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Effect of Subsurface Drainage Combined with Biochar on the Bacterial Community Composition of Coastal Saline Soil

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Abstract: Waterlogging and salinization are considered to be the main threats to agricultural productivity and land resources in coastal areas of China. Thus far, drainage and field soil improvement programs have been ineffective. In this article, we investigated the effect of subsurface drainage combined with biochar (B–S) on soil physicochemical properties and soil bacterial community structure in coastal saline soil. In this study, B–S significantly reduced soil electrical conductivity (EC) and soil water content (W) by 35% and 10.65% compared to no drainage (CK). Compared to CK and drainage alone (S), B–S significantly increased soil total nitrogen (TN) by 24.78% and 39.62%, soil available phosphorus (AP) by 28.29% and 69.82%, soil nitrate (NO_3^--N) by 64.65% and 35.45%, and significantly increased soil organic matter (SOM) by 74.69% and 66.10%, respectively. It also significantly increased alkaline phosphatase (ALP) and urease activities. The results of redundancy analysis (RDA) showed that CAT and urease made the greatest response to changes in environmental factors, indicating that CAT is more sensitive to changes in environmental alterations than ALP. AP was the dominant factor in the change in enzyme activity (R^2 = 53.0%, $p < 0.05$), followed by NO_3^--N (R^2 = 14.8%). SOM was the dominant factor in the variation in microbial abundance content (R^2 = 38.5%, $p < 0.05$), followed by ALP (R^2 = 20.0%, $p < 0.05$). The results of the study can provide guidance for effective land use and sustainable development of agricultural soil ecology in coastal areas.

Keywords: subsurface drainage; biochar; waterlogging; composition of soil bacterial community; soil enzyme activity

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1. Introduction

Accelerated land degradation, inadequate drainage, rising sea levels, and heavy rainfall have led to more than a third of the world's land being affected by waterlogging and soil salinization [1–4]. Waterlogging and salinization are the first to affect crop root activity; waterlogging replaces air in soil pores with water, leading to oxygen deprivation in crop roots, inhibiting root respiration and ultimately leading to crop death or yield reduction; salinization reduces the osmotic potential of the soil solution, making water uptake by roots difficult, which limits plant growth and development [5,6]. In addition, bacterial community structure and soil physicochemical properties can be affected by salinity and waterlogging stress [7,8]. The coastal region, with its hot summers, heavy rainfall, and exposure to prolonged saltwater intrusion, can exacerbate waterlogging and salinization problems over time without appropriate mitigation measures. In addition, the rehabilitation of soils affected by salinization and waterlogging offers a potential opportunity to meet the growing demand for food from a growing population. It is therefore crucial to ensure global food security through the improvement of saline and flooded lands and the development of sustainable agriculture.

Soil waterlogging and salinization can have direct or indirect effects on soil bacterial community structure and soil enzyme activity by altering soil nutrient effectiveness and aeration [9–12]. Whereas soil waterlogging is closely related to soil water content, Li et al. [13] found that soil water content was the main influencing factor on the dominant soil bacterial community. Borowik and Wyszkowska [14] studied the response of soil enzyme activity to soil water content and found that high soil-water content reduced the activity of catalase, urease, and alkaline phosphatase. Increased soil salinity also inhibited urease and alkaline phosphatase activities [15]. Soil salinity was also strongly negatively correlated with the microbial community richness index (Chao1, ACE) [16]. Chen et al. [17] showed that the relative abundance of the Proteobacteria and Actinobacteria increased with increasing salinity levels. In summary, soil waterlogging and salinization can have many adverse effects on soil ecology, and in coastal areas, where waterlogging and salinization are prominent, studies have shown that subsurface drainage is an effective measure to improve soil waterlogging and salinization [10,18], and that subsurface drainage not only changes soil moisture conditions through drainage, but also leaches soluble salts [19]. Li et al. [20] showed that subsurface drainage treatment not only significantly reduced soil salinity but also had a significant effect on the composition of the soil bacterial community. Qiu et al. [21] showed that drainage also promoted cohesion of soil particles, improved soil aeration, and accelerated the oxidation of soil organic matter (SOM). However, single drainage measures have limitations for saline land management and soil quality enhancement, and the combination of multiple improvement measures holds good promise for saline land improvement and sustainable land use [22].

Biochar has great potential to improve soil quality [23–25]. Zhihui Wang et al. [26] studied the effects of biochar on inter-root soil waterlogging and micro-ecological changes in saline maize and found that, after waterlogging, soil permeability was better with biochar additions, and soil capacity was reduced and soil respiration was improved. Application of biochar can affect soil physicochemical properties and alter microbial habitat, thereby affecting soil microbial activity and microbial community structure [27,28]. Several studies have found that changes in microbial communities may be related to changes in soil nutrients, pH, and physical properties following the addition of biochar [29,30]. Herrmann et al. [12] found that biochar affected the community structure of soil bacteria by increasing the pH of the soil and the amount of active soil phosphorus. Zheng et al. [31] found that biochar significantly increased soil organic matter content and urease activity, while peroxidase activity remained unchanged or decreased, and it significantly increased ACE, Chao1 index, and the relative abundance of Acidobacteria.

In conclusion, for coastal areas, heavy and prolonged rainfall during the rainy season is likely to cause internal flooding or inundation, which can easily lead to crop collapse or death if drainage is not timely or sufficient, seriously affecting agricultural production. Biochar, as an exogenous additive, will inevitably cause changes to the soil environment when added to the soil. If the drainage technology is combined with biochar, it can solve the problem of drainage and salt removal in coastal areas and improve the nutrient status of waterlogged soils. However, there has been little research on the effects of soil properties from a combination of engineering and chemical soil improvement measures such as subsurface drainage combined with biochar, and its effects on soil microorganisms and soil enzyme activity. There is therefore a great need to clarify the response of soil bacterial populations to soil physicochemical properties under subsurface drainage combined with biochar conditions in order to better understand the relationship between changes in soil bacterial communities and the environment. Therefore, this paper takes coastal saline soils as the research object to: (1) reveal the effects of subsurface drainage combined with biochar on soil physicochemical properties; (2) explore the effects of subsurface drainage on soil bacterial community structure; and (3) elucidate the main drivers of changes in bacterial community structure under the waterlogging conditions.

2. Materials and Methods

2.1. Site Description

The study was performed in Dongying Agricultural High-tech Industry Demonstration Zone, Dongying, China (37°27′ N, 118°30′ E). The climate of the study site is continental temperate monsoon. The region has a 12.8 °C annual mean temperature, 8.8 m of average altitude, 4944 h of frost-free period, and 2196 h annual mean total sunshine hours. It has annual precipitation of 555.9 mm and annual accumulative evaporation of 1900.8 mm. The groundwater at the site is 0.8 m~2.04 m. Deep soil loosening was conducted before the experiment. Compound fertilizer (N-P_2O_5-K_2O) was applied on 30 July at a rate of 225 kg hm^{-1}. Physicochemical characteristics of the test site are shown in Table 1. According to the World Reference Base for Soil Resources (WRB), the soil type of the test site is solonchaks [32]. Soil bulk density and saturated hydraulic conductivity were 1.426~1.490 g cm^{-3} and 2.352~6.00 cm d^{-1} for the different soil layers, respectively. An automatic weather station was set up near the edge of the field. Geographical location of the study area is shown in Figure 1. The variation in reference crop evapotranspiration (ET_0) and precipitation for three months are shown in Figure 2.

Table 1. Basic properties of soil before the start of the experiment.

Depth of Soil Layer (cm)	AP (mg/kg)	TN (g/kg)	SOM (g/kg)	EC (μs/cm)	pH	NO_3^--N (mg/kg)	NH_4^+-N (mg/kg)
0–20	18.00	0.53	8.22	1916	8.03	18.55	4.99

Figure 1. Geographical location of the study area.

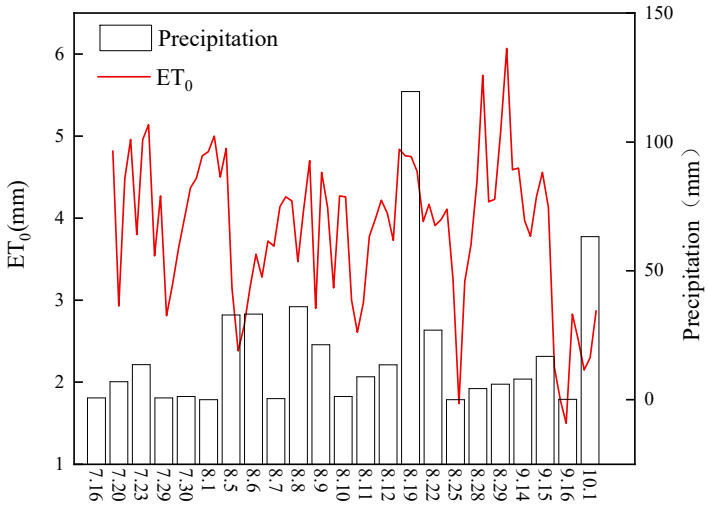

Figure 2. The changes in reference crop evapotranspiration (ET_0) and precipitation in three months. ET_0 is calculated using ET_0 Calculator V31.

2.2. Experiment Design

Three plots of subsurface drainage (depth of 1.1 m, pipe spacing of 30 m), subsurface drainage (depth of 1.1 m, pipe spacing of 30 m) combined with biochar (soil layer of 0~20 cm), and no drainage were set for investigating the effect of subsurface drainage combined with biochar on soil bacterial community structure and soil physicochemical properties under waterlogging. Subsurface drainage (depth of 1.1 m, pipe spacing of 30 m), subsurface drainage (depth of 1.1 m, pipe spacing of 30 m) combined with biochar (soil layer of 0~20 cm), and no drainage, are, respectively, recorded as S, B–S, and CK.

In May 2022, corrugated polyvinyl chloride pipes were buried under the test site with drainage holes on the surface of the pipes, and each pipe outlet was connected to a collector pipe, which was connected to a large catchment well, using a small pumping station for drainage. The slopes of the suction pipe and collection pipe were 2‰ and 3‰, respectively. The biochar was applied at 30 t ha^{-1} (on a dry-weight basis) and spread manually with a hand spreader in the field [33]. The day after application of biochar, it was incorporated to the top 20 cm soil depth with a rotary power harrow. The characteristics of biochar are shown in Table 2. Biochar was analyzed for no naphthalene, acenaphthylene, acenaphthene, fluorene, phenanthrene, etc. This indicates that the addition of this biochar to the soil will not pollute the soil and the environment.

Table 2. Basic parameters in biochar.

Feedstock	pH	C (%)	N (%)	Specific Surface Area (m^2/g)	Dry Bulk Density (g/cm^3)
Peanut shell	8.33	54.41	2.31	16.7	0.22

2.3. Sampling and Measurement of Soil Properties

On 31 August 2022, according to a simple random sampling scheme, a total of 27 soil samples were taken in three experimental fields at a sampling depth of 0~20 cm. The minimum distance between sampling points in each experimental field was 20 m. The sampling sites are shown in Figure 3. This means nine replicates per treatment. Each soil analysis sample was subdivided into three parts. The first part was a fresh soil sample, which was stored in a refrigerator at −4 °C and was used to determine soil ammonium (NH_4^+-N) and nitrate (NO_3^--N). The second part comprised fresh soil samples stored in a refrigerator at −80 °C for the determination of soil bacteria and soil enzyme activity.

The third part of the soil was air-dried and sieved to determine the physical and chemical properties of the soil: soil pH, soil electrical conductivity (EC), available phosphorus (AP), soil organic matter (SOM), and total nitrogen (TN).

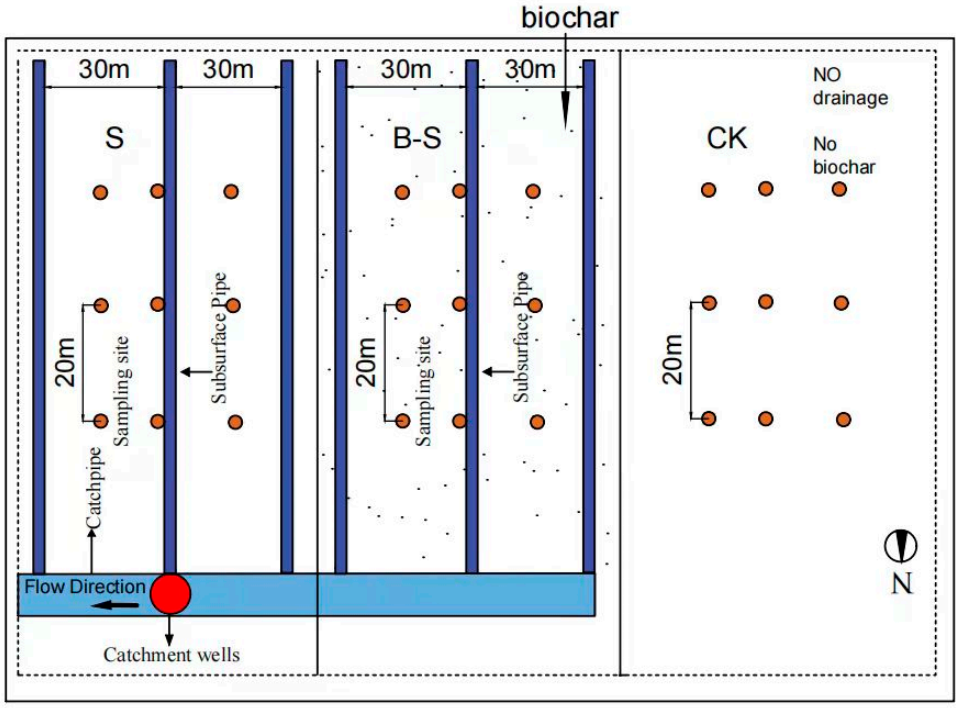

Figure 3. Subsurface pipe layout and sampling sites.

pH was measured on 1:2.5 soil-to-water mixtures using a pH meter (PHS-25, Shanghai, China). EC was measured on 1:5 soil-to-water mixtures at 25 °C by an electrical conductivity meter (DDSJ-308-a, Shanghai, China). Soil water content (W) was determined by the oven drying method. The NO_3^--N, NH_4^+-N, and TN were measured with a Continuous Flow Analyzer (AA3-HR, Germany) as described in [20]. The concentration of available phosphorus (AP) in the soil was determined using a UV/visible spectro-photometer (UV-1200, Tianmen, China) [34]. The potassium dichromate method was employed to determine SOM [35,36].

2.4. Soil Enzyme Activities

Determination of NH_3^--N produced by urease hydrolysis of urea was achieved using the indophenol blue colorimetric method in response to urease UE activity as described in [37]. The activities of soil catalase were measured according to [38]. Determination of soil alkaline phosphatase ALP activity was measured according to [39].

2.5. Soil DNA Extraction and Sequencing

The total DNA of the soil samples was extracted, primers (Forward primer, ACTCC-TACGGGAGGCAGCA; reverse primer, GGACTACHVGGGTWTCTAAT) were designed according to the conserved regions, and the sequencing junction was added at the end of the primers for PCR amplification, purification, quantification, and homogenization to form a sequencing library. Then, library quality control was performed, and the qualified libraries were sequenced by Illumina HiSeq 2500.

Microbial diversity analysis includes the following operations: quality control of initial sequencing sequences, including low-quality filtering and length filtering, to obtain high-quality sequences, and denoising/clustering the high-quality sequences and classification into OTUs or ASVs for diversity analysis, analysis of variance, and correlation analysis [40–44].

2.6. Statistical Analyses

Boxplots of bacterial alpha diversity index and barplots of soil physicochemical properties were plotted using Origin 2018, and the Tukey's truly significant difference (HSD) test was used to analyze the differences in these parameters in different soil treatments. Relative abundance of dominant bacterial phylum in soil samples was plotted using Origin 2018. Redundancy analysis was performed using Canoco 5.0 to explore the correlation between soil bacterial community structure and soil properties [45].

3. Results

3.1. Soil Physical and Chemical Properties

As shown in (Figure 4), both S and B–S amendments reduced EC, W, and NH_4^+-N compared to CK ($p < 0.05$). B–S significantly increased not only the NO_3^--N, but also the SOM, pH, AP, and TN ($p < 0.05$).

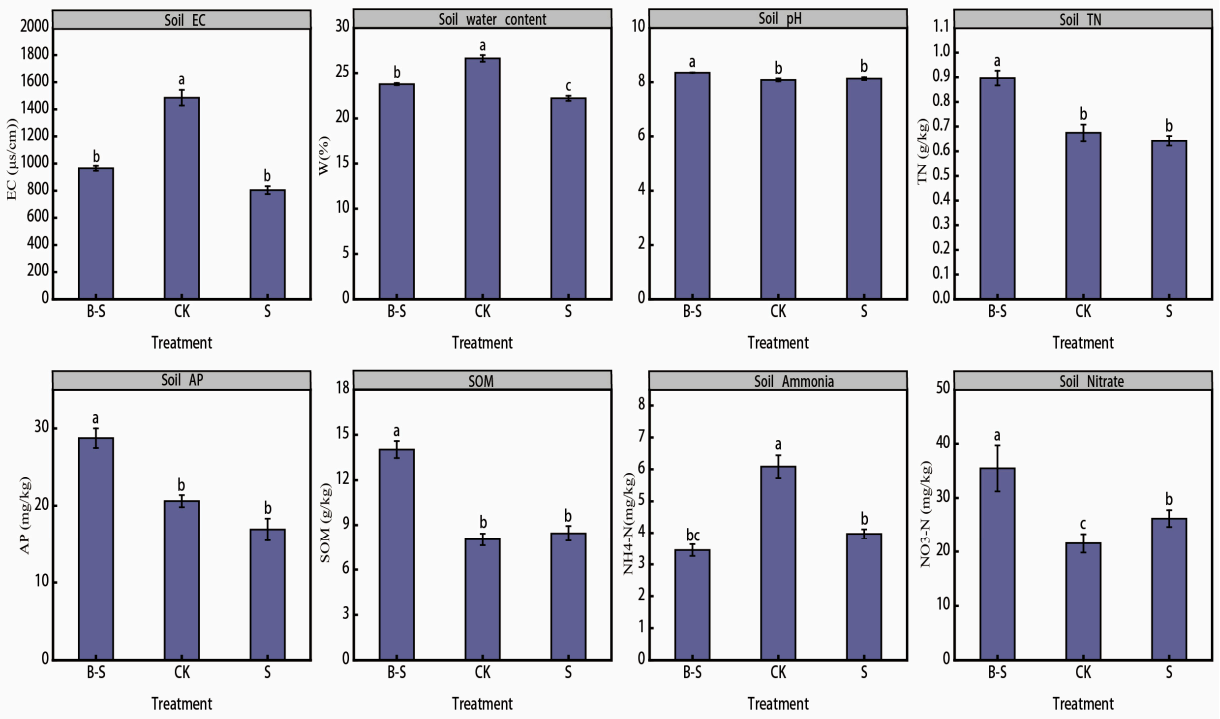

Figure 4. Differences in physicochemical properties of soils with different treatments (mean ± standard error, N = 9; a, b, and c in the table indicate significant differences between treatments.).

3.2. Changes in Soil Enzyme Activity

Both treatments, B–S and S, significantly increased soil enzyme activity, as shown in Table 3. Alkaline phosphatase (ALP) activity was significantly higher in CK than in S, while significantly lower than in B–S, probably because ALP activity was related to soil pH. Catalase (CAT) and soil urease were significantly higher in both B–S and S treatments than in CK ($p < 0.05$). Soil urease activity was significantly higher ($p < 0.05$) under B–S treatment compared to S. However, CAT activity was not significantly higher.

Table 3. Enzyme activity between treatments (mean ± standard error; N = 9).

Treatment	CAT (U/mL)	ALP (IU/L)	Urease (U/L)
B–S	68.15 ± 6.30 a	7.63 ± 0.24 a	587.97 ± 30.87 a
CK	47.94 ± 8.93 b	5.45 ± 0.36 b	433.08 ± 31.27 c
S	71.85 ± 6.39 a	4.47 ± 0.23 c	493.67 ± 33.12 b

Note(s): a, b, and c in the table indicate significant differences between treatments.

Redundancy analysis (RDA) between soil physicochemical properties and enzyme activity showed that soil enzyme activity was influenced by environmental factors (Figure 5). In RDA, pH, SOM, TN, AP, W, EC, NH_4^+-N, and NO_3^--N explained about 99.98% of the variation in enzyme activity, namely, 96.64% in the first axis and 3.35% in the second axis. Urease, ALP, and CAT were positively correlated with environmental factors AP, NO_3^--N, SOM, and pH, and negatively correlated with NH_4^+-N and EC. The strongest positive correlation was found between urease and TN, the strongest positive correlation was found between ALP and AP, and the strongest negative correlation was found between CAT and W. CAT and urease produced the greatest response to changes in environmental factors, indicating that CAT and urease are more sensitive to changes in environmental alterations than ALP. AP was the dominant factor in the change in enzyme activity (R^2 = 53.0%, $p < 0.05$), followed by NO_3^--N (R^2 = 14.8%).

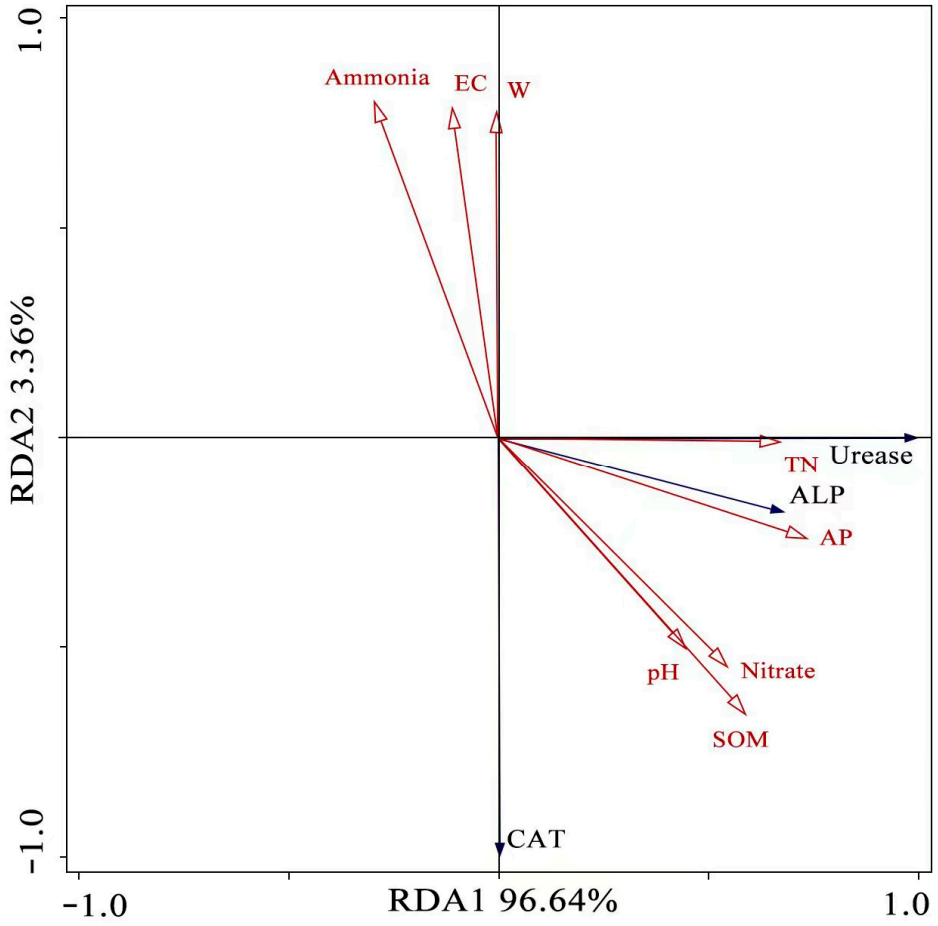

Figure 5. Redundancy analysis (RDA) of the correlation between soil parameters and enzyme activity.

3.3. Bacterial Community Diversity

The differences in soil bacterial community diversity between samples were evaluated by calculating Chao1 and Shannon indices (Figure 6). The results showed that the Chao1 and Shannon indices of the soil microbial community were significantly higher in both B–S and S treatments than in CK ($p < 0.05$). The Chao1 and Shannon indices of soil communities under subsurface drainage combined with biochar treatment were significantly higher than those of CK and S ($p < 0.05$). The results of the study indicate that subsurface drainage combined with biochar treatment had a significant effect on both soil community abundance and diversity.

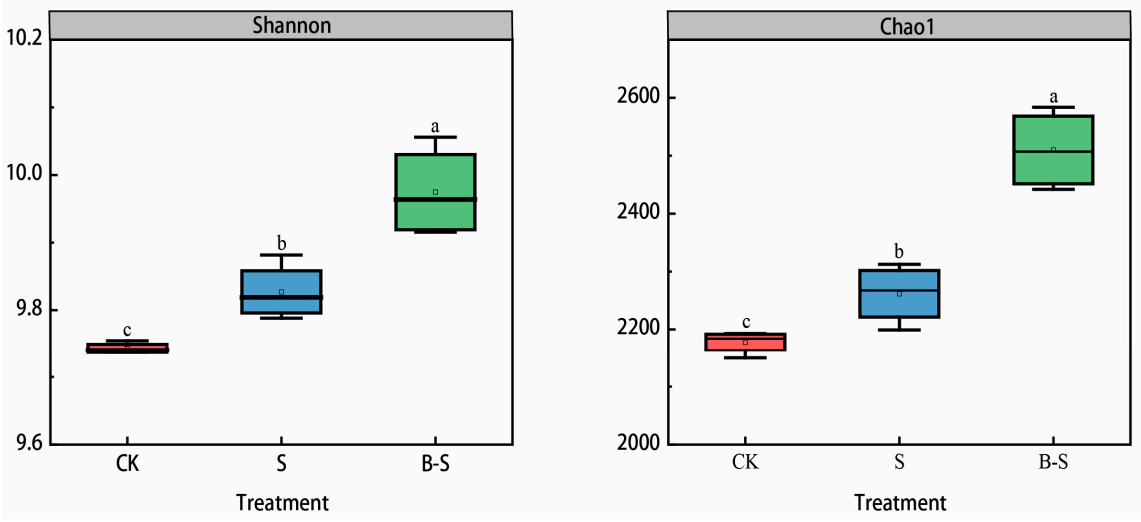

Figure 6. Alpha diversity of soil bacteria from different treatments, with different lowercase letters above each box in the same subplot indicating differences between groups (Tukey's HSD test, $p < 0.05$).

3.4. Changes in the Abundance and Composition of Microbial Communities

The two amendments altered not only the soil microbial diversity and abundance but also the soil community composition (Figure 7, Table 4). At the phylum level, the species composition was essentially the same in all soil samples, and the top nine bacterial phyla in terms of relative abundance were Proteobacteria, Gemmatimonadota, Bacteroidota, Actinobacteriota, Chloroflexi, Myxococcota, Methylomirabilota, Nitrospirota, and Acidobacteriota. The dominant phylum accounted for more than 93% of the bacterial sequences in all samples. Proteobacteria was the most abundant, accounting for 36.12~40.41% of the total composition. The relative abundance of Acidobacteriota phylum, Chloroflexi phylum, Gemmatimonadota phylum, and Myxococcota phylum was significantly different between the three treatments ($p < 0.05$). The relative abundance of Proteobacteria phylum in B–S treatment was significantly higher than the other two treatments. In B–S, the relative abundance of Methylomirabilota phylum and Nitrospirota phylum was significantly higher than in CK, while it was not significantly different from that of S treatment.

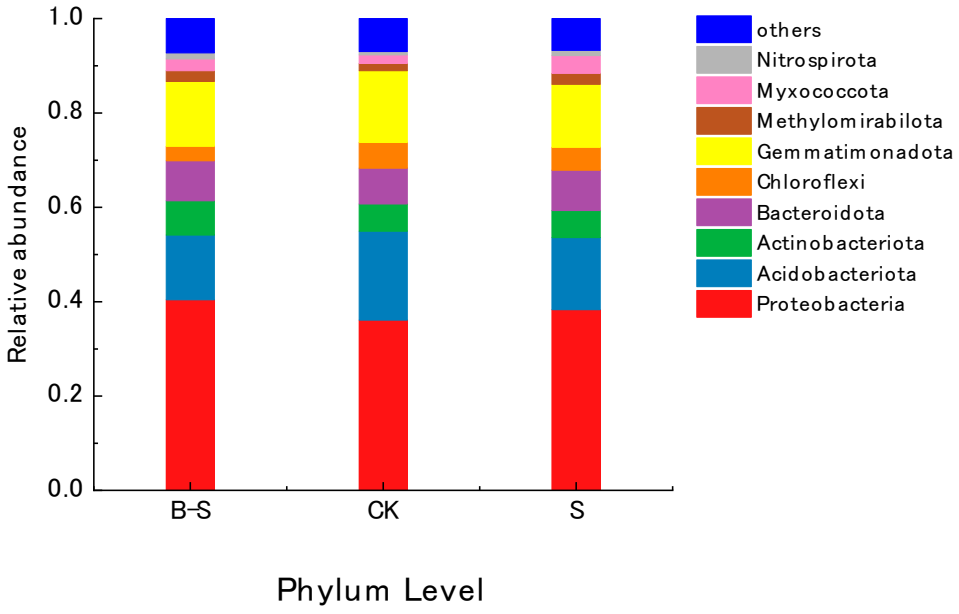

Figure 7. Relative abundance and community composition of the dominant bacterial phylum in the soil of each treatment.

Table 4. Effect of different treatments on the relative abundance (%) of dominant phyla in soil (mean ± standard error; N = 9).

Treatment	Proteobacteria	Acidobacteriota	Actinobacteriota	Bacteroidota	Chloroflexi	Gemmatimonadota	Methylomirabilota	Myxococcota	Nitrospirota
B–S	40.41 ± 2.27 a	15.31 ± 0.67 b	7.22 ± 0.35 a	8.51 ± 0.33 a	3.06 ± 0.23 c	13.75 ± 0.69 b	2.30 ± 0.14 a	2.49 ± 0.19 b	1.27 ± 0.17 a
CK	36.12 ± 0.88 b	18.81 ± 0.54 a	5.77 ± 0.11 b	7.61 ± 0.42 a	5.46 ± 0.15 a	15.21 ± 0.26 a	1.51 ± 0.19 b	1.80 ± 0.17 c	0.72 ± 0.07 b
S	38.30 ± 2.97 b	13.73 ± 0.20 c	5.72 ± 0.29 b	8.54 ± 0.18 a	4.34 ± 0.15 b	13.33 ± 0.55 c	2.31 ± 0.06 a	3.79±0.29 a	1.09 ± 0.09 a

Note(s): a, b, and c in the table indicate significant differences between treatments.

3.5. The Relationship between Soil Properties and Bacterial Abundance

RDA showed that the relative abundance of soil bacteria was influenced by environmental factors (Figure 8). In RDA, pH, SOM, TN, AP, W, EC, NH_4^+-N, and NO_3^--N explained about 94.35% of the variation in the relative abundance of soil bacteria, namely, 70.49% in the first axis and 23.86% in the second axis. Bacteroidota, Methylomirabilota, Myxococcota, Nitrospirota, Actinobacteriota, and Proteobacteria were positively correlated with environmental factors AP, NO_3^--N, SOM, pH, and ALP. Bacteroidota, Methylomirabilota, Myxococcota, Nitrospirota, Actinobacteriota, and Proteobacteria were negatively correlated with NH_4^+-N, EC, and W, but Chloroflexi, Acidobacteriota, and Gemmatimonadota showed positive correlation with them. The RDA showed that SOM was the dominant factor in the variation in bacterial abundance (R^2 = 38.5%, $p < 0.05$), followed by ALP (R^2 = 20.0%).

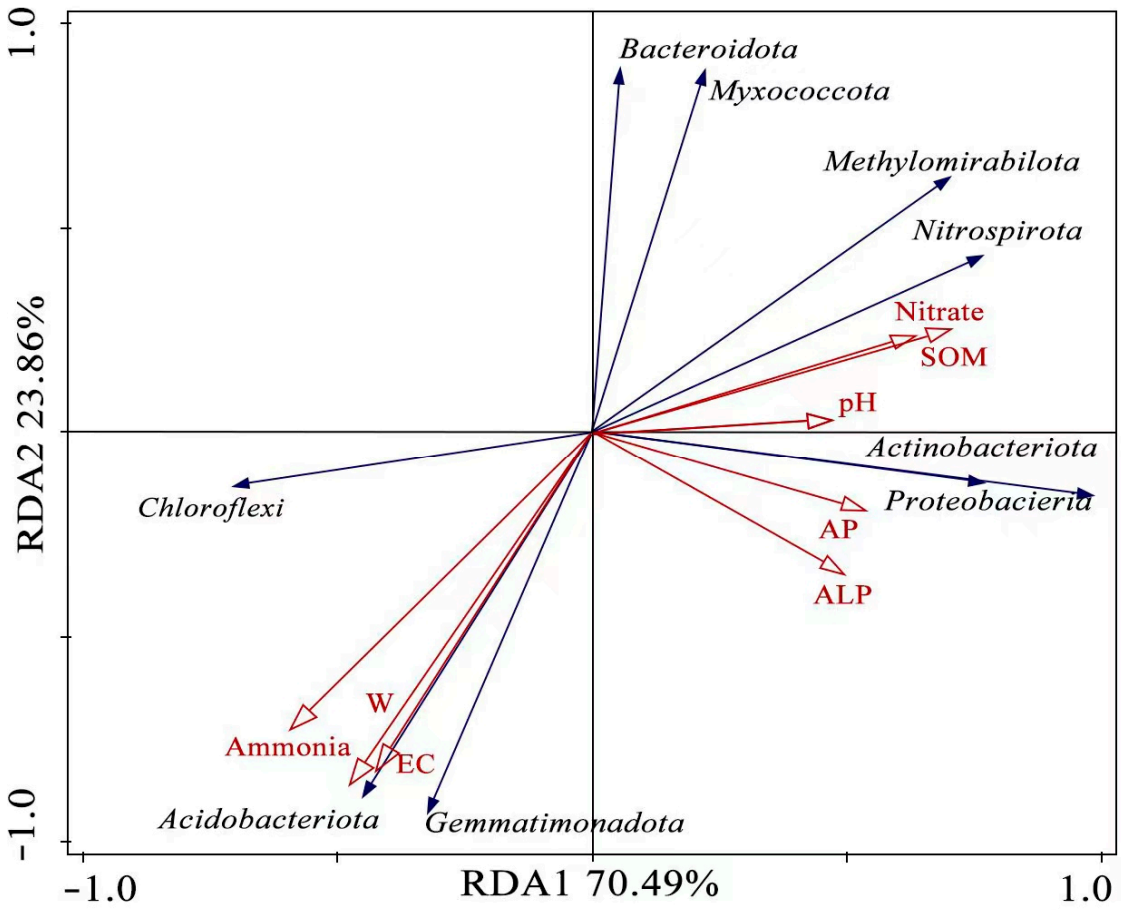

Figure 8. Redundancy analysis (RDA) of the correlation between soil parameters and soil bacterial community composition.

4. Discussion

4.1. Changes in Soil Physical and Chemical Properties

In saline areas with poor drainage, the way the land is improved and utilized is critical, because it affects the ecology of the soil. Different land improvement methods regulate soil physicochemical properties differently [20,46–48]. In this study, we found that the two measures had significant effects on soil EC, W, pH, NH_4^+-N, NO_3^--N, urease, and CAT, indicating that subsurface drainage combined with biochar had an important effect on the improvement of some soil physicochemical properties in the short term.

Compared with CK, the B–S treatment significantly reduced soil EC and soil water content. Probably because of the rainfall (27 mm) on 22 August 2022, a large amount of water accumulated on the soil surface and the water table rose. After strong drainage by subsurface drainage and salt removal techniques, the soil water content of the shallow soil was rapidly reduced, in addition to the rainwater dissolving and then leaching soluble salts into the subsoil, thus reducing the soil EC. However, the soil water content of B–S was significantly higher than that of S. This may be due to the relatively small particles of biochar blocking the large pores between soils or combining with soil inorganic minerals to reduce soil pores, thus decreasing the hydraulic conductivity of soil, and in addition, the larger specific surface area and smaller pores of biochar increase the water absorption capacity of the soil, thus reducing water loss [49]. B–S had a higher pH than that of the 0–20 cm soil layer due to the addition of biochar itself at 8.33, which may account for the significantly higher pH of B–S than the CK and S treatments, and the addition of biochar may have elevated the pH of the soil, which is consistent with the findings of Fan et al. [50].

Significant changes in soil nutrient status occurred after biochar addition, possibly due to retention of synthetic nutrients (e.g., applied fertilizers) or adsorption on biochar [51]. The CEC of soil increased after biochar application, which facilitated the fixation and adsorption of NH_4^+ [24,52,53]. Positively charged NH_4^+ may be adsorbed on soil colloidal particles or on negatively charged functional groups on biochar particles [54,55]. Therefore, biochar is beneficial to reducing the leaching of NH_4^+-N. However, in this study, both subsurface pipes combined with biochar treatment and subsurface drainage treatment were detected to have higher NO_3^--N content and lower ammonium nitrogen content, which may be mainly due to the higher urease activity and Nitrospirota abundance in the B–S and S treatments, which accelerated the nitrification rate of nitrogen. Furthermore, B–S treatment reduced soil nutrients compared with S, probably because biochar is a direct source of N on the one hand, and because of its larger surface area and higher CEC on the other hand.

Overall, the B–S treatment both effectively reduced EC and removed excess water through the subsurface drainage system, and improved soil nutrient retention through the unique physicochemical properties of biochar.

4.2. The Relationship between Soil Properties, Bacterial Abundance, and Soil Enzymes

Environmental conditions under different land use patterns have a large impact on soil microbial communities and diversity [56]. Subsurface drainage combined with biochar as an amendment can cause changes in soil ecosystem function and thus in the structure of microbial communities [57–60]. It is well documented that bacterial communities are sensitive to changes in soil properties in soils that are environmentally stable in their natural habitat [61,62]. In particular, soil chemical properties such as pH [63,64], SOM [23] and N [45] are the main drivers of soil microbial community response to environmental changes [65,66]. RDA showed that SOM was the dominant factor in the variation in bacterial abundance (R^2 = 38.5%, $p < 0.05$), which is consistent with [67]. Bacteroidota, Methylomirabilota, Myxococcota, Nitrospirota, Actinobacteriota, and Proteobacteria were negatively correlated with EC. Lu et al. [68] studied the effect of salt stress levels on soil microbial community structure and found that 1350 μS/cm soil EC is an inflection point beyond which soil salt stress only has a serious effect on microbial activity. It has been reported that increasing soil salinity does not significantly affect the abundance and

diversity of soil bacterial communities [69]. It has also been reported that increased soil salinity decreases soil nutrients, microbial diversity, biomass, and the metabolic activity of microorganisms [70]. In this study, Methylomirabilota and Nitrospirota were more negatively correlated with EC, and thus the relative abundance of Methylomirabilota and Nitrospirota in both S and B–S was higher than in CK, which was consistent with the pattern of EC. The positive correlation of Acidobacteriota with EC was stronger, so the relative abundance of Acidobacteriota in CK was higher than that in S and B–S. This may be due to different tolerance of different genotypes of microorganisms to osmotic stress, with some microorganisms failing to adapt to osmotic stress upon activation or death with increasing salinity, while some microbial communities tend to prefer highly osmotic environments [71].

The addition of biochar can provide a suitable habitat for microorganisms, thereby increasing the relative abundance of soil bacterial communities, because of its pore structure and adsorption of water and nutrients [59]. Doan et al. [72] found that the addition of biochar significantly increased the Simpson index. R. Yao et al. [73] identified the dominant phylum of soil bacteria when Proteobacteria, Bacteroidota, Acidobacteriota, and Chloroflexi were found in soil samples from coastal saline lands. In addition to these bacteria found in the soil samples of this study, Gemmatimonadota, Myxococcota, Methylomirabilota, Nitrospirota, and Actinobacteriota were also found as dominant bacterial phylum. The highest relative abundance of Proteobacteria among all treatments shown in this study is consistent with the results of Lucas et al. [74], who reported that Proteobacteria species can survive in salt and other extreme environments. Concentrates from high-temperature pyrolysis of biochar have proven to be an extremely easy carbon source for soil Actinobacteriota to decompose [75]. This may also be the reason why the relative abundance of Actinobacteriota under the added biochar treatment condition was significantly higher than the other two groups in this study. Gemmatimonadota have the ability of aerobic methanation and its relative abundance is negatively correlated with soil water content [76]. However, Ren et al. [77] reported that Gemmatimonadota were positively correlated with soil water content and Murphy et al. [78] reported that Myxococcota were aerobic bacteria and negatively correlated with soil water content, which is consistent with the relationship between W and relative abundance of Gemmatimonadetes and Myxococcota that was significantly affected by biochar and subsurface drainage in our study. In our study, the relative abundance of Acidobacteriota was found to be significantly lower in B–S compared to the other two groups, and Xu et al. [79] observed that Acidobacteriota are usually the dominant bacteria in oligotrophic and low-pH soils, and the decrease in their abundance may be due to the increase in soil pH and nutrient content after the addition of biochar. In this research, Chloroflexi showed a strong negative correlation with nitrate and SOM and a positive correlation with W. The relative fractional abundance of Chloroflexi in CK was significantly higher than that of B–S and S. Chloroflexi are parthenogenic anaerobes that can metabolize autotrophically through photosynthesis, and many microorganisms can grow in the inter-rhizosphere under anaerobic conditions [80]. Therefore, in terrestrial environments, the growth and reproduction of Chloroflexi are not dependent on the nutrient supply of the soil [81]. Yaliang et al. [82] reported that straw returned to the field significantly increased soil SOC content, but the relative abundance of Chloroflexi was significantly reduced. Lan et al. [83] reported that soil SOM content was positively correlated with the relative abundance of Methylomirabilota. The dominant genus in the phylum Nitrospirota, Nitrosomonas, can increase the inorganic nitrogen content of the soil by hydrolyzing urease [84]. In the present study, Nitrospirota and nitrate were positively correlated, and the relative abundance of both Nitrospirota and nitrate were highest in B–S. Members of Nitrospirota can also oxidize nitrite to nitrate, accelerating the rate of nitrogen nitrification [85]. In addition to this, the relative abundance of Nitrospirota phylum in coastal saline sites is also pH-dependent [86]. Soil enzyme activity controls soil organic matter decomposition rate and nutrient cycling processes [87]. Addition of biochar to the soil can increase the activity of enzymes related to N utilization such as urease [88].

Ebrahimi et al. [89] used gene expression programming (GEP) and artificial neural network (ANN) techniques for the determination of soil urease and alkaline phosphatase activities and showed that pH, EC, and SOM were the most effective parameters for the evaluation of urease and alkaline phosphatase activities. In addition to these factors, soil moisture conditions also affect soil enzyme activities. Zheng et al. [90] reported that soil urease and catalase were negatively correlated with mean annual precipitation.

5. Conclusions

This study showed the response of subsurface drainage combined with biochar measures on soil physicochemical properties and bacterial community composition. In this study, B–S significantly reduced EC and W by 35% and 10.65% compared to CK. Compared to CK and S, B–S significantly increased TN by 24.78% and 39.62%, AP by 28.29% and 69.82%, NO_3^--N by 64.65% and 35.45%, and significantly increased SOM by 74.69% and 66.10%, respectively. It also significantly increased ALP and urease activities. The RDA showed that CAT and urease had the greatest response to changes in environmental factors, indicating that CAT is more sensitive to changes in environmental alterations than ALP. AP was the dominant factor in the change inf enzyme activity (R^2 = 53.0%, $p < 0.05$), followed by NO_3^--N (R^2 = 14.8%). SOM was the dominant factor in the variation in microbial abundance content (R^2 = 38.5%, $p < 0.05$), followed by ALP (R^2 = 20.0%). The results of this study show that subsurface drainage combined with biochar can reduce EC and change soil moisture conditions in coastal areas, while also changing some of the physicochemical properties of the soil to affect soil enzyme activity and soil bacterial community composition. However, biochar is affected by raw materials and pyrolysis conditions, and biochar contains carcinogenic polycyclic aromatic hydrocarbons (PAHs). In addition, biochar can adsorb harmful substances such as heavy metals and organic matter from the soil due to its porous structure, alkaline properties, and abundance of functional groups. Therefore, the potential environmental risks of biochar need to be considered when it is applied to soils, and biochar with good amelioration effect, low contaminant content, and low environmental risk should be selected. Further assessment of the long-term positive and negative impacts of biochar on soil quality and crop yields in the region is also urgently needed in the future.

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