Research Square

Preprints are preliminary reports that have not undergone peer review.
They should not be considered conclusive, used to inform clinical practice,
or referenced by the media as validated information.

Effects of different growth patterns of Tamarix chinensis on saline-alkali soil: Implications for coastal restoration and management

Chen Gu (gu_c2@hdec.com)
Power China Huadong Engineering Corporation Limited https://orcid.org/0000-0001-7967-2026
Weibin Huang
Power China Huadong Engineering Corporation Limited
Qing Shao
Power China Huadong Engineering Corporation Limited
Jiyan Shi
Zhejiang University
Jianliang Rui
Power China Huadong Engineering Corporation Limited
Yanming Yu
Power China Huadong Engineering Corporation Limited
Zhinai Lu
Power China Huadong Engineering Corporation Limited
Yao Chen
Power China Huadong Engineering Corporation Limited
Xiaojun Chen
Power China Huadong Engineering Corporation Limited
Shudi Dong
Power China Huadong Engineering Corporation Limited
Chenghua Ye
Power China Huadong Engineering Corporation Limited
Ya Tuo
Environmental Development Center of the Ministry of Ecology and Environment: Sino-Japan Friendship Center for Environmental Protection https://orcid.org/0000-0002-0850-1630

Research Article

Keywords: Tamarix chinensis, Coastal saline-alkali soil, Phytoremediation, Soil property, Root-associated microbiome

Posted Date: June 30th, 2022

DOI: https://doi.org/10.21203/rs.3.rs-1728745/v1

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

Abstract

Objective: To better understand the wetland restoration, the physicochemical properties and microbial community in different compartments (rhizosphere and bulk soil) of the status of living and death *T. chinensis* covered soil zones were studied in a restored coastal tidal flat located on the Zhoushan island.

Results: There were differences between growth conditions in the levels of soil pH, salinity, SOM, and nutrient. The living status of *T. chinensis* exhibited higher capacity of decreasing saline-alkali soil than the death condition of plants, and the living condition of *T. chinensis* showed higher uptake of N, P, and K as compared with the death samples. *Proteobacteria*, *Bacteroidota*, and *Chloroflexi* were the predominant bacterial communities as revealed via high-throughput sequencing. This study contributed to our understanding of halophyte growth on coastal phytoremediation, and guide theoretically for management of *T. chinensis* population.

Introduction

Wetlands are one of the most fragile, productive, and valuable natural ecosystems. Saltmarshes are major components of coastal habitats. However, they have experienced a rapid decline globally mainly through human-induced disturbances and natural stressors (Li et al., 2019). A recent report from Chen et al. (2022) showed that the distribution of 7 major species in saltmarshes in the intertidal zone of China had declined from 151,324 ha in 1985 to 115,397 ha in 2019. Indeed, high soil salinity is the primary limiting factor influencing plant growth. Halophytic plants are one of the typical vegetation types in coastal ecosystem. They can tolerate high salinity due to their different exclusion, compartmentation, and excretion resistance mechanisms (Rathore et al., 2017). *Tamarix chinensis* Lour. is one of the salt-tolerant shrub species that is widely distributed in coastal habitats worldwide (Feng et al., 2018). This species is found in the western of USA, where it is considered as an invasive species (Swaminathan et al., 2020; Xie et al., 2020). In China, *T. chinensis* is the vital part of the coastal wetland ecological restoration projects of “Southern Mangrove and Northern Tamarisk” and “Blue Carbon” (Xie et al., 2019; Yang et al., 2021). As one of the dominant shrub in northern China, *T. chinensis* contributes largely to shoreline protection, carbon sequestration, and ecological function (Jiao et al., 2021; Xie et al., 2020). Moreover, this species is often used for saline soil rehabilitation in China due to its strong salt tolerance, drought, and flooding (Chen et al., 2019; Feng et al., 2018).

In response to the degradation of coastal ecosystems worldwide, there has triggered growing interest in developing techniques for the restoration of degraded coastal habitats. In China, the coastal restoration projects have multiplied in recent years, with more than 1 billion US dollars spent during the period of 2016 to 2019 (Liu et al., 2021). As an eco-friendly and cost-effective technology, phytoremediation is a promising way to improve the damaged wetland ecosystems and ameliorate saline soil (Zhou et al., 2020). Previous studies found that the establishment of halophytes on saline soil can change the soil properties (Feng et al., 2018). Jing et al. (2019) pointed out that halophytes could assist in coastal soil desalination, altered soil properties, enzyme activities. Furthermore, halophytes are capable of restoring

coastal wetlands by absorbing excess nutrients and pollutants (Jiang et al., 2015). Therefore, it is great potential for using halophytes to restore saline-alkali soil.

Microorganisms are abundant and diverse in soils. Microbes play significant roles in the biogeochemical cycle and ecological function of wetlands (Li et al., 2021). It has been reported that the distinct patterns of growth of halophytes could result in differential communities and degrees of microbial activities in root associated soil (Rathore et al., 2017). The rhizosphere is a habitat in which microorganisms are directly influenced by plant roots (Chaudhary et al., 2018). In general, the rhizosphere receives continuously input from the exudation of plant roots, which contribute to the rhizosphere a carbon-rich environment for the enrichment of microbial communities (Sasse et al., 2018). Zhang et al. (2011) emphasized that rhizosphere microbial processes are vital factors in determining the survival and sustainable growth of plant. Although many studies have focused on environmental variations on soil properties, and little attention has been paid to the difference of microbial community in the rhizosphere and non-rhizosphere soil between living and death halophytes after the establishment of vegetation. To the best of our knowledge, no study has been carried out yet to study the rhizosphere and bulk soil bacteria presented in the roots associated soils of different growth status of *T. chinensis.* Comparing the root-associated microbes between plants is crucial for understanding plant-microbe interactions during bioremediation mechanism.

A restored coastal tidal flat site located on the Zhoushan island was chosen in this study. The project was completed in December 2019. *Suaeda australis*, *Phragmites australis*, and *Tamarix chinensis* dominate the study area. After 2 years of vegetation, the majority of *T. chinensis* had strong salinity adaptability in this region. However, a minority of this species was gradually die-off. To effectively protect and restore saltmarshes, a deep understanding of growth and die-off pattern is necessary. Here, we hypothesized that the variations of root-associated bacteria were likely attributed to the changes of physicochemical property of living and death *T. chinensis*-covered soils. To further test the hypothesis, high-throughput sequencing technique was used to analyse the variations in the soil property and the diversity and composition of bacteria in different compartments (rhizosphere and bulk soil) from two status of living and death *T. chinensis* wetlands.

Material And Methods

Site description

3-year-old seedings of *T. chinensis* were collected from a coastal ecological restoration project site in Dinghai district (29°32’-30°04’N, 121°30’-123°25’E), Zhoushan island, Zhejiang Province (Fig. 1). It has a subtropical monsoon climate with an annual average temperature of approximately 16°C, and the annual average sunshine duration is 1941–2257 h (Lin et al., 2018). The coastline type of the study area is mainly composed of tidal flat wetlands. The replacement of invasive *S. alterniflora* with several local plant species in the mean high tide level was initiated in 2019 for coastal flat restoration, including *S. australis*, *P. australis*, *T. chinensis.* The living *T. chinensis*-covered zone and death zone of rhizosphere

and bulk soils were collected in this study. The living and death of *T. chinensis*-covered rhizosphere soil samples were named as TLR and TDR, while the living and death of *T. chinensis*-covered bulk soils were named as TLB and TDB. The bare mudflat without plants was termed as MUD. Soil samples were collected in January 2022. In each zone, wetland soils were collected with triplicates.

Soil collection and analysis

The roots of *T. chinensis* of living and death status were separately shaken vigorously to separate soil not tightly adhering to the roots (i.e., bulk soil) and attached to roots (i.e., rhizosphere soil). Before analysis, all visible plant residues, litter materials, macrofauna, and stone pieces were removed, and the soil samples were placed separately into aseptic bags and then brought back to the laboratory immediately. Bulk soil sample was divided into two parts. One part of bulk soil and MUD were used to determine the soil physical-chemical properties; the other set of bulk soil was maintained at -80°C for high throughput sequencing analyses. The rhizosphere soil was maintained at -80°C for high throughput sequencing analyses.

Soil pH in each sample was detected using a digital pH meter. Soil salinity was determined after drying residue method. Soil moisture content was analysed by the weight loss of the soil after drying at 105°C until weight stability. Soil organic matter (SOM) was measured using the dichromate titration method. Total nitrogen (TN), available nitrogen (AN), total phosphorous (TP), available phosphorous (AP) were determined by standard methods (Zhang et al., 2019). Soil total potassium (STK) and available potassium (SAK) were measured using graphite furnace atomic absorption spectrometry.

Soil DNA extraction and high throughput sequencing

The total genomic DNA was extracted from ~ 0.5 g of the samples using the Soil DNA Kit (D5625, OMEGA) following the manufacturer's protocols. The concentration and purity of the DNA were quantified by Qubit®3.0 (Life Invitrogen). The integrity of the DNA was verified by running electrophoresis on 2% agarose gel. The V4-V5 regions of 16S rRNA genes of the samples were then subjected to sequencing. The 16S rRNA genes were amplified using the primers 515F (5'- GTGCCAGCMGCCGCGG-3') and 907R (5'-CCGTCAATTCMTTTRAGTTT-3') by PCR (95°C for 5 min, followed by 27 ~ 30 cycles at 95°C for 30 s, 55°C for 30 s, and 72°C for 45 s and a final extension at 72°C for 5 min). PCR reactions were performed in 30 μL mixture containing 15 μL of 2 × Phanta Master Mix, 1 μL of each primer (10 μM), and 20 ng of template DNA. Amplicons were extracted from 2% agarose gels and purified using the AxyPrep DNA Gel Extraction Kit (Axygen Biosciences, Union City, CA, U.S.) according to the manufacturer's instructions and quantified using Qubit®3.0 (Life Invitrogen). The amplicon library was paired-end sequenced (2×250) on an Illumina Novaseq 6000 platform (Nanjing GenePioneer Co. Ltd) according to the standard protocols. The PCR chimeras were detected and filtered out using the Vsearch uchime-denovo algorithm. The PE reads were overlapped to assemble the final tag sequences with the minimum overlap length as 10 bp with PANDAseq (Masella et al., 2012). Quality filtering of MiSeq reads was carried out by PRINSEQ according to specific filtering conditions to obtain the highquality clean tags.

Analysis of sequencing data

The sequences with ≥ 97% similarity were assigned to the same operational taxonomic units (OTUs) by Vsearch (Version 2.15.0). The phylogenetic affiliation of each 16S rRNA gene sequence was analyzed by uclust against the silva (SSU132)16S rRNA database using confidence threshold of 90%. The rarefaction analysis based on QIIME (1.9.1) was conducted to reveal the diversity indices (Caporaso et al., 2010). Chao1 index was calculated to compare the diversity of the bacterial communities (Chao, 1984). Beta-diversity using both weighted and unweighted UniFrac was calculated by QIIME 1.9.1 (Lozupone et al., 2011). Principal coordinate analysis (PCoA) was conducted using the QIIME 1.9.1 to examine dissimilarities in community composition.

Results And Discussion

Soil characterization

It has been reported that plants could alter soil properties via nutrient cycling and litter decomposition (Cao et al., 2014). After 2 years of plantation, the physicochemical properties of soil in different conditions are presented in Table 1. The pH of MUD was 8.54, the pH of TDB was higher than TLB. Soil salinity was lower in soils under plant-covered sites than in MUD. These results indicated that *T. chinensis* could decrease soil pH and desalinization was occurred, the living status of *T. chinensis* exhibited higher capacity of decreasing saline-alkali soil than the death condition of plants. The SOM of plant-covered soils was obviously higher than MUD, with the highest SOM value in TLB. This result might be related to the litter decomposition and below-ground biomass (Cao et al., 2014; Chaudhary et al., 2015; Shao et al., 2015). A previous study showed that salinity and alkalinity could reduce the SOM accumulation in coastal wetlands (Xie et al., 2017). Wang et al. (2010) also illustrated that the increase in SOM could decrease the accumulation of salinity by improving soil porosity and water permeability. Levels of TN, TP, STK, and SAK decreased in the following order: MUD□TDB□TLB. These results indicated that the higher uptake of N, P, and K by *T. chinensis* to regulate N and P mineralization, osmotic adjustment (Rathore et al., 2017). Overall, the physicochemical properties of bulk soil were quite different between TLB and TDB.

Table 1
Soil physicochemical parameters of *T. chinensis* coverage

	TLB	TDB	MUD
pH	7.14	8.51	8.54
Moisture (%)	19.8	24.2	63.3
SOM (g/kg)	97.3	90.1	16.6
Salinity (g/kg)	5.05	14.1	28.7
TN (mg/kg)	316	350	504
AN (mg/kg)	34.0	39.2	40.6
TP (mg/kg)	174	484	520
AP (mg/kg)	11.3	18.4	14.2
STK (%)	1.01	1.49	1.62
SAK (mg/kg)	153	416	693

Bacterial community diversity

Soil microbial diversity is one of the direct indicators of soil health, fertility, and function (Xu et al., 2019). The responses of soil microbial communities were investigated by high throughput sequencing. As shown in Fig. 2, it can be seen that the rarefaction curve reached plateau, suggesting the bacterial diversity covered sufficiently at the sequencing depth. Chao1 richness was analysed to compare the levels of alpha diversity indices in different treatment (Fig. 3). The indices of Chao1 in TDR was markedly higher than TLR, indicating that the bacterial communities in the rhizosphere soil of death status were more diverse. In addition, there were no obvious differences in the bulk soils of the plant species in different conditions. Liu et al. (2016) exhibited the Chao1 index of dense *T. chinensis*-covered bulk soils was 1,475 in November and 1,607 in September, which is in line with the present study.

The sequence data was subjected to PCoA based on weighted UniFrac distance analysis. As shown in Fig. 4 (a), the first two PCs explained a total of 41.94% variance of bacterial communities in rhizosphere soils, the bacterial communities were clearly clustered into two groups, the condition of living plant species was separated from those of death treatment. Similarly to the rhizosphere soil communities, the first two PCs explained a total of 41.33% variance of bacterial communities, there was distinct two groups clustered between the living and death *T. chinensis*-covered bulk soils (Fig. 4 (b)). These results indicated that the different status of plant species in both rhizosphere and bulk soils could dramatically change the bacterial community diversity.

Predominant bacterial community composition at the phylum level

The composition of the bacterial communities at the phylum level in the bulk soil and rhizosphere soil from all the samples are presented in Fig. 5. In rhizosphere soils, the major phyla were *Proteobacteria*, *Bacteroidota*, *Chloroflexi*, *Acidobacteriota*, *Desulfobacterota*, *Planctomycetota*, *Gemmatimonadota*, *Actinobacteriota*, *Myxococcota*, *Latescibacterota*, which accounted for more than 90% of the bacterial sequences obtained from the rhizosphere soils. *Proteobacteria*, *Bacteroidota*, *Chloroflexi* were dominant in rhizosphere samples. As for bulk soils, the main phyla were *Proteobacteria*, *Bacteroidota*, *Chloroflexi*, *Acidobacteriota*, *Actinobacteriota*, *Gemmatimonadota*, *Planctomycetota*, and *Myxococcota*. Similarly to the rhizosphere soil communities, *Proteobacteria*, *Bacteroidota*, *Chloroflexi* were dominant in bulk soils. It has been reported that *Proteobacteria*, *Chloroflexi*, *Acidobacteria*, and *Bacteroidetes* were the dominant bacterial phyla in welands across China (An et al., 2019). Furthermore, Jing et al. (2019) demonstrated that *Proteobacteria*, *Bacteroidota*, *Chloroflexi* were the dominant bacterial phyla in the rhizosphere and bulk soils of halophytes in the saline coastal wetlands of the Yellow River Delta. However, a study in coastal saline-alkali soil under *T. chinensis* woodland at Bohai Bay revealed that *Proteobacteria*, *Acidobacteria*, and *Actinobacteria* were the dominant phyla (Liu et al., 2016). It is likely that the soil type, vegetation type, seasonality, the distance to seashore line might play important role in soil characteristics and shape the composition of the bacterial communities (Liu et al., 2016; Shao et al., 2015).

Proteobacteria was the major phylum in all the samples, which is consistent with the findings of previous studies on other halophyte covered soils such as *Atriplex triangularis*, *Suaeda glauca*, *Messerschmidia sibirica*, *Salicornia europaea*, and *Phragmites australis* (Jing et al., 2019; Tian and Zhang, 2017; Zhang et al., 2019; Zhao et al., 2016). The phylum *Proteobacteria* accounted for the largest proportion across samples might be attributed to its capacity to metabolize various substrates (Eilers et al., 2010; Zhao et al., 2020). Previous report showed that *Bacteroidota* might participate in the decomposition of organic matter (An et al., 2022). Ward et al. (2009) reported that *Acidobacteria* played a vital role in the cycling of organic matter derived from plants. Therefore, the relative abundance of theses phyla in the present study might be due to the higher root exudate in coastal soils of Zhoushan Island. For comparison, higher abundance of *Bacteroidota* was observed in TLB as compared with TLR, indicating the bacteria in bulk soils had higher capacity of degrading organic matter than that of rhizosphere soils in the healthy ecosystem of *T. chinensis*. Higher abundance of *Acidobacteria* was found in TDR and TDB samples compared with TLR and TLB, suggesting the bacteria in death plant soils exhibited higher decomposition of organic matter derived from plants. Besides, *Proteobacteria*, *Chloroflexi*, *Acidobacteriota* are fast growing Gram-negative bacteria, and their carbon sources are simple and easy to use (Yin et al., 2018). Thus, it is great potential for using halophytes such as *T. chinensis* to ecological restore the environment. Overall, bacterial community might be used as a bioindicator for coastal ecological restoration project and wetland degradation of *T. chinensis*.

Conclusions

In summary, the results of the present study supported the scientific hypothesis and could use as valuable references for coastal *T. chinensis* establishment and management in ecological restoration project. A comprehensive comparison of soil properties and bacterial communities in different

compartments (bulk soil and rhizosphere soil) of two status of living and death *T. chinensis* wetlands. *T. chinensis* could decrease pH and salinity of soil, the living status of *T. chinensis* exhibited higher capacity of decreasing saline-alkali soil than the death condition of plants. The physicochemical properties of bulk soil obviously differed between TLB and TDB. Lower values of Chao1 could be observed in living rhizosphere of *T. chinensis* soils than in death condition, while there were no obvious differences in the bulk soils of the plant species in different conditions. Results further revealed that the predominant bacterial communities were *Proteobacteria*, *Bacteroidota*, and *Chloroflexi*. This study could contribute to a better understanding of rhizosphere and bulk microbiota in *T. chinensis*-covered coastal wetland ecosystems.

Declarations

Funding

This work was supported by the grant from Postdoctoral Advance Programs of Zhejiang Province (ZJ2021022).

Conflict of interest

The authors declared that they have no conflicts of interest to this work.

References

1. An F, Niu Z, Liu T, Su Y (2022) Succession of soil bacterial community along a 46-year choronsequence artificial revegetation in an arid oasis-desert ecotone. Sci Total Environ 814:152496
2. An J, Liu C, Wang Q, Yao M, Rui J, Zhang S, Li X (2019) Soil bacterial community structure in Chinese wetlands. Geoderma 337:290–299
3. Cao D, Shi F, Koike T, Lu Z, Sun J (2014) Halophyte plant communities affecting enzyme activity and microbes in saline soils of the Yellow River Delta in China. Clean-Soil, Air, Water 42:1–8
4. Caporaso JG, Kuczynski J, Stombaugh J et al (2010) QIIME allows analysis of high-throughput community sequencing data. Nat Methods 7:335–336
5. Chao A (1984) Nonparametric estimation of the number of classes in a population. Scand J Stat 11:265–270
6. Chaudhary DR, Gautam RK, Yousuf B, Mishra A, Jha B (2015) Nutrients, microbial community structure and functional gene abundance of rhizosphere and bulk soils of halophytes. Appl Soil Ecol 91:16–26
7. Chaudhary DR, Kim J, Kang H (2018) Influence of different halophyte vegetation on soil microbial community at temperate salt marsh. Microb Ecol 75:729–738
8. Chen G, Jin R, Ye Z, Li Q, Gu J, Luo M, Luo Y, Christakos G, Morris J, He J, Li D, Wang H, Song L, Wang Q, Wu J (2022) Spatiotemporal mapping of salt marshes in the intertidal zone of China during 1985–

2019. J Remot Sens 2022:9793626

9. Chen H, Yang C, Ren A, Guo K, Feng X, Li J, Liu X, Sun H, Wang J (2019) The evapotranspiration of Tamarix and its response to environmental factors in coastal saline land of China. Water 11:2273
10. Eilers KG, Lauber CL, Knight R, Fierer N (2010) Shifts in bacterial community structure associated with inputs of low molecular weight carbon compounds to soil. Soil Biol Biochem 42:896–903
11. Feng X, An P, Li X, Guo K, Yang C, Liu X (2018) Spatiotemporal heterogeneity of soil water and salinity after establishment of dense-foliage *Tamarix chinensis* on coastal saline land. Ecol Eng 121:104–113
12. Jiang TT, Pan JF, Pu XM, Wang B, Pan JJ (2015) Current status of coastal wetlands in China: degradation, restoration, and future management. Estuar Coast Shelf S 164:265–275
13. Jiao L, Sun T, Zhang P, Yang W, Shao D, Zheng S (2021) Effect of floral traits mediated by plant-soil feedback on the relationship between plant density and fecundity: Case study of *Tamarix chinensis* in the Yellow River Delta, China. Glob Ecol Conserv 26:e01479
14. Jing C, Xu Z, Zou P, Tang Q, Li Y, You X, Zhang C (2019) Coastal halophytes alter properties and microbial community structure of the saline soils in the Yellow River Delta, China. Appl Soil Ecol 134:1–7
15. Li J, Chen Q, Li Q, Zhao C, Feng Y (2021) Influence of plants and environmental variables on the diversity of soil microbial communities in the Yellow River Delta Wetland, China. Chemosphere 274:129967
16. Li S, Xie T, Pennings SC, Wang Y, Craft C, Hu M (2019) A comparison of coastal habitat restoration projects in China and the United States. Sci Rep 9:14388
17. Lin W, Cen J, Xu D, Du S, Gao J (2018) Wetland landscape pattern changes over a period of rapid development (1985–2015) in the ZhouShan Islands of Zhejiang province, China. Estuar Coast Shelf S 213:148–159
18. Liu W, Zhang W, Liu G, Zhang Y, Zhang G (2016) Microbial diversity in the saline-alkali soil of a coastal *Tamarix chinensis* woodland at Bohai Bay, China. J Arid Land 8:284–292
19. Liu Z, Fagherazzi S, Li J, Cui B (2021) Mismatch between watershed effects and local efforts constrains the success of coastal salt marsh vegetation restoration. J Clean Prod 292:126103
20. Lozupone C, Lladser ME, Knights D, Stombaugh J, Knight R (2011) UniFrac: an effective distance metric for microbial community comparison. ISME J 5:169–172
21. Masella AP, Bartram AK, Truszkowski JM, Brown DG, Neufeld JD (2012) PANDAseq: paired-end assembler for illumina sequences. BMC Bioinformatics 13:1–7
22. Rathore AP, Chaudhary DR, Jha B (2017) Seasonal patterns of microbial community structure and enzyme activities in coastal saline soils of perennial halophytes. Land Degrad Dev 28:1779–1790
23. Sasse J, Martinoia E, Northen T (2018) Feed your friends: do plant exudates shape the root microbiome? Trends Plant Sci 23:25–41

24. Shao X, Yang W, Wu M (2015) Seasonal dynamics of soil labile organic carbon and enzyme activities in relation to vegetation types in Hangzhou bay tidal flat wetland. PLoS ONE 10:e0142677
25. Swaminathan P, Ohrtman M, Carinder A, Deuja A, Wang C, Gaskin J, Fennell A, Clay S (2020) Water deficit transcriptomic responses differ in the invasive *Tamarix chinensis* and *T. ramosissima* established in the Southern and Northern United States. Plants 9:86
26. Tian X, Zhang C (2017) Illumina-based analysis of endophytic and rhizosphere bacterial diversity of the coastal halophyte *Messerschmidia sibirica*. Front Microbiol 8:2288
27. Wang XY, Xin YZ, Gao DM, Li FM, Morgan J, Xing BS (2010) Microbial community characteristics in a degraded wetland of the Yellow River Delta. Pedosphere 20:466–478
28. Ward NL, Challacombe JF, Janssen PH, Bernard H, Coutinho PM, Martin W et al (2009) Three genomes from the phylum *Acidobacteria* provide insight into their lifestyles in soils. Appl Environ Microbiol 75:2046–2056
29. Xie L, Wang B, Xin M, Wang M, He X, Wei Q, Shi X, Sun X (2019) Characteristics of vegetation carbon, nitrogen, and C/N ratio in a *Tamarix chinensis* coastal wetland of China. Clean-Soil, Air, Water 47:1800452
30. Xie L, Wang B, Xin M, Wei Q, Wang W, He X, Wang J, Shi X, Sun X (2020) Impacts of coppicing on *Tamarix chinensis* growth and carbon stocks in coastal wetlands in northern China. Ecol Eng 147:105760
31. Xie X, Pu L, Wang Q, Zhu M, Xu Y, Zhang M (2017) Response of soil physicochemical properties and enzyme activities to long-term reclamation of coastal saline soil, Eastern China. Sci Total Environ 607–608:1419–1427
32. Xu Y, Seshadri B, Bolan N, Sarkar B, Ok YS, Zhang W, Rumpel C, Sparks D, Farrell M, Hall T, Dong Z (2019) Microbial functional diversity and carbon use feedback in soils as affected by heavy metals. Environ Int 125:478–488
33. Yang H, Xia J, Cui Q, Liu J, Wei S, Feng L, Dong K (2021) Effects of different *Tamarix chinensis*-grass patterns on the soil quality of coastal saline soil in the Yellow River Delta, China. Sci Total Environ 772:145501
34. Yin P, Yin M, Cai Z, Wu G, Lin G, Zhou J (2018) Structural inflexibility of the rhizosphere microbiome in mangrove plant *Kandelia obovata* under elevated CO_2. Mar Environ Res 140:422–432
35. Zhang X, Zhang L, Zhang L, Ji Z, Shao Y, Zhou H, Bao Y, Qu Y, Liu L (2019) Comparison of rhizosphere bacterial communities of reed and *Suaeda* in Shuangtaizi river estuary, Northeast China. Mar Pollut Bull 140:171–178
36. Zhao Q, Bai J, Gao Y, Zhao H, Zhang G, Cui B (2020) Shifts in the soil bacterial community along a salinity gradient in the Yellow River Delta. Land Degrad Dev 31:2255–2267
37. Zhao S, Zhou N, Zhao ZY, Zhang K, Tian CY (2016) High-throughput sequencing analysis of the endophytic bacterial diversity and dynamics in roots of the halophyte *Salicornia europaea*. Curr Microbiol 72:557

38. Zhou D, Yu J, Guan B, Li Y, Yu M, Qu F, Zhan C, Lv Z, Wu H, Wang Q, Yang J (2020) A Comparison of the development of wetland restoration techniques in China and other nations. Wetlands 40:2755–2764

Figures



Figure 1

Location of the study area

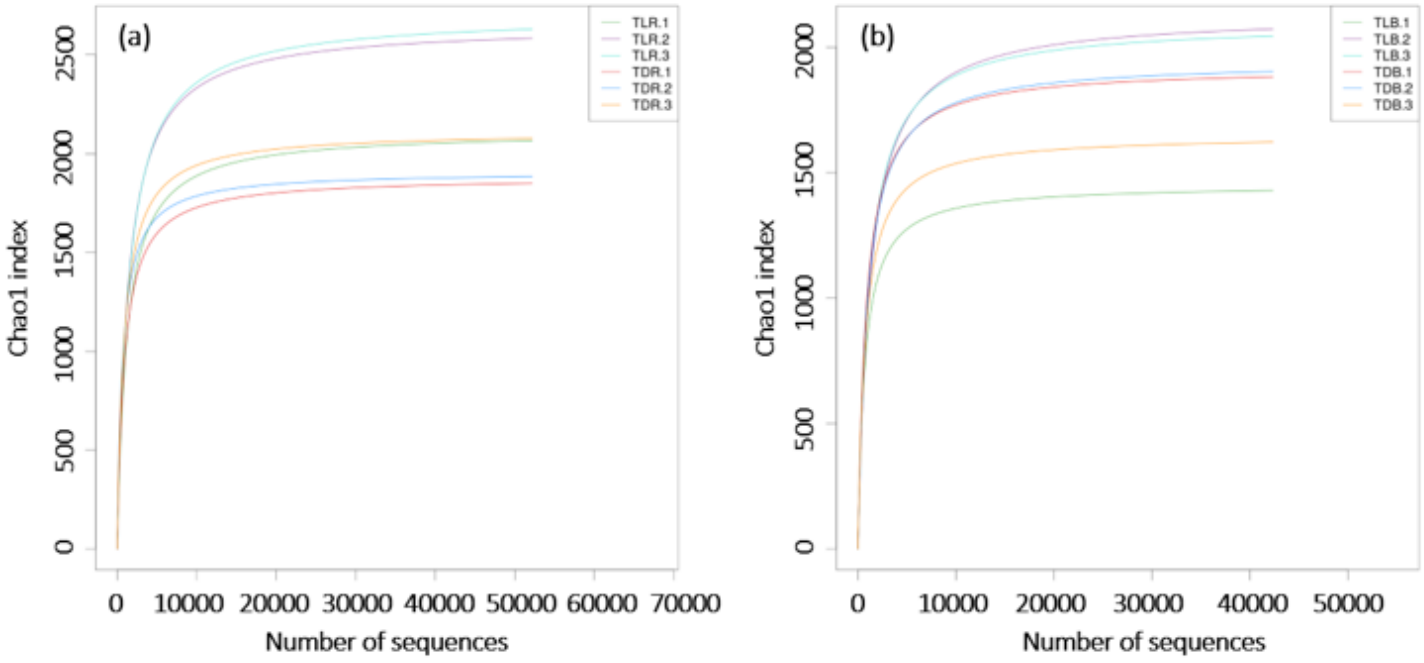


Figure 2

Rarefaction curves of all samples

Figure 3

Chao1 index of all samples

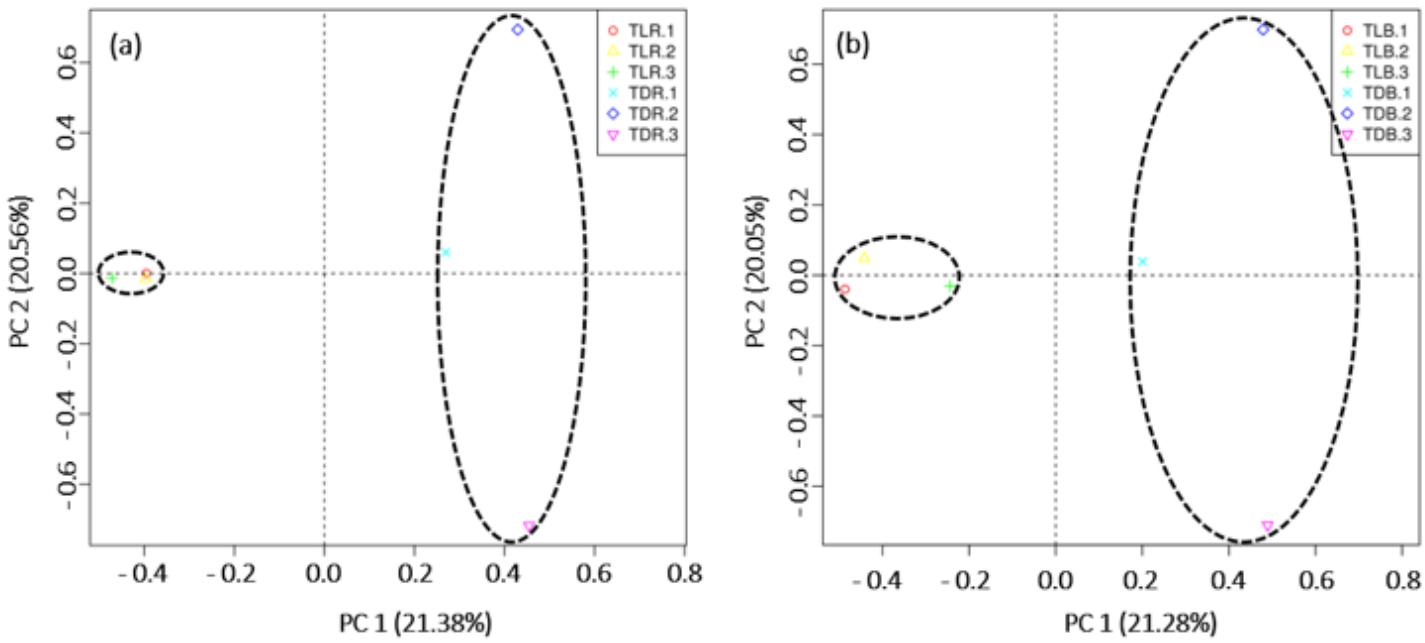


Figure 4

PCoA based on sequence data of 16S rRNA genes of (a) rhizosphere soil and (b) bulk soil

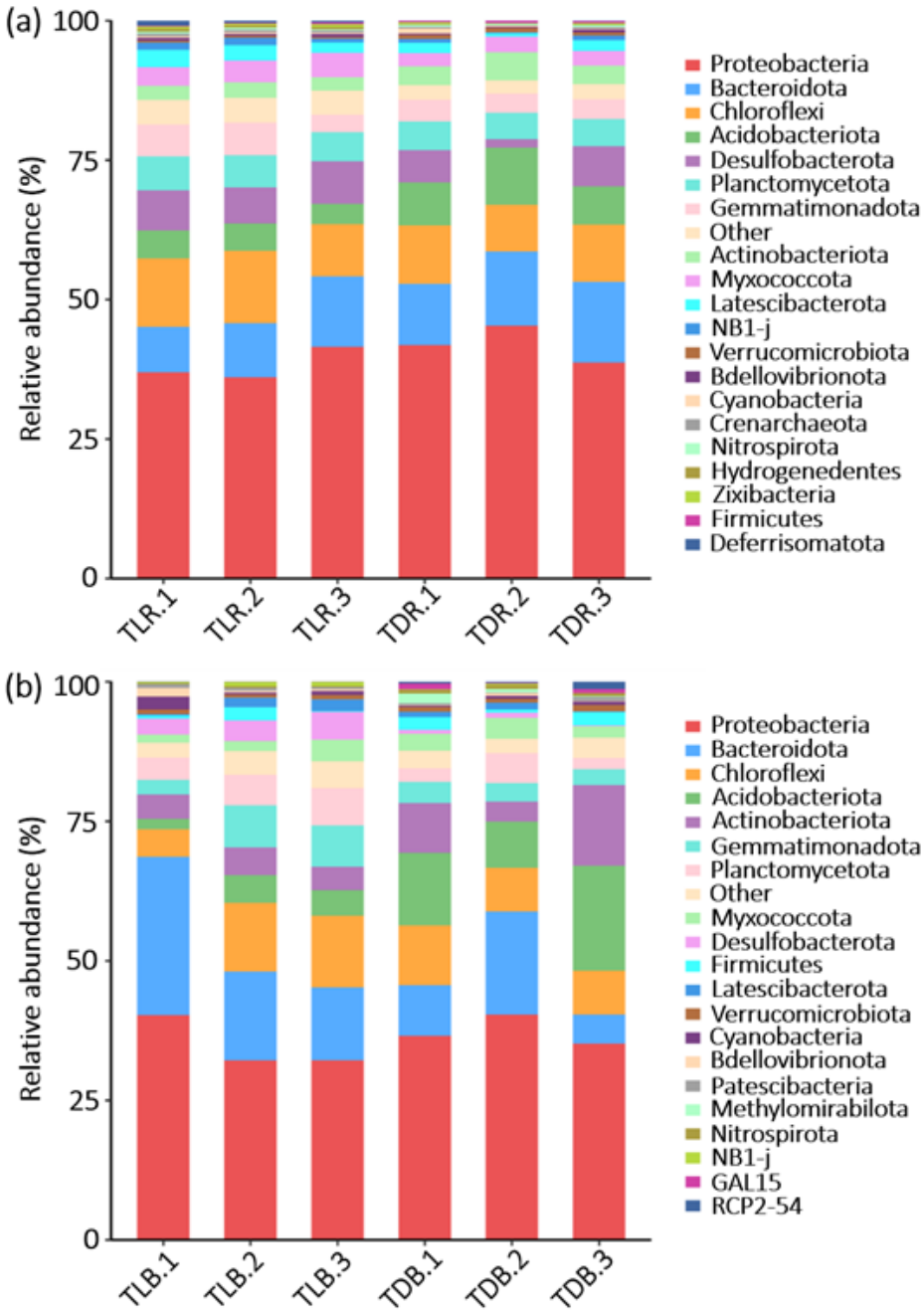


Figure 5

Bacterial community composition at phylum-level classification of (a) rhizosphere soil and (b) bulk soil