method [30]. Soil alkaline phosphatase (S-AKP), urease (S-UE), and catalase (S-CA) activities were extracted and measured using enzyme activity kits and a microplate reader (Epoch2, BioTek, Shoreline, WA, USA) [30].

Soil enzyme activity detection kits were procured from Beijing Biological Technology Co., Ltd., Beijing, China.

2.4. Soil DNA Extraction and High-Throughput Sequencing Analysis

Total DNA was extracted using the FastDNA® SPIN Kit for Soil Microbiome (Norcross, MP, USA). DNA concentration and purity were determined using a Nanodrop2000 (Thermo Scientific, Wilmington, DE, USA), and extracted genomic DNA was examined by electrophoresis on a 1% agarose gel. Specific primers with barcoding markers were synthesized for sequencing amplicons in the V3-V4 region using 16S rRNA. Bacterial PCR primers were 338F (5′-ACTCCTACGGGAGGCAGCAG-3′) and 806R (5′-GGACTACHVGGGTWTCTAAT-3′). Each sample was amplified three times by PCR, and the aggregated PCR products were used to construct a library and sequenced on both ends using the Illumina NovaSeq platform (Shanghai Meiji Biomedical Technology Co., Ltd., Shanghai, China). QIIME2 was employed for quality control and analysis of the original sequencing data. After isolating PE reads from Illumina sequencing, double-end reads were controlled and filtered for sequencing quality, with overlapping reads spliced to obtain optimized data after quality control splicing. DADA2/Deblur and other sequence denoising methods were utilized to process the optimized data, obtaining representative sequence and abundance information of amplicon sequence variants (ASVs) [31].

2.5. Statistic Analyses

Based on the results of ASV analysis, the alpha diversity index was calculated by random sampling of the sample sequences. Nonmetric multidimensional scaling (NMDS) analysis based on Bray–Curtis distance was used to demonstrate beta diversity. Linear discriminant analysis effect size (LEfSe) based on the R software (version 4.1.0) package was used to find the species characteristics that best explained the differences between groups in two or more groups of samples. Pearson correlation analysis was used to analyze the correlation between soil microbial community and soil factors. Redundancy analysis (RDA) was used to analyze the relationship between soil bacterial community and soil chemical properties (class level).

All data were processed using Microsoft Excel 2019 (version 16.0.15629) and SPSS (version 20.0, IBM, Armonk, NY, USA), and one-way ANOVA was performed. Duncan's new multiple-distance method was used to test the significance of the applied treatment. Canoco5 software (version 5.02; accessed on 15 November 2023, http://www.canoco5.com/). All graphics were obtained by Origin software (version 9.65.169, Origin Lab, accessed on 15 November 2023, https://www.originlab.com/).

3. Results

3.1. Soil Physico-Chemical Characteristics

Significant differences were observed in soil pH and EC among treatments ($p < 0.05$; Table 1). Compared to the control, soil pH and EC were notably reduced by 1.3% and 15.4% with W treatment and by 4.1% and 5.8% with BW treatment. Soil organic carbon content ranged from 9.0 g/kg to 10.66 g/kg across treatments, with no significant variance in available nutrient content (AP, AK, and AN). In comparison to CK, BW treatment resulted in increases of 17.2%, 17.9%, and 18.2% in SOC, AP, and AN, respectively. Conversely, compared to CK treatment, SOC, AK, and AN decreased with W treatment, with AK content experiencing the highest decrease at 9%. Notably, significant differences were found in soil urease and alkaline phosphatase activity ($p < 0.05$), with the highest activity recorded in BW treatment, showing a 25.8% increase in S-UE and a 126% increase in S-AKP compared to CK.

Table 1. Soil physical and chemical properties under different treatments.

Treatments	pH	EC us/cm	SOC g/kg	AK mg/kg	AP mg/kg	AN mg/kg	S-CAT (μmol/d/g)	S-UE (U/g)	S-AKP (U/g)
W	8.40 ± 0.06 a	352.66 ± 15.79 ab	9.00 ± 0.37 ab	259.66 ± 15.36 a	25.75 ± 0.15 a	59.53 ± 3.52 a	117.19 ± 0.34 a	209.66 ± 29.87 ab	278.64 ± 36.78 b
BW	8.17 ± 0.02 b	393.00 ± 103.49 ab	10.66 ± 1.51 a	270.66 ± 20.43 a	27.43 ± 2.92 a	72.03 ± 8.14 a	118.33 ± 1.72 a	220.52 ± 29.72 a	900.63 ± 137.19 a
CK	8.51 ± 0.06 a	417.00 ± 20.11 a	9.10 ± 0.40 ab	285.5 ± 2.04 a	23.26 ± 1.12 a	60.95 ± 0.43 a	117.04 ± 0.09 a	175.33 ± 5.01 b	398.39 ± 79.15 b

W: paddy field, BW: paddy field application of bio-organic fertilizer, CK: dry field; EC: electrical conductivity, SOC: soil organic carbon, AK: soil-available potassium, AP: soil-available phosphorus, AN: soil alkalolytic nitrogen, S-CAT: soil catalase, S-UE: soil urease, S-AKP: soil alkaline phosphatase. Different lowercase letters indicate significant differences between W, BW, and CK within the same stand (Duncan's multiple-range tests, $p < 0.05$). All data are presented as mean value ± standard deviation ($n = 3$).

3.2. Soil Fungi Diversity and Community Structure

Analysis revealed 1533 fungal ASVs in each treatment (Figure 1), with CK, W, and BW treatments containing 525, 777, and 793 ASVs, respectively, and 176 ASVs common among all treatments. Significant differences in fungal diversity indices were observed among treatments ($p < 0.05$; Table 2). Compared to CK, ACE and Shannon indices increased notably by 74% and 34% with W treatment and by 36% and 24% with BW treatment, respectively. However, the Simpson index, representing community diversity, significantly decreased in organic treatments (W and BW), with W and BW showing reductions of 76% and 59% compared to CK, respectively.

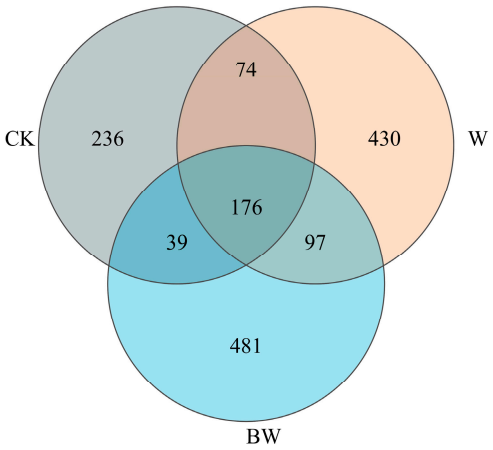


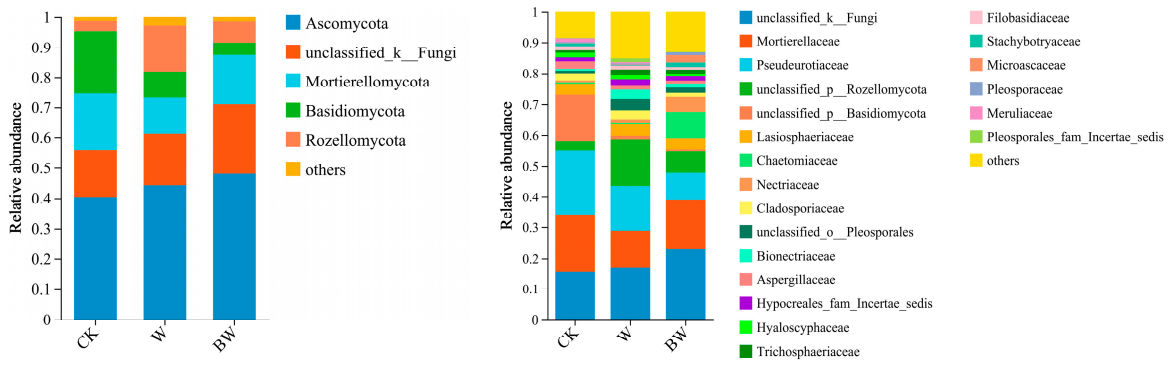
Figure 1. Venn diagram of soil fungal ASVs.

Table 2. Diversity indices of fungal communities under different treatments.

Treatments	Sobs	ACE	Chao	Shannon	Simpson
W	380.33 ± 70.53 a	415.15 ± 26.57 a	415 ± 26.44 a	4.27 ± 0.23 a	0.03 ± 0.01 b
BW	315.66 ± 56.81 a	318.26 ± 58.53 ab	317.81 ± 57.94 ab	3.89 ± 0.17 a	0.06 ± 0.01 b
CK	236 ± 53.09 a	237.46 ± 54.52 b	237.49 ± 54.79 b	3.12 ± 0.25 b	0.16 ± 0.03 a

W: paddy field, BW: paddy field application of bio-organic fertilizer, CK: dry field. Different lowercase letters indicate significant differences between W, BW, and CK within the same stand (Duncan's multiple-range tests, $p < 0.05$). All data are presented as mean value ± standard deviation ($n = 3$).

The dominant fungal phyla following materials addition were Ascomycota (40–48%), unclassified_k__Fungi (15–22%), Mortierellomycota (12–18%), Basidiomycota (4–20%), and Rozellomycota (3–15%), comprising over 98% of the total abundance at the phylum level (Figure 2a). Basidiomycota abundance notably increased by 13% in BW treatment compared to CK, while Rozellomycota decreased by 12%. At the genus level (Figure 2b), main fungal phyla, such as unclassified_k__Fungi, Mortierella, Pseudeurotium, unclassified_p__Rozellomycota, unclassified_p__Basidiomycota, unclassified_f__Chaetomiaceae, Schizothecium, and Cladosporium, accounted for 65–78% of total fungal abundance. The relative abundance of unclassified_p__Basidiomycota significantly increased by 14% in BW treatment compared to CK.

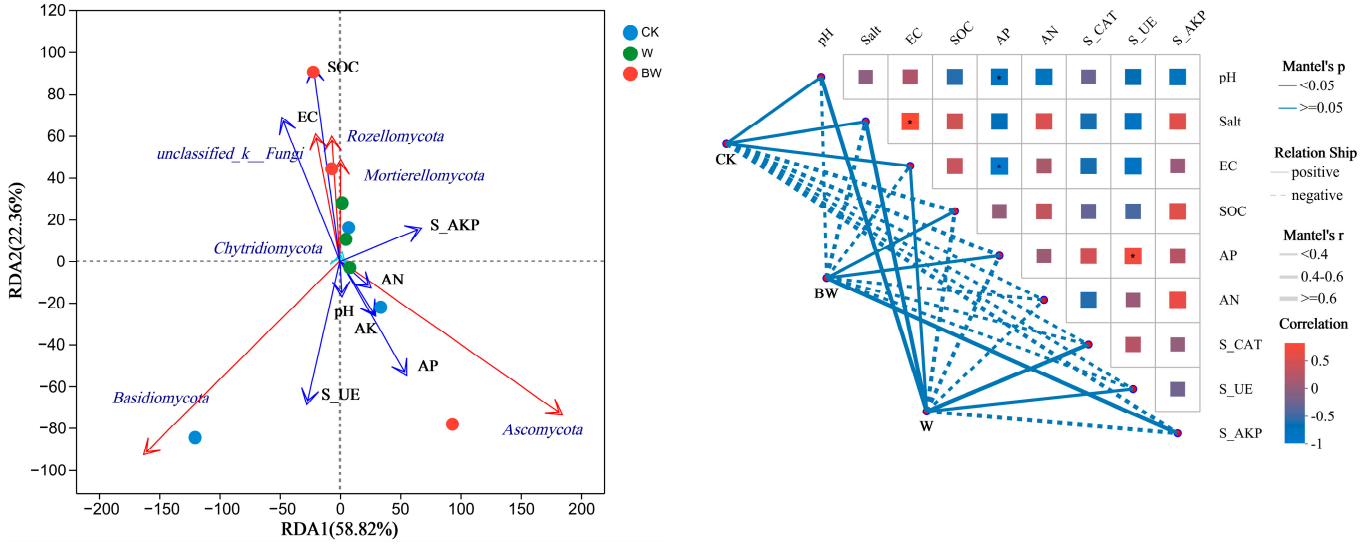


(**a**) (**b**)

Figure 2. The composition of soil fungal communities at the phylum level (**a**) and family level (**b**) under different treatments.

3.3. Relationship between Soil Fungi and Environment Factors

Redundancy analysis (RDA) reflected the relationship between soil fungi and environmental factors (Figure 3a), with 81.18% of the variation in the fungal microbial community explained by selected factors. Soil EC and SOC exhibited relatively high r^2 values, indicating their significant effect on fungal species distribution (Table 3). Furthermore, significant correlations were found between soil pH and AN with soil fungi microbial, with BW treatment negatively related to soil pH and salt but positively related to soil SOC, AP, and S-AKP (Figure 3b). Conversely, CK/W exhibited a positive correlation with soil pH and salt and a negative correlation with soil SOC and AP.



(**a**) (**b**)

Figure 3. Analysis of soil properties affecting the distribution of soil fungal community structure: (**a**) redundancy analysis of soil properties and soil fungal communities and (**b**) correlation analysis between soil properties (Mantel test).

Table 3. Redundancy analysis results of soil fungi at phylum level.

Index	RDA1	RDA2	r^2	*p*-Value
pH	0.0976	−0.9952	0.0122	0.983
EC	−0.576	0.8175	0.361	0.273
SOC	−0.2327	0.9725	0.473	0.202

Table 3. *Cont.*

Index	RDA1	RDA2	r^2	*p*-Value
AK	0.7466	−0.6653	0.074	0.764
AP	0.7108	−0.7034	0.3095	0.281
AN	0.8926	−0.4509	0.0355	0.83
S-UE	−0.3725	−0.928	0.2814	0.433
S-AKP	0.9743	0.2253	0.2358	0.423

The EC, SOC, AK, AP, AN, S-UE, and S-AKP represent soil electrical conductivity, organic carbon, available soil potassium, available soil phosphorus, available soil nitrogen, soil urease, and soil alkaline phosphatase, respectively.

3.4. Functional Gene Prediction of Soil Fungi under Various Measures

The functional gene composition of the fungal community under different treatments is depicted in Figure 4. Saprotrophs dominated, including Dung Saprotroph, Animal Pathogen-Soil Saprotroph, and Plant Pathogen, accounting for 80–95% of relative abundance. The relative abundance of Plant Pathogen in W and BW treatments was notably higher than CK, while "Animal Pathogen-Dung Saprotroph-Endophyte-Epiphyte-Plant Saprotroph-Wood Saprotroph" was relatively higher in BW treatment.

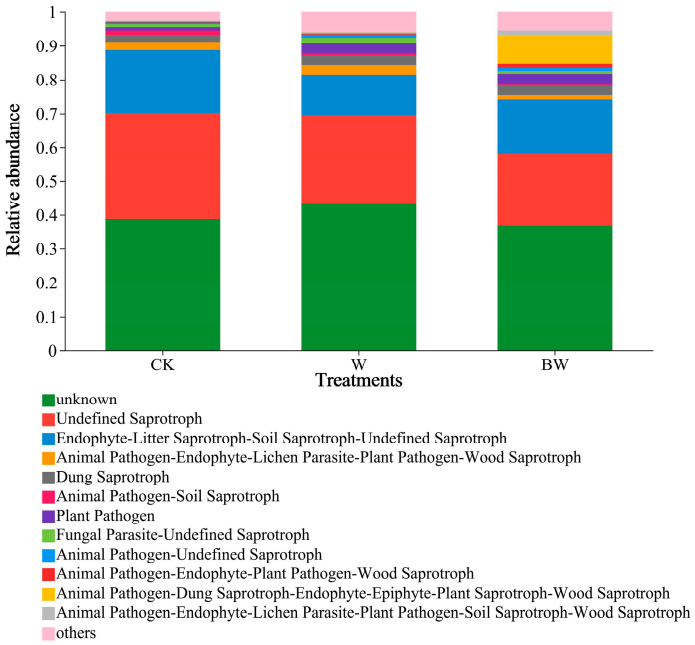


Figure 4. Functional gene composition of the fungal community under different treatments.

4. Discussion

4.1. Effects of Drought to Water Combined with Biological Organic Fertilizer on Soil Physical and Chemical Properties

Irrigation leaching proves effective in managing saline soil [17]. In this study, combining water leaching with exogenous organic materials notably reduced soil conductivity and pH (Table 1), aligning with previous findings [29,30]. This reduction is attributed to the downward migration of soluble salt ions in surface soil alongside water movement, inducing temporary salt compression [31]. The addition of bio-organic fertilizer supplements exchangeable Ca^{2+} in soil, displacing Na^{+} pairs, reducing soil viscosity, and alleviating plant stress [32]. Humic acid H^{+} in bio-organic fertilizer neutralizes alkaline OH- in soil, reducing salt-based ions and facilitating desalination and alkali elimination in saline soil surface layers [5].

However, excessive water leaching can deplete soil nutrients. Consequently, apart from organic carbon, available nutrient contents such as AP, AK, and AN in treatment W

were lower than the control but significantly higher in BW treatment than CK and W treatments. Bio-organic fertilizer, enriched with easily decomposable organic carbon, transforms into available nutrients post-mineralization, supplementing root soil nutrient stock and mitigating leaching effects [3,33,34]. Additionally, soil urease and alkaline phosphatase activities in W and BW treatments were significantly higher than CK (Table 1). These activities, indicative of soil microbial nitrogen and phosphorus utilization, reflect increased nutrient availability due to combined irrigation and bio-organic fertilizer application, promoting salt leaching and providing a conducive environment for soil microorganisms [23]. Thus, soil enzyme activities related to nitrogen and phosphorus utilization increased significantly.

4.2. Responses of Soil Fungal Communities to Changes in Soil Environment

In our study, ACE and Shannon indices in W and BW treatments were significantly higher than CK, while the Simpson index was significantly lower (Table 2). These findings echo those of Lu et al. [35], suggesting that bio-organic fertilizer application and changes in cultivation practices enhance soil fungal diversity and richness. Microbial community alpha diversity often correlates with ecosystem stability and functionality [9,12]. We speculate that organic material addition boosts soil fungal microbial diversity by increasing available nutrient pools and physical micro-habitats [35,36]. Soils rich in AN and AP foster microbial growth and reproduction, promoting high microbial diversity [21,37]. Moreover, irrigation directly influences soil fungal diversity, community composition, and functional groups [19], impacting C and N cycles, plant growth, and soil microbial community structure and function [33].

At the phylum level (Figure 2), Ascomycota, Basidiomycota, and Mortierellomycota play key roles in soil fungal communities, consistent with findings in agricultural cropping soil fungal communities [38]. Ascomycota, the primary organic matter decomposer, thrives in nutrient-rich environments [15,20]. Basidiomycota abundance significantly increased in the BW treatment, also known for organic matter decomposition [14,17]. Competition between microbial taxa from Ascomycota and Basidiomycota may enhance community complexity [39]. Additionally, unclassified_p__Basidiomycota belonging to Basidiomycota was a keystone taxon in soil fungal communities at the genus level (Figure 3), potentially playing a crucial role in monitoring agricultural ecosystems, especially with combined organic fertilizer and straw return systems [20]. Our study also showed that organic material addition and irrigation synergistically improved the relative abundance of Mortierellomycota (Figure 2). Previous studies have demonstrated that Mortierellomycota, as beneficial fungi, can improve nutrient conditions and stress resistance of host plants in symbiosis with plants [40]. These findings collectively indicate a shift in soil fungal community composition under dryland soil modification.

4.3. Prediction and Analysis of Key Factors and Functional Genes Affecting Soil Fungal Community

Soil nutrient variability is widely recognized as a crucial factor influencing changes in fungal community structure [2,12]. In our study, the composition and distribution of the soil fungal community closely correlated with soil physical and chemical properties. Redundancy analysis (RDA) results indicated that EC and SOC were the most significant environmental factors affecting soil fungal species distribution (Table 3), consistent with previous studies on degenerated soil restoration [27]. Microbial activity is reliant on the availability of organic carbon [38,41], with heterotrophic microorganisms utilizing organic carbon as an energy source and component of their biomass [11]. In our study, the soil fungal community in the BW treatment showed a positive relationship with soil SOC and AP while exhibiting a negative relationship with SOC and AP in W and CK treatments (Figure 3b). This suggests that the microbial environment improved with organic fertilizer addition. Additionally, Zhang et al. [42] demonstrated that microbial gene quantity was positively correlated with available soil resources (C, P) under moderately disturbed conditions. Soil pH is a crucial validation factor for saline soil environment restoration [43].

Its gradual decrease was significantly negatively correlated with soil fungal community composition in the BW treatment (Figure 3b). This indicates that soil pH, EC, organic matter, and available phosphorus are likely the main factors driving changes in soil fungal community structure [16]. Soil pH can alter microbial community structure by affecting nutrient availability, such as available phosphorus and organic matter [43].

Fungal functional groups, based on FUNGuild analysis in our study, responded similarly to organic material addition and irrigation, with saprophytic fungi being the dominant functional guilds (Figure 4), consistent with Ji et al.'s findings [44]. Organic material addition significantly increased soil organic matter, favoring saprophytic fungi involved in organic matter decomposition [8]. Moreover, habitats with better soil moisture were more conducive to the propagation of saprophytic fungi [18]. Although there were no significant differences in fungal communities between different treatments, numerous studies have demonstrated that fungal communities exhibit strong drought tolerance due to the formation of a large hyphal network for long-distance nutrient and water transport [16,38]. However, short-term interventions like irrigation and fertilization in our study may have less impact on soil fungal functional groups [27]. Additionally, while FUNGuild provides a valuable analysis of fungal functions based on existing literature, its classification may not be comprehensive, warranting further research for better understanding.

5. Conclusions

The combination of drought and water modification with bio-organic fertilizer significantly increased soil organic carbon, available phosphorus, available potassium, and enzyme activities while decreasing soil pH and EC. Short-term application of bio-organic fertilizer enhanced the biodiversity of the soil fungal community but had minimal impact on fungal community structure. At the phylum level, Ascomycota, Mortierellomycota, and Basidiomycota were the predominant fungal groups. At the genus level, fungi under Basidiomycota dominated. Soil pH, EC, soil organic carbon, available phosphorus, and soil enzyme activity were identified as the main factors influencing the soil fungal community. Saprophytic fungi constituted the primary functional group in the fungal community. The relative abundance of plant pathogenic fungi increased with the application of bio-organic fertilizer combined with drought and water improvement. Further verification is necessary to assess the long-term effects of bio-organic fertilizer application in coastal saline soil under flooding conditions. These findings contribute to enhancing the scientific foundation for the efficient utilization and development of saline soil resources in coastal areas.

Author Contributions: Conceptualization, G.L. and R.Y.; methodology, G.L.; software, M.X.; validation, C.C., G.L. and R.Y.; formal analysis, M.X.; resources, G.L.; data curation, X.W.; writing—original draft preparation, M.X.; writing—review and editing, G.L. and R.Y.; visualization, C.C.; supervision, G.L. and X.W.; project administration, X.W.; funding acquisition, G.L., C.C. and X.W. All authors have read and agreed to the published version of the manuscript.

Funding: This research was supported by the Sub-topic of the National Key Research and Development Program, grant number 2021YFD190090504, the Strategic Priority Research Program of the Chinese Academy of Sciences grant number XDA0440000, and the Natural Science Foundation Project of Henan Province grant number 222300420497. Special thanks are given to the referees and the editors for their instructive comments, suggestions, and editing of the manuscript.

Data Availability Statement: The data presented in this study are available upon request from the corresponding author. The data are not publicly available due to privacy restrictions.

Conflicts of Interest: The authors declare no conflicts of interest.

References

1. Li, S.; Yang, Y.; Li, Y.; Gao, B.; Tang, Y.; Xie, J.; Zhao, H. Remediation of saline-sodic soil using organic and inorganic amendments: Physical, chemical, and enzyme activity properties. *J. Soils Sediments* **2019**, *20*, 1454–1467. [CrossRef]
2. Yao, R.-J.; Li, H.-Q.; Yang, J.-S.; Wang, X.-P.; Xie, W.-P.; Zhang, X. Biochar Addition Inhibits Nitrification by Shifting Community Structure of Ammonia-Oxidizing Microorganisms in Salt-Affected Irrigation-Silting Soil. *Microorganisms* **2022**, *10*, 436. [CrossRef] [PubMed]
3. Wu, L.; Zhang, K.; Zhu, X.; Lu, T.; Wang, X. Effects of amendments on carbon and nitrogen fractions in agricultural soils of Yellow River Delta. *Geosci. Lett.* **2023**, *10*, 22. [CrossRef]
4. Taher, D.; Nofal, E.; Hegazi, M.; El-Gaied, M.A.; El-Ramady, H.; Solberg, S.Ø. Response of Warm Season Turf Grasses to Combined Cold and Salinity Stress under Foliar Applying Organic and Inorganic Amendments. *Horticulturae* **2023**, *9*, 49. [CrossRef]
5. Yao, R.; Yang, J.; Zhu, W.; Li, H.; Yin, C.; Jing, Y.; Wang, X.; Xie, W.; Zhang, X. Impact of crop cultivation, nitrogen and fulvic acid on soil fungal community structure in salt-affected alluvial fluvo-aquic soil. *Plant Soil* **2021**, *464*, 539–558. [CrossRef]
6. Zhou, M.; Liu, X.; Meng, Q.; Zeng, X.; Zhang, J.; Li, D.; Wang, J.; Du, W.; Ma, X. Additional application of aluminum sulfate with different fertilizers ameliorates saline-sodic soil of Songnen Plain in Northeast China. *J. Soils Sediments* **2019**, *19*, 3521–3533. [CrossRef]
7. Yang, L.; Bian, X.; Yang, R.; Zhou, C.; Tang, B. Assessment of organic amendments for improving coastal saline soil. *Land Degrad. Dev.* **2018**, *29*, 3204–3211. [CrossRef]
8. Zhang, X.; Qu, J.; Li, H.; La, S.; Tian, Y.; Gao, L. Biochar addition combined with daily fertigation improves overall soil quality and enhances water-fertilizer productivity of cucumber in alkaline soils of a semi-arid region. *Geoderma* **2020**, *363*, 114170. [CrossRef]
9. Farooqi, Z.U.R.; Qadir, A.A.; Alserae, H.; Raza, A.; Mohy-Ud-Din, W. Organic amendment–mediated reclamation and build-up of soil microbial diversity in salt-affected soils: Fostering soil biota for shaping rhizosphere to enhance soil health and crop productivity. *Environ. Sci. Pollut. Res.* **2023**, *30*, 109889–109920. [CrossRef]
10. Gardner, T.G.; Frene, J.P.; Lawson, S.S.; Lue Sue, N.D.; Handy, J.; Crawford, R.H. The Impact of Tree Species on Microbial Community Structure and Soil Function on Forest Plantations in the Central Hardwoods Region (CHR). *Forests* **2023**, *14*, 859. [CrossRef]
11. Wang, X.; Feng, J.; Ao, G.; Qin, W.; Han, M.; Shen, Y.; Liu, M.; Chen, Y.; Zhu, B. Globally nitrogen addition alters soil microbial community structure, but has minor effects on soil microbial diversity and richness. *Soil Biol. Biochem.* **2023**, *179*, 108982. [CrossRef]
12. Li, J.; Chen, L.; Zhang, J.; Zhang, C.; Ma, D.; Zhou, G.; Ning, Q. Organic amendments with high proportion of heterocyclic compounds promote soil microbiome shift and microbial use efficiency of straw-C. *Front. Microbiol.* **2023**, *14*, 1087709. [CrossRef]
13. Peng, X.; Liu, J.; Duan, X.; Yang, H.; Huang, Y. Key Soil Physicochemical Properties Regulating Microbial Community Structure under Vegetation Restoration in a Karst Region of China. *Ecosyst. Health Sustain.* **2023**, *9*, 0031. [CrossRef]
14. Edwards, K.R.; Bárta, J.; Mastný, J.; Picek, T. Multiple environmental factors, but not nutrient addition, directly affect wet grassland soil microbial community structure: A macrocosm study. *FEMS Microbiol. Ecol.* **2023**, *99*, fiad070. [CrossRef]
15. Somenahally, A.C.; McLawrence, J.; Chaganti, V.N.; Ganjegunte, G.K.; Obayomi, O.; Brady, J.A. Response of soil microbial Communities, inorganic and organic soil carbon pools in arid saline soils to alternative land use practices. *Ecol. Indic.* **2023**, *150*, 110227. [CrossRef]
16. Wang, Y.; Zhao, X.; Omidvar, N.; Liu, M.; Zou, D.; Zhang, M. Insight into functional mechanisms of percarbamide and nitrification inhibitors in degrading fungicide residues and shaping microbial communities in soil-plant systems. *J. Environ. Manag.* **2023**, *345*, 118687. [CrossRef]
17. Han, L.; Qin, H.; Wang, J.; Yao, D.; Zhang, L.; Guo, J.; Zhu, B. Immediate response of paddy soil microbial community and structure to moisture changes and nitrogen fertilizer application. *Front. Microbiol.* **2023**, *14*, 1130298. [CrossRef]
18. Zhang, H.; Xi, J.; Lv, Q.; Wang, J.; Yu, K.; Zhao, F. Effect of Aerated Irrigation on the Growth and Rhizosphere Soil Fungal Community Structure of Greenhouse Grape Seedlings. *Sustainability* **2022**, *14*, 12719. [CrossRef]
19. Gao, S.; He, Q.; Huang, D.; Wang, Z.; Mao, J.; Xie, X.; Su, Y.; Qiu, Q.; Li, J.; Chen, Z. Responses of Fungal Community Structure and Functional Composition to Short-Term Fertilization and Dry Season Irrigation in *Eucalyptus urophylla* × *Eucalyptus grandis* Plantation Soils. *Forests* **2022**, *13*, 854. [CrossRef]
20. Wang, Y.; Liu, L.; Luo, Y.; Awasthi, M.K.; Yang, J.; Duan, Y.; Li, H.; Zhao, Z. Mulching practices alter the bacterial-fungal community and network in favor of soil quality in a semiarid orchard system. *Sci. Total Environ.* **2020**, *725*, 138527. [CrossRef] [PubMed]
21. Guan, H.; Zhang, Y.; Mao, Q.; Zhong, B.; Chen, W.; Mo, J.; Wang, F.; Lu, X. Consistent effects of nitrogen addition on soil microbial communities across three successional stages in tropical forest ecosystems. *Catena* **2023**, *227*, 107116. [CrossRef]
22. Xiao, M.; Liu, G.; Jiang, S.; Guan, X.; Chen, J.; Yao, R.; Wang, X. Bio-Organic Fertilizer Combined with Different Amendments Improves Nutrient Enhancement and Salt Leaching in Saline Soil: A Soil Column Experiment. *Water* **2022**, *14*, 4084. [CrossRef]
23. Ni, P.; Wang, S.; Liu, B.; Sun, H. Effects of Organic Manure and Biochar-Based Fertilizer Application on Soil Water and Salt Transport in Brackish Water Irrigated Soil Profile. *J. Soil Sci. Plant Nutr.* **2023**, *23*, 3120–3136. [CrossRef]
24. Amer, M.M.; Aboelsoud, H.M.; Sakher, E.M.; Hashem, A.A. Effect of Gypsum, Compost, and Foliar Application of Some Nanoparticles in Improving Some Chemical and Physical Properties of Soil and the Yield and Water Productivity of Faba Beans in Salt-Affected Soils. *Agronomy* **2023**, *13*, 1052. [CrossRef]

25. Suddarth, S.R.P.; Ferreira, J.F.S.; Cavalcante, L.F.; Fraga, V.S.; Anderson, R.G.; Halvorson, J.J.; Bezerra, F.T.C.; Medeiros, S.A.S.; Costa, C.R.G.; Dias, N.S. Can Humic Substances Improve Soil Fertility under Salt Stress and Drought Conditions? *J. Environ. Qual.* **2019**, *48*, 1605–1613. [CrossRef]
26. Khan, I.; Mahmood, S.; Chattha, M.U.; Bilal Chattha, M.; Ahmad, S.; Awan, M.I.; Alqahtani, F.M.; Hashem, M.; Alhaithloul, H.A.S.; Qari, S.H.; et al. Organic Amendments Improved the Productivity and Bio-Fortification of Fine Rice by Improving Physiological Responses and Nutrient Homeostasis under Salinity Stress. *Plants* **2023**, *12*, 1644. [CrossRef] [PubMed]
27. Zhang, C.; Mi, W.; Xu, Y.; Zhou, W.; Bi, Y. Long-term integrated rice-crayfish culture disrupts the microbial communities in paddy soil. *Aquac. Rep.* **2023**, *29*, 101515. [CrossRef]
28. Kalanaki, M.; Ritzema, H.; Bamshad, R.; Jones, E.; Fazilatnia, M. Application of bio-desalinization for reclamation of salt-affected soil under composted cow manure and deficit irrigation with saline water. *Paddy Water Environ.* **2020**, *18*, 469–479. [CrossRef]
29. Guo, K.; Liu, X. Effect of initial soil water content and bulk density on the infiltration and desalination of melting saline ice water in coastal saline soil. *Eur. J. Soil Sci.* **2019**, *70*, 1249–1266. [CrossRef]
30. Cao, J.; Zhao, P.; Wang, D.; Zhao, Y.; Wang, Z.; Zhong, N. Effects of a Nanonetwork-Structured Soil Conditioner on Microbial Community Structure. *Biology* **2023**, *12*, 668. [CrossRef]
31. Chen, C.; Lv, Q.; Tang, Q. Impact of bio-organic fertilizer and reduced chemical fertilizer application on physical and hydraulic properties of cucumber continuous cropping soil. *Biomass Convers. Biorefinery* **2022**, *14*, 921–930. [CrossRef]
32. Bello, S.K.; Alayafi, A.H.; Al-Solaimani, S.G.; Abo-Elyousr, K.A.M. Mitigating Soil Salinity Stress with Gypsum and Bio-Organic Amendments: A Review. *Agronomy* **2021**, *11*, 1735. [CrossRef]
33. Sun, Y.P.; Yang, J.S.; Yao, R.J.; Chen, X.B.; Wang, X.P. Biochar and fulvic acid amendments mitigate negative effects of coastal saline soil and improve crop yields in a three year field trial. *Sci. Rep.* **2020**, *10*, 8946. [CrossRef] [PubMed]
34. Sun, Z.; Lin, M.; Du, C.; Hao, Y.; Zhang, Y.; Wang, Z. The use of manure shifts the response of α-diversity and network while not β-diversity of soil microbes to altered irrigation regimes. *Appl. Soil Ecol.* **2022**, *174*, 104423. [CrossRef]
35. Lu, Y.; Lyu, M.; Xiong, X.; Deng, C.; Jiang, Y.; Zeng, M.; Xie, J. Understory ferns promote the restoration of soil microbial diversity and function in previously degraded lands. *Sci. Total Environ.* **2023**, *870*, 161934. [CrossRef]
36. Zheng, X.; Lin, C.; Guo, B.; Yu, J.; Ding, H.; Peng, S.; Sveen, T.R.; Zhang, Y. Effects of re vegetation restoration on soil bacterial community structure in degraded land insubtropical China. *Eur. J. Soil Biol.* **2020**, *98*, 103184. [CrossRef]
37. Dong, W.Y.; Zhang, X.Y.; Dai, X.Q.; Fu, X.L.; Yang, F.T.; Liu, X.Y.; Sun, X.M.; Wen, X.F.; Schaeffer, S. Changes in soil microbial community composition in response to fer tilization of paddy soils in subtropical China. *Appl. Soil Ecol.* **2014**, *84*, 140–147. [CrossRef]
38. Lin, Y.; Kong, J.; Yang, L.; He, Q.; Su, Y.; Li, J.; Wang, G.; Qiu, Q. Soil Bacterial and Fungal Community Responses to Throughfall Reduction in a Eucalyptus Plantation in Southern China. *Forests* **2021**, *13*, 37. [CrossRef]
39. Liu, Q.; Wang, S.; Li, K. Responses of soil bacterial and fungal communities to the long-term monoculture of grapevine. *Appl. Microbiol. Biotechnol.* **2021**, *105*, 7035–7050. [CrossRef]
40. Johnson, J.M.; Ludwig, A.; Furch, A.C.U. The beneficial root-colonizing fungus Mortierella hyaline promotes the aerial growth of Arabidopsis and activates calcium-dependent responses that restrict Alternaria brassicae-induced disease development in roots. *Mol. Plant-Microbe Interact.* **2019**, *32*, 351–363. [CrossRef]
41. Zhu, X.; Mao, L.; Chen, B. Driving forces linking microbial community structure and functions to enhanced carbon stability in biochar-amended soil. *Environ. Int.* **2019**, *133*, 105211. [CrossRef]
42. Zhang, W.W.; Wang, C.; Xue, R.; Wang, L.J. Effects of salinity on the soil microbial community and soil fertility. *J. Integr. Agric.* **2019**, *18*, 1360–1368. [CrossRef]
43. Zou, L.; Bai, Y.P.; Huang, J.; Xiao, D.R.; Yang, G. Soil pH and dissolved organic carbon shape microbial communities in wetlands with two different vegetation types in Changdu area, Tibet. *J. Mt. Sci.* **2023**, *20*, 750–764. [CrossRef]
44. Ji, C.; Huang, J.; Zhang, X.; Yang, G.; Xing, S.; Fu, W.; Hao, Z.; Chen, B.; Zhang, X. Response of soil fungal community to chromium contamination in agricultural soils with different physicochemical properties. *Sci. Total Environ.* **2023**, *879*, 163244. [CrossRef]

Disclaimer/Publisher's Note: The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of MDPI and/or the editor(s). MDPI and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.