

Rhizosphere microorganisms and soil physicochemical properties of restored wetland plant communities at cutting slash of *Populus deltoides* in Dongting Lake

Sijia Tan (✉ 1075642992@qq.com)

Central South University of Forestry and Technology

Lijuan Jiang

Central South University of Forestry and Technology

Jingyi Liu

Central South University of Forestry and Technology

Zhangquan Zeng

Hunan Academy of Forestry

Yaqin Xiao

Hunan Academy of Forestry

Xiaoli Wu

Hunan Academy of Forestry

Yandong Niu

Hunan Academy of Forestry

Research Article

Keywords: Dongting Lake, Restoration slash, Renewal plant community, Soil physicochemical properties, Rhizosphere microorganism

Posted Date: October 18th, 2022

DOI: <https://doi.org/10.21203/rs.3.rs-1648020/v1>

License:   This work is licensed under a Creative Commons Attribution 4.0 International License.

[Read Full License](#)

Version of Record: A version of this preprint was published at Wetlands on May 10th, 2023. See the published version at <https://doi.org/10.1007/s13157-023-01696-1>.

Abstract

Carex spp. and *Artemisia selengensis* communities are typical renewal wetland plant communities at cutting slash of *Populus deltoides*. However, how rhizosphere microorganisms and soil factors interact during natural restoration in plant communities is unknown. Plots containing *Carex* spp. and *Artemisia selengensis* in the slash area were investigated, and the *P. deltoides* plantation area at a lake shore was sampled as a control. The results revealed that the richness and diversity indices of the fungal community in the *Carex* spp. community were higher than those in the *A. selengensis* and *P. deltoides* undergrowth communities. Ascomycota was the dominant phylum in the soil of *Carex* spp. community whereas Basidiomycota was the dominant phylum in the *A. selengensis* community. The richness and diversity indices of the rhizosphere bacterial community in the control were higher than those in communities of *Carex* spp. and *A. Selengensis*. Proteobacteria and Actinobacteria were the dominant phyla of the rhizosphere bacterial community in the control plot. Soil water content (WC), proportion of clay (CY), and nutrient content, as well as catalase activity (CAT) in the soil of *Carex* spp. community were the highest, whereas those in the control were the lowest. Conversely, the bulk density (BK) and proportion of gravel in the control plot were the highest. RDA found that the CY, organic matter (OM), ammonium nitrogen (AN) and nitrate nitrogen (NN) content in the soil were the key factors affecting the structure and composition of the rhizosphere microbial community.

Introduction

Since the 1980s, plantations of *P. deltoides*, an exotic species, have been established on a large scale around the Dongting Lake area, changing not only the native wetland vegetation species but also drastically reducing their diversity. Consequently, the soil texture of the wetland changed, that is, proportion of soil gravel increased, and the water retention capacity decreased. To restore the degraded wetland ecosystem and its function (Ren et al. 2016; Lavenne et al. 2019), *P. deltoides* trees were removed from the Dongting Lake area, thus ecological restoration on the *P. deltoides* cutting slash is paramount. Therefore, basic theoretical research to provide guidance for the restoration should be carried out. The identification of the interaction and coupling relationship between roots, soil, and rhizosphere microorganisms is essential for evaluating the stability of the wetland ecosystem structure and its function.

Wetland soil provides nutrients and water for wetland plant growth; in turn, wetland plants produce and release substances that can affect soil material turnover, soil enzyme and microorganism activity, thus affecting soil properties (Hien et al. 2014; Cochrane et al. 2018; Zahra et al. 2019). Nutrient cycling within plants and in soil are closely related to microbial decomposition. Microorganisms influence soil fertility by mineralizing and solidifying soil nutrients, consequently affecting the growth of aboveground plants (Stefanowicz et al. 2021). The rhizosphere is the contact area between plants and soil and is region of soil where microorganisms are the most active; it is also an important starting point for studying the activities and functions of soil microorganisms (Feudis et al. 2016; Liu et al. 2020). Therefore, increasing attention has been paid in recent years to the research on rhizosphere microorganisms and the soil

environment in wetland plant communities. Although numerous studies have been conducted on the relationship between rhizosphere microorganisms and soil properties, these studies have largely focused on how to employ rhizosphere microorganisms to regulate the soil environment and promote plant growth and development in response to stress (Bakker et al. 2015; Pivato et al. 2017). However, there has been little research on the interaction and coupling relationship between plant communities, rhizosphere microorganisms, and soil environment during wetland restoration. In this study, the plant communities of restoration in the *P. deltoides* slash removal at Dongting Lake were investigated, whereas the plant communities on the *P. deltoides* lake shore were used as the control. To obtain fundamental ecological information on wetland restoration in slash sites and biodiversity conservation in wetlands, the rhizosphere microbial community structure, soil physicochemical properties, and their correlation and influence mechanism among different plant communities were examined.

Materials And Methods

Field experimental site

Overview of field experimental site

The study site is located in the Hengling Lake area (28°30' ~ 29°3' N, 112°38' ~ 112°57' E), shown in Fig. 1. It is a key part of Dongting Lake in central-south China and gathers all the incoming water from the Xiangjiang, Zijiang and Yuanshui Rivers, as well as most of the incoming water from Lishui River and three inlets of the Yangtze River. Moreover, it is an essential channel for flood discharge in the middle and lower reach of the Yangtze River Basin. Due to the perennial alluviation of rivers, Hengling Lake has a typical subtropical inland wetland ecosystem, with various wetland landscapes, such as beaches, meadows, swamps, and water bodies. There are rich vegetation types in this area, with 397 species belonging to 196 genera and 106 families. Herbs, such as *Polygonum hydropiper*, *Artemisia selengensis*, *Miscanthus lutarioriparius*, *Phragmites australis*, *Hemisteptia lyrata* and *Oenanthe javanica*, are the dominant species in this area.

Sampling Site

In April 2021, two typical wetland communities of *Carex* spp. and *A. selengensis*, which naturally restored in *P. deltoides* cutting slash with the same site conditions, were used as experimental plots, and the *P. deltoides* plantation at the lake shore was taken as the control plot (CK). Each plot had an area of approximately 200 m × 200 m, and each plot has three belt transects (50 m × 200 m). A total of 45 quadrats (2 m × 2 m) were set in each transect according to the five-point sampling method (details are shown in Table 1).

Table 1
Status of experimental plots

sampling site code	longitude and latitude	constructive specie	Restoration age(year)
CK	112°48'48.06"E,28°45'33.16"N	<i>Populus deltoides</i>	-
AS	112°49'51.16"E,28°46'22.26"N	<i>Artemisia selengensis</i>	three
CX	112°47'47.87"E,28°44'25.39"N	<i>Carex</i> spp.	three
Note: CX: <i>Carex</i> spp. community; AS: <i>Artemisia selengensis</i> community; CK: the control plot, the same below.			

Materials Collection

Non-rhizosphere soil

A 1 m deep section was dug in each quadrat, and 1 kg of topsoil (surface layer 0–20 cm) was collected with an undisturbed soil sampler and put into Ziplock bag for chemical and physical analysis. A portion of the soil samples was stored in a refrigerator to determine the indices of fresh soil, while another portion was air-dried and sieved through 2 mm and 0.149 mm sieves to determine the chemical properties of the soil. The undisturbed surface layer soil (0–20 cm) was collected using a cutting ring and transferred to the laboratory for the analysis of soil bulk density, water content, and other physical properties (Shao et al. 2020).

Rhizosphere Soil

Based on the distribution of plant roots of the section, roots with soil were dug out, and soil on the root surfaces was then gently brushed off with a sterile brush and collected as rhizosphere soil samples (Chen et al., 2019). According to the sample belt transects, the rhizosphere soil of each sample square was evenly mixed, placed into a sterilized centrifuge tube, and then quickly placed into liquid nitrogen in low temperature preservation and transferred to Shanghai Majorbio Bio-pharm Technology Co., Ltd for extraction and sequencing of rhizosphere microorganisms.

Soil Physicochemical Properties

The drying constant weight method was used to determine the bulk density (BK), porosity (PV), and water content (WC) of soil samples; The soil particle size composition was determined by laser particle size analyzer (Bettersize 2000, China). The soil catalase activity (CAT) was measured using a kit + enzyme-labeled instrument (Epoch, USA). The soil samples were mixed with distilled water; the pH value and electrical conductivity (EC) of the soil were measured using a portable analyzer (YSI, USA). The soil

organic matter (OM) was measured using the potassium dichromate external heating method; an elemental analyzer was used to measure total nitrogen (TN) of the soil sample. Nitrate-nitrogen (NN) content was measured using phenol disulfonic acid colorimetry, and ammonium nitrogen (AN) was measured using Nessler's reagent method (Gong et al. 2006), total phosphorus (TP) was determined using the sodium hydroxide melting-molybdenum antimony colorimetric method, whereas the available phosphorus (AP) was measured using the 0.5 mol·L⁻¹ sodium bicarbonate extraction-molybdenum antimony colorimetric method (Pan et al. 2015).

DNA Extraction And Amplicon Sequencing

Total microbial genomic DNA was extracted from the rhizosphere soil samples using the E.Z.N.A.® Soil DNA Kit (Omega Bio-tek, Norcross, GA, U.S.), according to the manufacturer's protocol. Moreover, the integrity, concentration, and purity of DNA were determined via 1.0% agarose gel electrophoresis and a NanoDrop® ND-2000 spectrophotometer (Thermo Scientific Inc., USA); the DNA was kept at -80 °C prior to further use.

The hypervariable region V3-V4 of the bacterial 16S rRNA gene were amplified with primer pairs 338F(5'-ACTCCTACGGGAGGCAGCAG-3') and 806R (5'-GGACTACHVGGGTWTCTAAT-3') (Liu et al. 2016) using an ABI GeneAmp® 9700 PCR thermocycler (ABI, CA, USA). The PCR amplification was performed in a mixture including 4 µL 5 × Fast Pfu buffer, 2 µL of 2.5 mM dNTPs, 0.8 µL of each primer (5 µM), 0.4 µL of Fast Pfu polymerase, 0.2 µL of bovine serum albumin, 10 ng of template DNA, and ddH₂O to a final volume of 20 µL. Moreover, the PCR amplification conditions were as follows: initial denaturation at 95 °C for 3 min, followed by 27 cycles of denaturing at 95 °C for 30 s, annealing at 55 °C for 30 s, extension at 72 °C for 45 s, single extension at 72 °C for 10 min, and end at 10 °C.

The region ITS of the fungi gene were amplified with the primer pairs ITS1F (5'-CTTGGTCATTTAGAGGAAGT

AA-3') and ITS2R (5'-GCTGCGTTCTTCATCGATGC-3') (Jana et al. 2020) using an ABI GeneAmp® 9700 PCR thermocycler (ABI, CA, USA). The PCR amplification mixture containing 2 µL 10 × buffer, 2 µL 2.5 mM dNTPs, 0.8 µL each primer (5 µM), 0.2 µL rTaq polymerase, 0.2 µL of bovine serum albumin, 10 ng of template DNA, and ddH₂O to a final volume of 20 µL. The PCR amplification conditions were as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles of denaturing at 95 °C for 30 s, annealing at 55 °C for 30 s and extension at 72 °C for 45 s, and single extension at 72 °C for 10 min, and end at 10 °C.

All samples were amplified with triplicate. The PCR product was extracted from 2% agarose gel and purified using the AxyPrep DNA Gel Extraction Kit (Axygen Biosciences, Union City, CA, USA), according to the manufacturer's protocol, and quantified using a Quantus™ Fluorometer (Promega, USA). Purified amplicons were pooled in equimolar amounts and paired-end sequenced on an Illumina MiSeq PE300 platform (Illumina, San Diego, USA) according to the standard protocols provided by Majorbio Bio-pharm

Technology Co., Ltd (Shanghai, China). The raw sequencing reads were deposited into the NCBI Sequence Read Archive (SRA) database (Accession Number: MJ20210610077).

Sequence Data Analysis

Raw FASTQ files were de-multiplexed using an in-house Perl script before being quality-filtered by fastp version 0.19.6 (Chen et al. 2018) and merged by FLASH version 1.2.7 (Tanja et al. 2011). The optimized sequences were then clustered into operational taxonomic units (OTUs) using UPARSE 7.1 (Edgar et al. 2013) with a sequence similarity level of 97%. The most abundant sequence for each OTU was selected as a representative sequence. To minimize the effects of sequencing depth on alpha and beta diversity measures, the number of fungi and bactergene sequences from each sample were rarefied to 10,000, which still yielded an average Goods coverage of 97%. The taxonomy of each OTU representative sequence was analyzed using an RDP Classifier version 2.2 (Wang et al. 2007) against a database (silva138/16s_bacter and unite8.0/its_fungi) with a confidence threshold of 0.7. The statistical applications Excel and SPSS (22.0) were used to analyze data from vegetation and soil physics and chemistry.

Statistical Analyses

Excel and SPSS (22.0) software were used to statistically analyze data of vegetation, soil physics, and soil chemistry. One-way ANOVA and Turkey HSD analyses were used to test the significant differences among different data groups. Differences were either significant ($P < 0.05$) or extremely significant ($P < 0.01$).

Importance value (%) = (relative frequency + relative coverage + relative abundance) / 3

The Majorbio Cloud platform (<https://cloud.majorbio.com>) was used for bioinformatic analysis of the soil microbiota. Based on the OTUs information, rarefaction curves and alpha diversity indices including observed OTUs, Chao richness, Shannon index, and Good's coverage were calculated using mothur v1.30.1 (Schloss et al. 2009). The similarity of microbial communities in different samples was assessed using principal coordinate analysis (PCoA) based on Bray–Curtis dissimilarity using the Vegan v2.5-3 package. The linear discriminant analysis (LDA) effect size (LefSe) (Segata et al. 2011) (<http://huttenhower.sph.harvard.edu/LEfSe>) was used to detect the significantly abundant taxa (phylum to genera) of microbial communities among the various groups (LDA score > 2, $P < 0.05$). The distance-based redundancy analysis (db-RDA) was performed using the Vegan v2.5-3 package to investigate the effect of soil physicochemical properties on soil microbial community structures.

Results

Plant community characteristics in different experimental plots

Table 2
Species composition of plant communities at differential experimental plot

sampling site code	Herbaceous dominant species	Species number	Species of top 5 importance value
CK	-	11	<i>Artemisia selengensis</i> (18.71), <i>Oenanthe javanica</i> (14.38), <i>Polygonum hydropiper</i> (12.08), <i>Rorippa indica</i> (10.63), <i>Cardamine hirsuta</i> (9.07)
AS	<i>Artemisia selengensis</i>	14	<i>Artemisia selengensis</i> (30.44), <i>Trigonotis peduncularis</i> (7.11), <i>Phragmites australis</i> (6.73), <i>Mazus pumilus</i> (6.46), <i>Polygonum hydropiper</i> (6.30)
CX	<i>Carex brevicuspis</i> , <i>Carex dispalata</i>	22	<i>Carex brevicuspis</i> (17.70), <i>Carex dispalata</i> (15.84), <i>Polygonum hydropiper</i> (7.05), <i>Miscanthus lutarioriparius</i> (6.11), <i>Galium spurium</i> (6.07)

As shown in Table 2, the dominant species of plant communities differed among the three experimental plots. There were 22 species in the *Carex* spp. community; *Carex brevicuspis* and *Carex dispalata* were the dominant species and *Polygonum hydropiper*, *Miscanthus lutarioriparius*, and *Galium spurium* were the associated species in the community. There were 14 kinds of plants in the *A. selengensis* community; among them, *Artemisia selengensis* was the most significant and constructive species, and *Trigonotis peduncularis*, *Phragmites australis*, *Mazus pumilus* were associated species. There were 11 kinds of herbaceous plants in the control plot, among which *Artemisia selengensis*, *Polygonum hydropiper*, *Oenanthe javanica*, *Rorippa indica*, and *Cardamine hirsuta* were key understory species, but there were no discernable dominant herbaceous species.

Physical And Chemical Properties Of Soil From Different Plant Communities

Table 3
Physical and chemical properties of Soil from different plant communities

index	CK	AS	CX
water content (%)	24.23 ± 0.68 ^c	29.95 ± 1.71 ^b	38.50 ± 2.12 ^a
Bulk density (g·cm ⁻³)	1.39 ± 0.03 ^a	1.31 ± 0.10 ^a	1.02 ± 0.07 ^b
Clay (%)	3.27 ± 0.07 ^b	3.41 ± 0.20 ^b	3.86 ± 0.11 ^a
Silt (%)	90.23 ± 0.54 ^a	90.27 ± 0.44 ^a	90.55 ± 1.14 ^a
Gravel (%)	6.50 ± 0.60 ^a	6.32 ± 0.62 ^a	5.59 ± 1.23 ^a
Porosity (%)	38.29 ± 0.61 ^a	28.89 ± 5.10 ^b	30.76 ± 0.96 ^b
Catalase activity (U·g ⁻¹)	4.72 ± 0.24 ^b	5.81 ± 0.43 ^a	5.92 ± 0.24 ^a
pH value	6.56 ± 0.09 ^a	6.24 ± 0.13 ^b	6.40 ± 0.12 ^{ab}
electrical conductivity (uS·cm ⁻¹)	23.00 ± 0.50 ^c	38.10 ± 1.57 ^b	46.57 ± 3.13 ^a
total nitrogen (g·kg ⁻¹)	1.10 ± 0.04 ^b	1.16 ± 0.04 ^b	1.40 ± 0.04 ^a
Ammonium nitrogen (mg·kg ⁻¹)	0.24 ± 0.03 ^a	0.35 ± 0.07 ^a	0.26 ± 0.13 ^a
Nitrate nitrogen (mg·kg ⁻¹)	0.78 ± 0.01 ^b	1.06 ± 0.28 ^{ab}	1.32 ± 0.17 ^a
Total phosphorus (g·kg ⁻¹)	0.56 ± 0.01 ^b	0.60 ± 0.04 ^b	0.74 ± 0.09 ^a
Available phosphorus (mg·kg ⁻¹)	7.20 ± 1.21 ^b	16.23 ± 2.58 ^a	20.40 ± 2.53 ^a
Organic matter (g·kg ⁻¹)	14.27 ± 0.17 ^b	19.77 ± 2.16 ^a	21.13 ± 0.82 ^a
Note: The data in the table were mean standard deviation, and different lowercase letters indicate significant differences.			

All three experimental plots had acidic soils (Table 3), with pH values ranging from 6.24 to 6.56. Moreover, soil EC ranged from 23.00 to 46.57 (uS·cm⁻¹). The soil particle size composition was primarily silt, accounting for 90.23–90.55% of the total soil.

The soil of the *Carex spp.* community had the highest WC, oportion of clay(CY), proportion of silt, CAT, EC, TN, NN, TP, AP, and OM content, followed by the *A. selengensis* community, and those in the control plot, had the lowest. Conversely, soil BK and the proportion of gravel in the control were the highest, followed by the soil of *A. selengensis* community, then that of the *Carex spp.* community (the lowest). The soil PV and pH value of the control were the highest, followed by the *Carex spp.* community, and were the lowest in the *A. selengensis* community. The AN content in soil was the highest in the *A. selengensis* community, followed by the *Carex spp.* community, and was the lowest in the control.

The soil BK and pH value were lower in *A. selengensis* and *Carex spp.* communities, whereas soil WC, CY, EC, TN, and OM content were higher, soil nutrient content was elevated, and soil water storage capacity as well as environmental quality were improved, compared with the control.

Structure Of Rhizosphere Microbial Communities In Different Plant Communities

Effective sequencing data

After sequencing, 45,314 optimized fungal sequences were obtained in rhizosphere soil of the three experimental plots. Based on sequence similarities of 97.00%, they were divided into 1,979 fungal OTUs, including 15 phyla, 53 classes, 127 orders, 254 families, 465 genera, and 679 species. We obtained a 23,609 optimized bacterial gene sequences, which could be divided into 3,950 bacterial OTUs, including 47 phyla, 141 classes, 317 orders, 478 families, 777 genera, and 1,526 species.

As shown in Fig. 2, there were 169 fungi OTUs in rhizosphere soil shared by the three experimental plots, 108 OTUs shared by the control and *A. selengensis* community, 105 OTUs shared by the control and *Carex spp.* community, and 152 OTUs shared by the *A. selengensis* and *Carex spp.* communities. Among the three experimental plots, the *Carex spp.* community had the greatest number of unique OTUs (582). The number of unique OTUs in the *A. selengensis* community (431) was nearly identical to that in the control (432). In the rhizosphere soil of the three experimental plots, there were 1,481 bacteria OTUs, 342 of which were shared with the control and *A. selengensis* community, 629 with the control and *Carex spp.* community, and 278 with the *A. selengensis* and *Carex spp.* communities. Among the three experimental plots, the control had the largest number of unique OTUs (522), followed by the of *Carex spp.* community (384), and the *A. selengensis* community (314).

To summarize, the number of OTUs of rhizosphere microorganisms varied between experimental plots. Among the three experimental plots, the largest number of fungal OTUs in rhizosphere soil was from the *Carex spp.* community with 1,008 OTUs, followed by the *A. selengensis* community with 860 OTUs, and the lowest was in the control with 814 OTUs. However, the control had the most bacterial OTUs in the rhizosphere soil (2,974), followed by the *Carex spp.* community (2,772) and the *A. selengensis* community (2,415).

Abundance And Diversity Of Microbial Communities In Rhizosphere Soil

Table 4
Alpha index of rhizosphere soil microbial community (OTU level)

	sampling site code	Chao index	Shannon index
fungi	CK	391.66 ± 66.59	4.19 ± 0.08
	AS	464.67 ± 75.99	3.64 ± 0.37
	CX	482.31 ± 74.08	4.33 ± 0.43
bacteria	CK	2653.73 ± 20.08	6.51 ± 0.10
	AS	2139.68 ± 37.42	5.89 ± 0.08
	CX	2256.67 ± 211.52	5.92 ± 0.47
Note: The data in the table were mean standard deviation.			

In this study, the Chao index was employed to assess the richness of microbial communities in rhizosphere soil samples; the higher the Chao index, the higher the richness of microbial communities. The Shannon index was used to determine the diversity of microbial communities in the rhizosphere soil samples; the lower the Shannon index, the lower the diversity of microbial communities.

The findings revealed that the richness and diversity of rhizosphere microbial communities differed significantly amongst the three experimental plots (Table 4). Among them, the richest and most diverse fungal community was in the rhizosphere soil of the *Carex spp.* community. The richness of fungal community in the rhizosphere soil of the *A. selengensis* community was greater than that of the control, but the diversity of was lower. Among the three communities, however, the control had the most rich and diverse rhizosphere bacterial communities.

Species Composition Of Fungal And Bacterial Communities

The bacterial and fungal species composition (from phylum, family, genus, to OTU level) in the rhizosphere soil of the three experimental plots was investigated to determine the relationship between underground microbial communities and aboveground plant communities. There were also Unclassified (sequence without classification information in the database) and Norank (in the middle level of the taxonomic pedigree of the database but was not named yet).

Figure 3A analyzes the composition of fungal communities (at the phylum level) in the rhizosphere soil of the three experimental plots. The dominant fungal phyla were Ascomycota (48.22–65.27%) and Basidiomycota (21.27–36.01%), followed by Rozellomycota (0.73–7.08%), Mortierellomycota (1.42–3.95%), Glomeromycota (0.31–3.45%), Chytridiomycota (0.53–2.16%), and some unclassified_k_Fungi (7.12–8.38%). Ascomycota were the most abundant in the rhizosphere soil of the *Carex spp.* community, followed by those in the control plot, and the least abundant was in that of the *A. selengensis* community. Basidiomycota, Glomeromycota, and Chytridiomycota were the most abundant in the *A. selengensis*

community, followed by the control plot, and were the least abundant in the *Carex spp.* community. The control plot had the highest concentration of Rozellomycota, followed by the *Carex spp.* community, while the *A. selengensis* community had the lowest concentration. Mortierellomycota abundance was highest in the control, followed by that in the *A. selengensis* community, and it was the lowest in the rhizosphere soil of the *Carex spp.* community.

The dominating rhizosphere fungi in the three experimental plots were substantially different at the genus level (Fig. 3C). The genera with the highest abundance in the control plot were ranked as follows: *Saitozyma* (8.84%), *Inocybe* (5.44%), *Emericelopsis* (4.75%), *Cladosporium* (4.04%), *Penicillium* (3.74%), and *Mortierella* (3.68%), with a total relative abundance of 30.49%. In the rhizosphere soil of the *Carex spp.* Community, *Limonomyces* (8.56%), *Talaromyces* (7.85%), *Apiospora* (4.38%), *Fusarium* (3.55%), *Cladosporium* (3.4%), and *Paraphaeosphaeria* (3.3%) were the most abundant, with a total relative abundance of 31.04%. The *unclassified_c_Agaricomycetes* (Agaricomycetes) (14.96%), *Paraphoma* (3.63%), *Talaromyces* (9.2%), *Didymella* (4.9%), *Saitozyma* (4.54%), and *Emericelopsis* (3.06%) had the highest relative abundance in the rhizosphere soil of the *A. selengensis* community, with a total relative abundance of 40.29%.

The dominant phyla in the bacterial communities in the rhizosphere soil of the three experimental plots (Fig. 3B), were Proteobacteria (20.82–23.86%), Actinobacteriota (13.28–28.91%), Acidobacteriota (13.64–22.07%) and Chloroflexi (11.89–17.65%), followed by Methyloirradiota (1.01–4.56%), Myxococcota (3.29–4.27%), Verrucomicrobiota (0.37–1.85%), Desulfobacterota (1.54–2.85%), Bacteroidia (1.3–2.97%), Nitrospirata (0.97–2.07%), Latescibacterota (0.65–1.2%), Firmicutes (1.89–7.47%), and Gemmatimonadota (2.11–6.38%). Among these, Verrucomicrobiota and Desulfobacterota are more relatively abundant in the rhizosphere soil of the *Carex spp.* Community. Proteobacteria and Firmicutes had the largest abundance in the rhizosphere soil of the *A. selengensis* community, followed by that of the *Carex spp.* Community, and were the least abundant in the control plot. The abundance of Actinobacteriota and Gemmatimonadota in the rhizosphere soil of the *Carex spp.* Community was the highest, followed by that of the control, and the lowest was in the of *A. selengensis* community. The abundance of Acidobacteriota was the highest in the rhizosphere soil of the *A. selengensis* community, followed by that in the control plot, and the lowest was in the *Carex spp.* community rhizosphere soil; The abundance of Chloroflexi in the rhizosphere soil of control was the highest, then that of the *A. selengensis* community rhizosphere soil, the lowest was in the rhizosphere soil of the *Carex spp.* community; Nitrospirata was most abundant in the control plot, followed by the *Carex spp.* Community and *A. selengensis* community.

The dominant rhizosphere bacteria in the three experimental plots were also different at the family level (Fig. 3D, excluding unclassified families). Xanthobacteraceae (6.71%), Gemmatimonadaceae (4.44%), Roseiflexaceae (2.89%), Streptomycesaceae (2.42%), and Gaiellaceae (2.1%) had the highest relative abundance in the control plot; overall relative abundance was 18.56%. Nocardioideaceae (13.67%), Gemmatimonadaceae (6.29%), Xanthobacteraceae (5.72%), and Sphingomonadaceae (2.25%) were abundant in the rhizosphere soil of *Carex spp.* community, accounting for 27.93% of the overall relative

abundance. The rhizosphere bacteria with the highest abundance in the *A. selengensis* community rhizosphere soil were Xanthobacteraceae (10.3%), Bacillaceae (3.96%), Methylobacteriaceae (2.91%), Anaerolineaceae (2.59%), Solibacteraceae (2.5%), and Gemmatimonadaceae (2.05%), with a total relative abundance of 24.31%.

The closer the points on the principal coordinate analysis (PCoA) diagram are to one another, the more similar the species composition of the communities. As shown in Fig. 4, the PCoA results indicated that the contribution rates of the first axes of fungi and bacteria were 23.11% and 38.94%, and that the contribution rates of the second axes were 20.74% and 23.92%. At the OTU level, there were significant differences in the species composition of the microbial community among the three plant communities; however, the variation in microbial community composition of the same plant community at different sampling sites was not significant.

Overall, the results demonstrated that the composition of microbial communities in rhizosphere soil of the three experimental plots differed significantly at the genus, family, and OTU levels, despite having similar phyla. The dominant phyla of rhizosphere fungal communities of the three experimental plots were Ascomycota and Basidiomycota. The total relative abundance of Basidiomycota and Ascomycota in the *Carex spp.* community were the highest (86.54%), followed by the *A. selengensis* community (84.23%), and the control plot (79.06%). Proteobacteria, Actinobacteriota, Acidobacteriota, and Chloroflexi were the dominant phyla of rhizosphere bacterial communities in the three experimental plots. The total relative abundance of Proteobacteria, Actinobacteriota, Acidobacteriota, and Chloroflexi was highest (75.42%) in the *Carex spp.* community, followed by the control (74.54%), and lowest in the *A. selengensis* community (73.32%).

Redundancy Analysis Of Rhizosphere Microbial Community Distribution And Soil Physicochemical Properties

Table 5

Relationship between rhizosphere microbial community abundance and soil environmental factors

environmental factor		correlation coefficient	
		Axis 1	Axis 2
fungi	NN	0.9236	-0.3834
	AN	-0.9885	0.1511
	AP	-0.0992	-0.9951
	OM	-0.6553	-0.7554
	pH	0.6787	0.7344
	CY	0.9772	-0.2124
bacteria	NN	-0.2022	0.9793
	AN	-0.2986	0.9544
	OM	-0.0331	0.9995
	WC	-0.7644	0.6448
	PV	-0.2585	-0.966
	CY	-0.9261	0.3772
Note: NN: Nitrate nitrogen; AN: Ammonium nitrogen; AP: Available phosphorus; OM: Organic matter; CY: Clay			

PV: porosity; WC: Water content

Redundancy analysis (RDA) of microbial communities (at the phylum level) and major soil factors was conducted to investigate the relationship between microbial communities and soil properties (see Fig. 5 and Table 5). Considering the rhizosphere fungal community (Fig. 5A), Ascomycota was positively correlated with soil pH value, CY, and NN content, and negatively correlated with AN and OM content. In contrast, Basidiomycota was positively correlated with AN, OM, and AP content, and negatively correlated with NN content and pH value. In general, the key soil factors that affect rhizosphere fungal community differences were AN, NN, OM content, pH value, and CY.

Acidobacteriota was positively correlated with OM, and negatively correlated with PV, CY, and WC in the rhizosphere bacterial community (Fig. 5B). Similarly, Proteobacteria was positively correlated with soil OM content and negatively correlated with soil WC and CY. In contrast, Actinobacteriota were positively correlated with PV, CY, AN, NN, and OM content. Chloroflexi was positively correlated with PV and negatively correlated with WC, CY, OM, NN, and AN content. Overall, the key soil factors that caused differences in bacterial community structure were PV, CY, OM, and NN content. Moreover, CY, OM, AN, and

NN content were the main soil factors that were behind the differences in the structure and composition of rhizosphere microbial communities in the soil of various plant communities.

Discussion

Plant communities and soil physicochemical properties during wetland restoration

Spatial variations of nutrients in wetland soils are often accompanied by changes in vegetation coverage and distribution (Yumei. 2019). A previous study identified soil moisture as a key factor affecting wetland restoration (Jin et al. 2020; Wu et al. 2021). Wetland hydrological restoration can augment vegetation response, resulting in an increase in species richness and a decrease in PI value (enhancement of aquatic plant characteristics) (Bartholomew et al. 2020). Apart from soil moisture, soil nutrient was another key component affecting wetland restoration. Wetland degradation caused soil nutrient loss, which would be recovered throughout the restoration process. Moreover, since plants are an important source of soil nutrient, vegetation restoration is conducive to the accumulation of soil nutrient, and both can be restored simultaneously (Yang et al. 2020). Another study (Huang et al. 2021) demonstrated that the properties of soil nutrient elements were different under different restoration approaches. Farmland to wetland restoration is preferable than farmland to forest restoration for plant restoration and growth, as well as soil carbon and nitrogen metabolism and balance. Moreover, different plant communities have different effects on soil nitrogen, phosphorus, and other nutrients (Dibar et al. 2020). For example, the *Carex spp.* community has strong ability to absorb and retain all nutrients in the soil, whereas the *Eleocharis valleculosa* community has a weak effect on all nutrients in the soil (Zhang et al. 2021).

This study demonstrated that soil sampled from the three plant communities showed diverse physicochemical properties. Of the three plant communities, the soil of the *Carex spp.* community had the highest EC, CY, CAT, WC and nutrient content (such as TN, TP, NN, AP, OM), whereas those in the control plot had the lowest. However, soil BK and gravel proportion were the highest in the control, and the lowest in the soil of the *Carex spp.* community. To some extent, vegetation restoration enhanced the properties of soil that had been degraded by *P. deltoides*. The *Carex spp.* community had the most abundant species, a relatively high aboveground vegetation biomass and coverage, and a gradually accumulating surface litter, improving the soil property. The combined activity of soil enzymes and microorganisms altered the soil texture, and progressively increased the soil nitrogen, phosphorus, potassium and OM content. In comparison, the control vegetation had lower biomass and coverage, as well as less surface matter accumulation. Additionally, a considerable quantity of water was required for the fast-growing *P. deltoides*, which intensified water and nutrient loss in the soil, resulting in nutritional depletion.

Rhizosphere Microbial Communities In Different Plant Communities

Plant roots and soil microorganisms mostly interact in the rhizosphere, where their interactions play a significant ecological role (Adil et al. 2017). Many bacteria, fungi, archaea, protozoa, and microorganisms with diversity functions were found in the rhizosphere. *Taxus wallichiana* var. *chinensis* rhizosphere microbial communities in subtropical and temperate regions of China comprised at least 7 fungal and 31 bacterial phyla (Hao et al. 2016). The richness and diversity of rhizosphere fungal communities of six distinct halophytes in Ebinur Lake wetland differed; however, at the phylum level, Ascomycota dominated the fungal communities in the rhizosphere soil of all six halophytes, followed by Basidiomycota (Zhang et al. 2021). Similarly, at the phylum level, the dominant bacteria shared by different plant communities in Huixian karst wetland Proteobacteria, Chloroflexi, Acidobacteriota, Actinobacteriota, and Bacteroidia (Tu et al. 2019). Most previous studies have found that the structures of rhizosphere microbial communities of different plants are similar at the phylum level (Urbina et al. 2018; Zhang et al. 2019). According to some research, plants are highly sensitive to rhizosphere microorganisms, and soil composition is vital to their stability (Tkacz et al. 2015). Plant nutritional preferences influenced soil nutritional status, which was a major driver of the production of plant-specific microflora (Cai et al. 2017). Therefore, the composition of dominant microbial phyla in different soil types was similar, and its diversity and richness were different (Ma et al. 2020).

The findings of this study were similar to those of the aforementioned previous investigations. The richness and diversity of rhizosphere microbial communities varied amongst the three experimental plots, but at the phylum level, Basidiomycota and Ascomycota were dominant. Proteobacteria, Chloroflexi, Acidobacteriota, Actinobacteriota, and Bacteroidia were the most common rhizosphere bacteria groups, indicating that the plant communities in the three experimental plots were different, and their varying nutritional preferences resulted in differences in soil physicochemical properties and enzyme activities. Despite the fact that all three experimental plots contained the same dominant phyla of the rhizosphere microbial community, their diversity and richness varied.

Relationship Between Rhizosphere Microbial Community And Soil Factors

Rhizosphere microbial community structure was influenced by soil properties, vegetation types, and other factors. The primary environmental factors impacting the rhizosphere microbial community structure differ based on the study area habitat. Plants growing in high salinity soil usually have a dense and diverse root microbial community in coastal areas (Santos et al. 2021). Therefore, soil salinity was the most important factor affecting microbial community structure (Vasquez-Cardenas et al. 2015). In inland wetlands, water level and vegetation types were recently discovered to have a significant influence on soil microbial communities (Ren et al. 2022), and the former has a greater influence than the latter. Moreover, Zhang et al. (2020) demonstrated that water level fluctuation, along with soil TN, WC, and TP, is the most important factor that impacts the rhizosphere microbial community and its dominant flora. Moreover, the study of Qin et al. (2019) revealed that soil CY affects bacterial biomass indirectly by changing root

length, soil pH value, phosphorus and nitrogen contents, whereas fungal biomass increase is related to the increase of aboveground vegetation yield.

In this study, we found that OM, AN, NN, and CY were the primary determinants of the differences in the structure and composition of rhizosphere microbial communities among various plant communities. This was because microbial communities play an important role in the cycling of soil carbon, nitrogen, and phosphorus, and the rhizosphere selects its classification and function (Hossain et al. 2020). Therefore, rhizosphere microorganisms are affected by root exudates, soil properties, and plant growth stages (Knief et al. 2011; Mendes et al. 2014).

Conclusion

This study found that the above-ground plant community on the slash of natural restoration richer than the *P. deltoides* plantation on the lake shore. The rhizosphere fungal community was richer in the cutting slash under ecological restoration, effectively improving the efficiency of decomposing OM in soil into nitrogen, phosphorus, and potassium required by plants, as well as increasing soil nutrients and WC, and improving soil quality. Therefore, in the process of the ecological restoration of damaged wetlands, plant communities, rhizosphere soil microorganisms, and soil environment are closely related, and their interactions supports the restoration of wetland ecosystem structure and function.

Declarations

Date Availability

The datasets generated and analysed during the current study are available from the corresponding author on reasonable request.

Authors'Contributions

YD Niu, XL Wu, ZQ Zeng, YQ Xiao conceived and designed the research. SJ Tan, JY Liu executed the research. SJ Tan performed data analysis. JY Liu, SJ Tan, LJ Jiang wrote the manuscript.

Funding

The research was supported by the following funds: The Key R&D Program of Hunan Province (Nos. 2019NK2021, and 2020NK2012), Special project of the central government for local scientific and Technological Development of Hunan Province (No. 2020ZYT001), and The Key R&D Project of Science and Technology Granted by Hunan Government (No. 2019Sk2191).

Conflicts of Interest/Competing Interests

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.

References

1. Adil E, Ali A, Reda M, Mohamed A, Fouad M, Nouredine H (2017) Plant-driven selection of microbes in the rhizosphere and plant-microbe feedbacks. *Revue Marocaine des Sciences Agronomiques et Vétérinaires* 5(3):238–247
2. Bakker MG, Chaparro JM, Manter D K, Vivanco JM (2015) Impacts of bulk soil microbial community structure on rhizosphere microbiomes of *Zea mays*. *Plant Soil* 392(1–2):115–126
3. Bartholomew MK, Anderson CJ, Berkowitz JF (2020) Wetland vegetation response to groundwater pumping and hydrologic recovery. *Wetlands* 40(6):1–11
4. Cai F, Pang G, Miao YZ, Li RX, Li R, Shen QR, Chen W (2017) The nutrient preference of plants influences their rhizosphere microbiome. *Appl Soil Ecol* 110:146–150
5. Chen SF, Zhou YQ, Chen Y, Gu J (2018) fastp: an ultra-fast all-in-one FASTQ preprocessor. *Bioinformatics* 34(17):i884–i890
6. Chen SM, Waghmode TR, Sun RB, Kuramae EE, Hu CS, Liu BB (2019) Root-associated microbiomes of wheat under the combined effect of plant development and nitrogen fertilization. *Microbiome* 7:1–13
7. Cochrane A (2018) Salt and waterlogging stress impacts on seed germination and early seedling growth of selected endemic plant species from western Australia. *PLANT ECOL* 219(6):633–647
8. Dibar DT, Zhang K, Yuan SQ, Zhang JY, Zhou ZZ, Ye XX (2020) Ecological stoichiometric characteristics of Carbon (C), Nitrogen (N) and Phosphorus (P) in leaf, root, stem, and soil in four wetland plants communities in Shengjin Lake. *China PLoS one* 15(8):e0230089
9. Edgar RC (2013) UPARSE: highly accurate OTU sequences from microbial amplicon reads. *Nat Methods* 10(10):996–998
10. Feudis MD, Cardelli V, Massaccesi L, Bol R, Willbold S, Cocco S (2016) Effect of beech (*Fagus sylvatica* L.) rhizosphere on phosphorus availability in soils at different altitudes (central Italy). *Geoderma* 276:53–63
11. Gong XF, Zhang J, Zhang ZH, Zhou Y (2006) Measurement of $\text{NH}_3\text{-N}$ in soil with Nessler's reagent colorimetry. *Environmental Science & Technology* (01):43–44 + 117
12. Hao DC, Song SM, Mu J, Hu WL, Xiao PG (2016) Unearthing microbial diversity of *Taxus* rhizosphere via MiSeq high-throughput amplicon sequencing and isolate characterization. *Sci Rep* 6(1):22006
13. Hien E, Masse D, Favre BS, Nazaret S (2014) Impact of the application of urban waste on bacterial community in cultivated soil in the suburban area of Ougadougou, Burkina Faso. *Acta Hort* 1021:315–323
14. Hossain MZ, Sugiyama SI (2020) Relative importance of soil microbes and litter quality on decomposition and nitrogen cycling in grasslands. *Ecol Res* 35(5):912–924
15. Huang J, Yuan ZN (2021) Ecological stoichiometric characteristics of Soil SOC, TN, and TP under different restoration methods in Qixing River wetland. *J King Saud University-Science* 33(4):101407

16. Jana V, Petr B (2013) Fungal community on decomposing leaf litter undergoes rapid successional changes. *ISME J* 7(3):477–486
17. Jin X, Sun XX, Li HX, Zhao DH, Li D, Wang L, Man XL (2020) Changes of plant species diversity and biomass with reclaimed marshes restoration. *J Forestry Res* 32:1–10
18. Knief C, Delmotte N, Chaffron S, Stark M, Vorholt JA (2011) Metaproteogenomic analysis of microbial communities in the phyllosphere and rhizosphere of rice. *ISME J* 6(7):1378–1390
19. Lavenne AD, Cudennec C (2019) Assessment of freshwater discharge into a coastal bay through multi-basin ensemble hydrological modelling. *Sci Total Environ* 669(JUN15):812–820
20. Liu CS, Zhao DF, Ma WJ, Guo YD, Wang AJ, Wang QL, Lee DJ (2016) Denitrifying sulfide removal process on high-salinity wastewaters in the presence of *Halomonas* sp. *Appl Microbiol Biotechnol* 100(3):1421–1426
21. Liu FD, Mo X, Kong WJ, Song Y (2020) Soil bacterial diversity, structure, and function of *Suaeda salsa* in rhizosphere and non-rhizosphere soils in various habitats in the Yellow River Delta, China. *Sci Total Environ* 740:140144
22. Ma XJ, Thakar SB, Zhang HM, Yu ZQ, Meng L, Yue JY (2020) Bioinformatics Analysis of the Rhizosphere Microbiota of Dangshan Su Pear in Different Soil Types. *Curr Bioinform* 15(12):503–514
23. Mago T, Salzberg SL (2011) FLASH: fast length adjustment of short reads to improve genome assemblies. *Bioinformatics* 27(21):2957–2963
24. Marie S, Cindy D, Valeria T, Ngonkeu ELM, Diégane D, Aboubacry K, Gilles B, Lionel M(2020) Influence of plant genotype and soil on the wheat rhizosphere microbiome: evidences for a core microbiome across eight African and European soils. *FEMS microbiology ecology* 96(6)
25. Mendes LW, Kuramae EE, Navarrete AA, Van VJA, Tsai SM (2014) Taxonomical and functional microbial community selection in soybean rhizosphere. *ISME J* 8(8):1577–1587
26. Pan SC, Wang XL, Chen M, Tan XN (2015) Determination of the effective phosphorus in soil by full Spectrum direct Reading plasma emission spectrometry. *Multipurp Utilization Mineral Resour* 3:59–61
27. Pineda A, Zheng SJ, van Loon JJ, Pieterse CM, Dicke M (2010) Helping plants to deal with insects: the role of beneficial soil-borne microbes. *Trends Plant Sci* 15(9):507–514
28. Pivato B, Bru D, Busset H, Deau F, Matejicek A, Philippot L, Moreau D, Positive (2017) effects of plant association on rhizosphere microbial communities depend on plant species involved and soil nitrogen level. *SOIL BIOL BIOCHEM* 114:1–4
29. Qin K, Dong XJ, Jifon J, Leskovar DI (2019) Rhizosphere microbial biomass is affected by soil type, organic and water inputs in a bell pepper system. *Appl Soil Ecol* 138:80–87
30. Ren B, Xie YH, Li YZ (2016) Understory Floristic Diversity in Poplar Plantations in the Dongting Lake Wetlands, China. *Wetlands* 40(5):1–12

31. Ren Q, Yuan JH, Wang JP, Liu X, Ma SL, Zhou LY, Miao LJ, Zhang JC (2022) Water Level Has Higher Influence on Soil Organic Carbon and Microbial Community in Poyang Lake Wetland Than Vegetation Type. *Microorganisms* 10(1):131–131
32. Santos SS, Rask KA, Vestergård M, Johansen JL, Ekelund F (2021) Specialized microbiomes facilitate natural rhizosphere microbiome interactions counteracting high salinity stress in plants. *Environ Exp Bot* 186(12):104430
33. Schloss PD, Westcott SL, Ryabin T, Hall RJ, Hartmann M, Hollister EB, Lesniewski RA, Oakley BB, Parks DH, Robinson CJ, Sahl JW, Stres B, Thallinger GG, Van Horn DJ, Weber FC (2009) Introducing mothur: Open-Source, Platform-Independent, Community-Supported Software for Describing and Comparing Microbial Communities. *Appl Environ Microbiol* 75:7537
34. Segata N, Izard J, Waldron L, Gevers D, Miropolsky L, Huttenhower GC (2011) Metagenomic biomarker discovery and explanation. *Genome Biol* 12:R60
35. Shao TY, Zhao JJ, Liu AH, Long XH (2020) Effects of soil physicochemical properties on microbial communities in different ecological niches in coastal area. *Appl Soil Ecol* 150:103486
36. Stefanowicz AM, Rożek K, Stanek M, Rola K, Zubek S (2021) Moderate effects of tree species identity on soil microbial communities and soil chemical properties in a common garden experiment. *For Ecol Manag* 482:118799
37. Tkacz A, Cheema J, Chandra G, Grant A, Poole PS (2015) Stability and succession of the rhizosphere microbiota depends upon plant type and soil composition. *ISME J* 9(11):2349–2359
38. Tu Y, Li HX, Jiang L, Dong K, Wang DQ (2019) Bacterial communities structure and diversity in rhizosphere of different plants from Huixian Wetland, Guangxi. *Ecol Environ Sci* 28(02):252–261
39. Vasquez-Cardenas D, van de Vossenberg J, Polerecky L, Malkin SY, Schauer R, Hidalgo-Martinez S, Confurius V, Middelburg JJ, Meysman FJR, Boschker HTS (2015) Microbial carbon metabolism associated with electrogenic Sulphur oxidation in coastal sediments. *ISME J* 9(9):1966–1978
40. Wang Q (2007) Naive Bayesian classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy. *Appl. Environ. Microbiol* 73
41. Wu GL, Li XL, Gao J (2021) The evolution of hummock-depression micro-topography in an alpine marshy wetland in Sanjiangyuan as inferred from vegetation and soil characteristics. *Ecol Evol* 11(9):3901–3916
42. Yang YL, Mou XJ, Wen BL, Liu XT (2020) Soil Carbon, Nitrogen and Phosphorus Concentrations and Stoichiometries Across a Chronosequence of Restored Inland Soda Saline- Alkali Wetlands, Western Songnen Plain, Northeast China. *Chin Geogra Sci* 30(5):934–946
43. Yumei K (2019) Influence of Grassland Degradation on Soil and Vegetation Characteristics in Inner Mongolia, China. *Pedologist* 55(3):332–342
44. Zahra A, Mostafa M, Reza B, Javad M, Ruhollah TM, Ruth K (2019) Soil enzyme activity variations in riparian forests in relation to plant species and soil depth. *Arab J Geosci* 12(23):1–9
45. Zhang QJ, Yu XB, Qian JX, Xiong T (2012) Distribution characteristics of plant communities and soil organic matter and main nutrients in the Poyang Lake Nanji Wetland. *Acta Ecol Sin* 32(12):3656–

46. Zhang X, Chen T, Niu YH, Li Y, Hu WG (2021) Research on diversity of fungi community in rhizosphere soil of six halophytes in Ebinur Lake Wetland. *Acta Microbiol Sinica* 61(12):3965–3976

47. Zhang XK, Wang HL, Li ZF, Xie J, Ni JJ (2020) Hydrological and soil physiochemical variables determine the rhizospheric microbiota in subtropical lakeshore areas. *PeerJ* 8:e10078

Figures

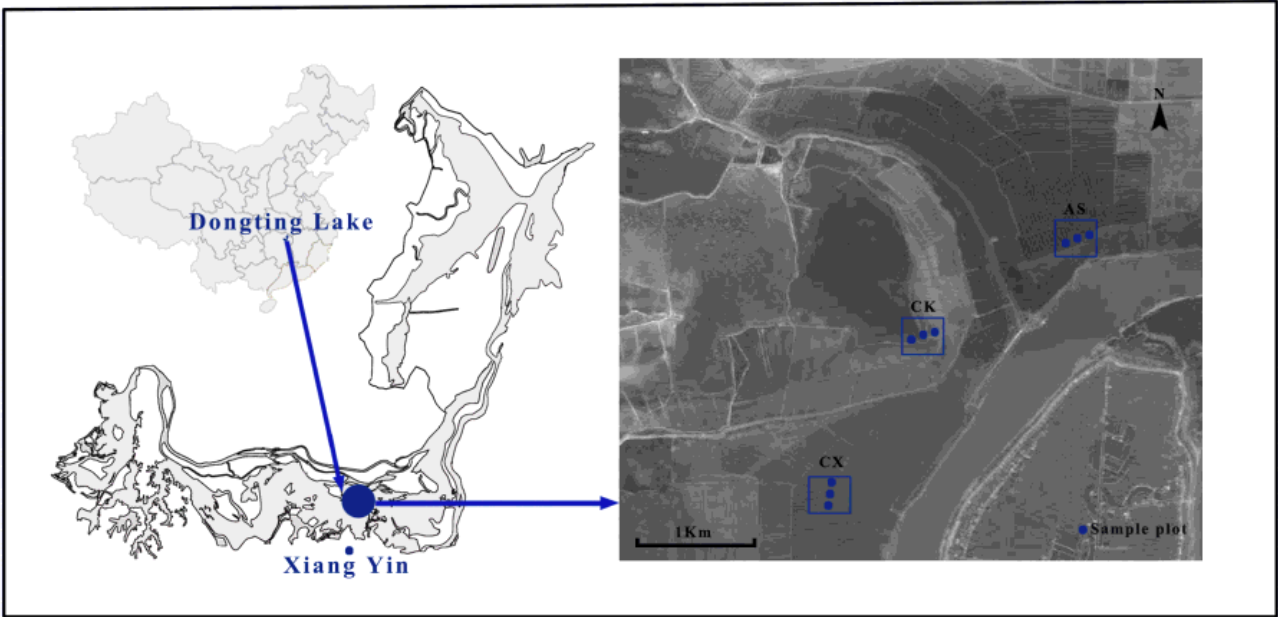


Figure 1

The position of study site

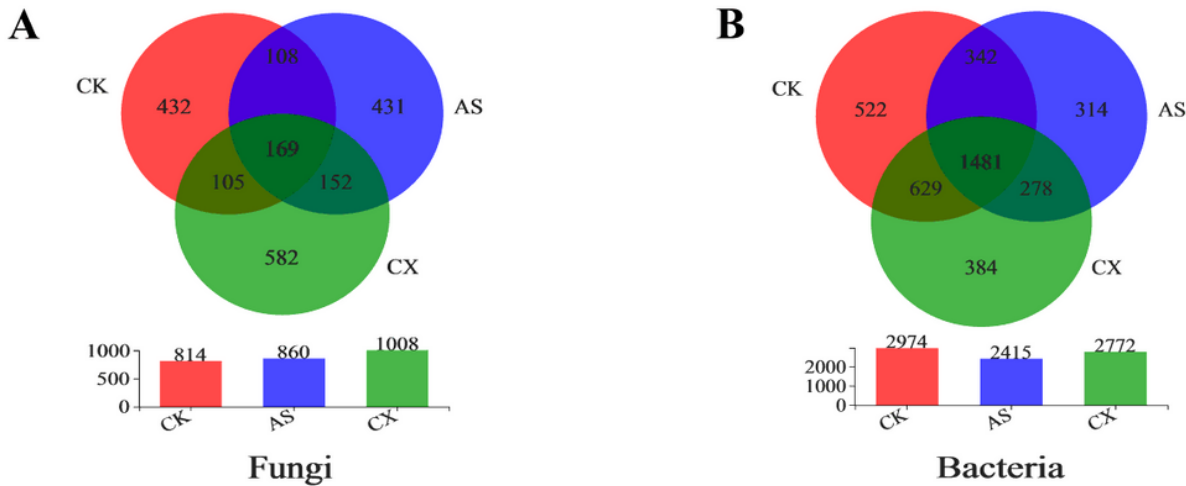


Figure 2

Venn diagrams on microbial in rhizosphere soil

Note: CX: *Carex* spp. community; AS: *Artemisia selengensis* community; CK: the control plot, the same below.

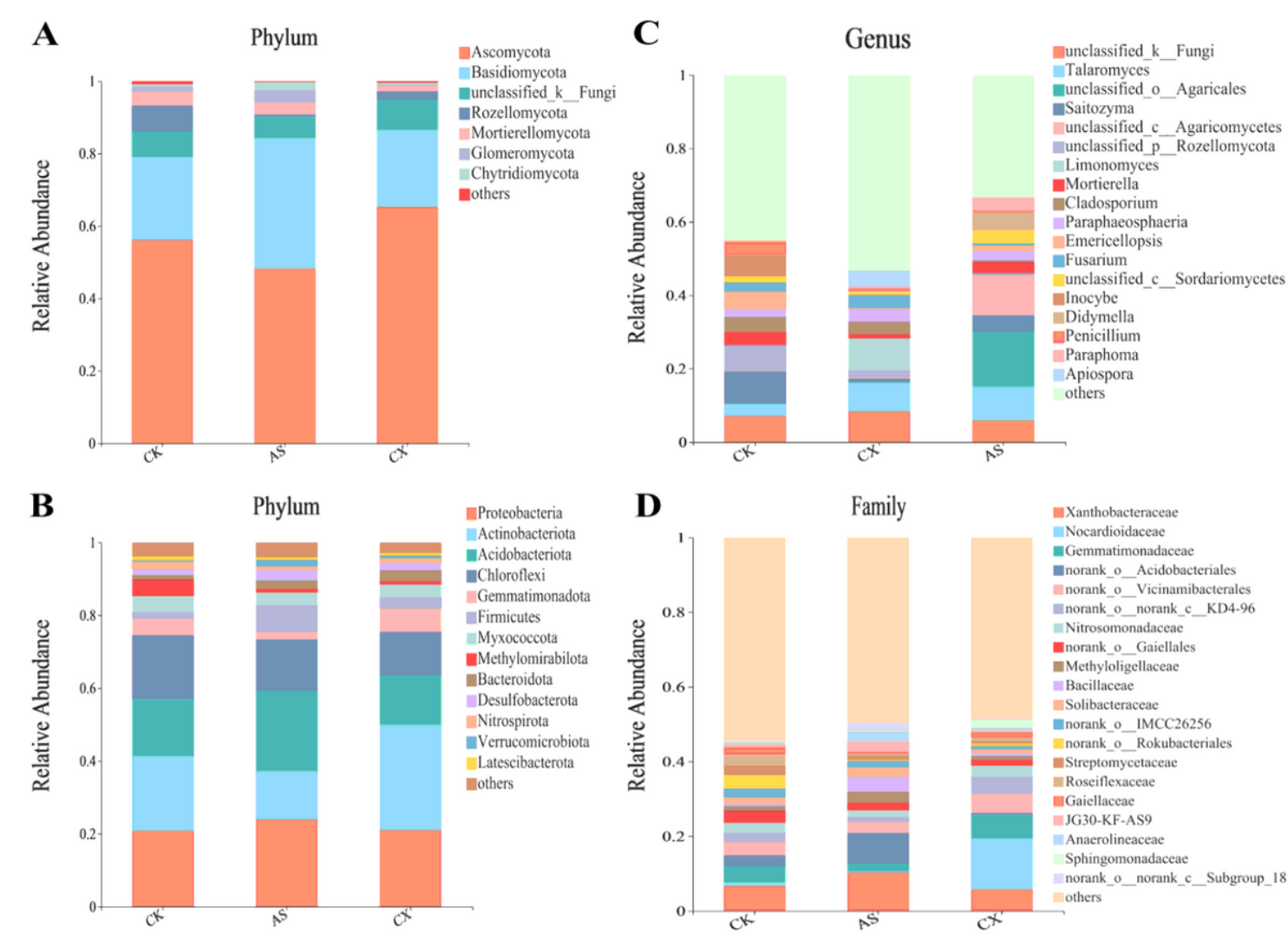


Figure 3

Relative abundance at phylum, genus, and family level; A,B:The abundance of less than 1% in all samples is merged into others and displayed in the figure; C:The abundance of less than 3% in all samples is merged into others and displayed in the figure; D:The abundance of less than 2% in all samples is merged into others and displayed in the figure

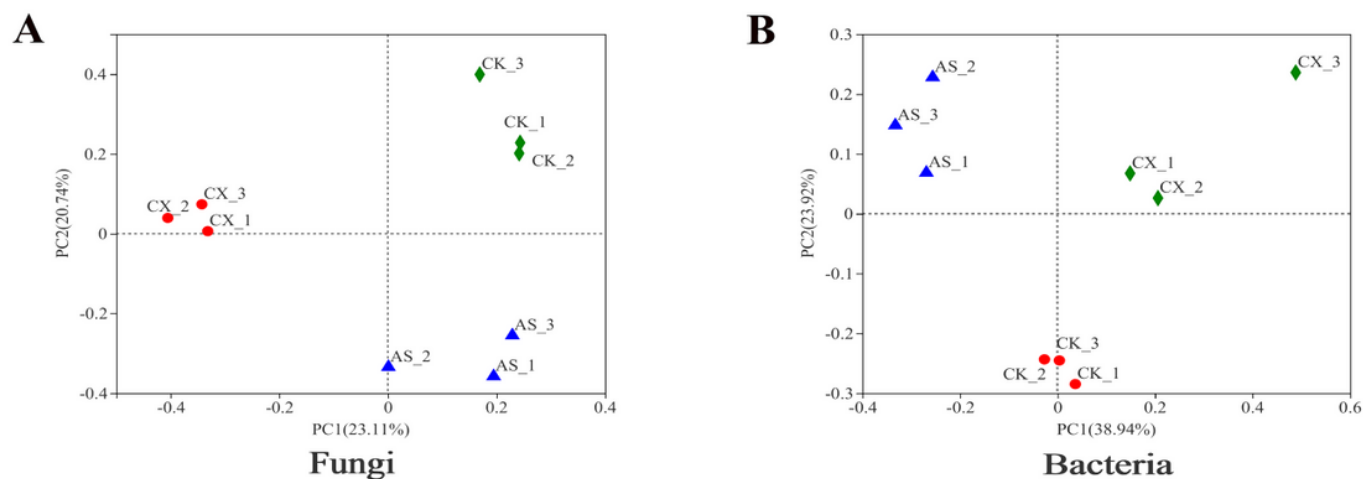


Figure 4

Principal coordinates analysis on microbial communities in rhizosphere soil

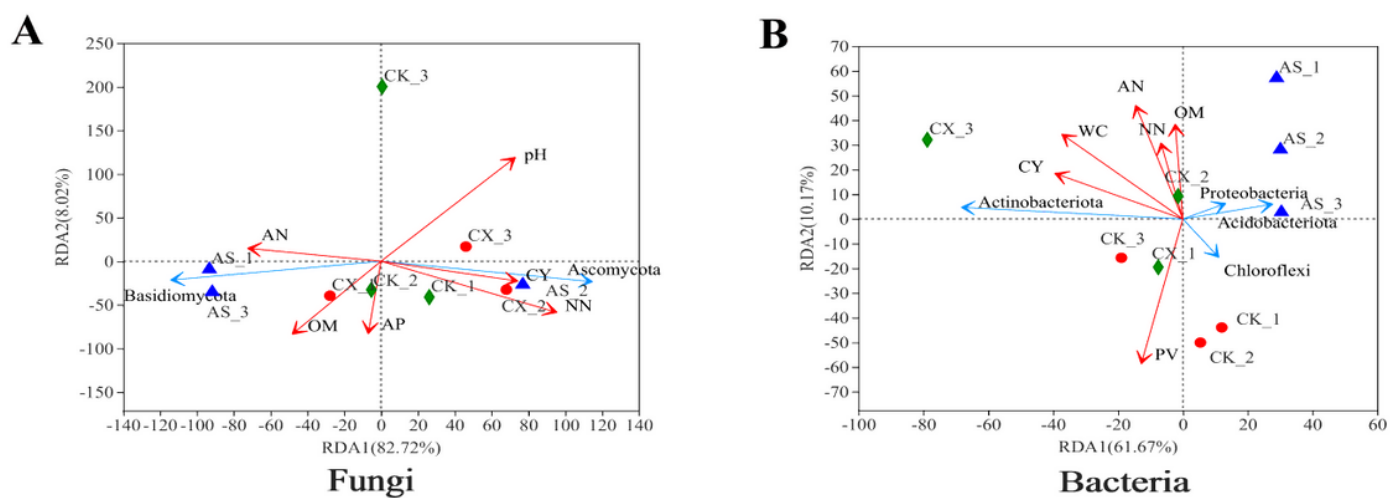


Figure 5

Redundancy analysis of rhizosphere microbial community and soil property factors (RDA)

Note: NN: Nitrate nitrogen; AN: Ammonium nitrogen; AP: Available phosphorus; OM: Organic matter; CY: Clay; PV: porosity; WC: Water content