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Distinct Rhizosphere microbial cmmunity sturucture of *Taraxacum koksaghyz* Rodin in Saline - Alkaline Environments

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Abstract:*Taraxacum koksaghyz* Rodin (TKS), known as Russian dandelion, is a promising alternative source of natural rubber and can grow in saline-alkali habitats. To adapt to different soil environments, TKS may develop unique rhizosphere microbial communities under saline-alkali conditions. Therefore, understanding the rhizosphere microbial community structure of TKS in saline-alkali soils can help reveal the microbial diversity and functional potential of important soil microorganisms associated with this rubber-producing plant. In this study, we investigated the rhizosphere microbial community structure of wild TKS populations inhabiting saline-alkaline soils of tekec and Zhaosu Counties in Xinjiang, China. Soil physicochemical parameters and microbial diversity were characterized using high-throughput sequencing of bacterial 16S rRNA and fungal ITS regions. The results revealed pronounced heterogeneity between the two regions: Zhaosu soils exhibited higher salinity and alkalinity but also greater nutrient availability (OM and TN), while tekec soils were relatively less saline but nutrient-poor. Bacterial communities were dominated by Bacillus, Actinomarinales, and Geminicoccaceae, whereas Mortierella, Fusarium, and Metarhizium prevailed among fungi. Increasing salinity significantly reduced bacterial richness and evenness, yet favored dominance of halotolerant taxa. Redundancy and correlation analyses indicated that Na^+, Cl^-, and SO_4^{2-} were the primary drivers of bacterial community shifts, while fungal assemblages were more strongly influenced by Ca^{2+}, Mg^{2+},

HCO_3^-, and organic matter. These findings suggest that microbial adaptation in TKS rhizospheres is shaped by a complex interplay between ion composition and nutrient availability. The co-enrichment of halophilic Bacillus and stress-associated fungi such as Mortierella offers a valuable perspective for understanding the microbial diversity and community characteristics of TKS rhizosphere soils under saline-alkaline stress, and may provide a basis for further exploring plant-microbe interactions in saline-alkaline habitats.Ultimately, these findings lay a theoretical foundation for the improvement of soil and crop yield in saline-alkali land.

Key words: *Taraxacum koksaghyz* Rodin; rhizosphere microbial community;saline–alkaline soils; bacterial community; fungal community.

Introduction

Natural rubber r (NR, cis-1,4-polyisoprene) is is an essential high molecular weight biopolymer that is widely used in transportation, medical devices, defense, and industrial manufacturing. Owing to its unique elasticity, resilience, and heat-dissipation properties, NR remains difficult to fully replace with synthetic alternatives. At present, the global supply of high-quality NR still depends predominantly on *Hevea brasiliensis*, which creates both biological and geographical vulnerability in the natural rubber production system.Therefore, identifying alternative rubber-producing crops is of considerable agronomic and strategic importance (Salehi et al., 2021). *Taraxacum koksaghyz* Rodin (TKS), also known as Russian dandelion, native to the Tianshan Valley of Kazakhstan and the Tekec River basin of Xinjiang, China.

Among the alternative candidates, Taraxacum kok-saghyz Rodin (TKS), also known as Russian dandelion, is considered one of the most promising temperate-zone rubber crops because it produces high-quality rubber in roots and can be cultivated outside the traditional Hevea belt.TKS is native to Central Asia and adjacent regions, including the Tianshan Valley of Kazakhstan and parts of Xinjiang, China. According to previous reports and our preliminary field observations, wild TKS occurs in heterogeneous habitats, including valley bottoms, wet floodplain environments, and salinized meadow soils with sulfate–sodium characteristics (Uteulin et al. 2023).These field characteristics suggest that TKS may possess ecological traits enabling persistence in salt-affected habitats. However, the ecological basis of this adaptation remains poorly understood.

Plant adaptation to salinity has traditionally been interpreted mainly through host genetic

differentiation and physiological regulation. However, increasing evidence indicates that root-associated microorganisms are also integral to plant performance under abiotic stress. The rhizosphere microbiome can contribute to osmotic adjustment, ion homeostasis, antioxidant defense, nutrient acquisition, and immune regulation, and is therefore increasingly regarded as a functional extension, or "second genome," of the plant (Li et al., 2021; Liu et al., 2022; Acharya et al., 2024). In saline soils, plants are not merely passive recipients of surrounding microbes; instead, they can selectively recruit beneficial root-associated bacterial assemblages through rhizosphere filtering and stress-induced changes in root exudation (Li et al., 2021; Liu et al., 2022).

Soil microorganisms are increasingly recognized as an important biological resource for mitigating the adverse effects of salinization on plant growth and ecosystem function (King et al., 2022; Zhang et al., 2024). Many salt-tolerant plant growth-promoting bacteria, including members of Pseudomonas, Bacillus, and Azotobacter, have been reported to improve plant growth and stress resistance in saline–alkali soils (Zhang et al., 2018; Acharya et al., 2024). Moreover, recent studies suggest that plants may recruit not only individual beneficial taxa but also functionally coordinated bacterial consortia to enhance salt tolerance, indicating that community assembly itself may be a component of plant stress adaptation (Wang et al, 2018; Zhang et al., 2024).

At the community level, several studies from geographically distinct saline–alkali ecosystems have reported a recurrent dominance of Proteobacteria, Actinobacteriota/Actinobacteria, Bacteroidota/Bacteroidetes, and Firmicutes, although their relative abundances vary with host identity and soil physicochemical properties. For example, Nan et al. (2022) showed that Proteobacteria, Bacteroidetes, Actinobacteria, Firmicutes, and Gemmatimonadetes were dominant in saline–alkali soils of Gansu Province. Similarly, Li et al. (2021) found that the rhizosphere bacterial communities of four halophytes from southern Xinjiang were dominated by Firmicutes, Proteobacteria, Actinobacteria, and Bacteroidetes. Recent reviews have further emphasized that salinity-related environmental filtering plays a major role in shaping microbial diversity and function in saline soils (Nan et al., 2022; Wang et al, 2018; Zhang et al., 2024).

These findings provide an important conceptual basis for studying TKS in its native saline habitats. If wild TKS can persist in salt-affected soils, an important unresolved question is whether this ecological success is associated with the assembly of a distinctive rhizosphere bacterial community, and whether variation in soil physicochemical properties helps explain that community structure. In

this sense, characterizing the rhizosphere bacterial community is not an isolated descriptive objective; rather, it is a necessary step toward understanding the microbial ecological basis of salt-associated habitat adaptation in TKS.

Therefore, the central question of this study is whether the rhizosphere of wild Taraxacum kok-saghyz growing in saline–alkali soils harbors a distinctive bacterial community associated with soil environmental filtering and salt-associated habitat adaptation. To address this question, we characterized rhizosphere bacterial diversity and community composition using high-throughput sequencing and analyzed their relationships with key soil physicochemical properties. We hypothesized that wild T. kok-saghyz would be associated with bacterial taxa commonly linked to saline tolerance, and that variation in salinity-related soil properties would significantly correlate with bacterial community assembly.

Methods

Sampling site description

Rhizosphere soil samples of Taraxacum kok-saghyz Rodin (rubber grass) were collected from natural wild populations in the Yili Tekes River Basin, Xinjiang Uygur Autonomous Region, China. Prior to sampling, communication was established with the relevant local administrative authorities, and permission for field sampling was obtained. Formal collection permits were not required. The plant species involved in this study is not listed as endangered or protected. The collection and use of plant materials complied with institutional, national, and local regulations, as well as relevant guidelines.

The plant material was formally identified by Liang jie Yang, based on the taxonomic description of Taraxacum koksaghyz Rodin in Acta Instituti Botanici Academiae Scientiarum URSS, Series I, Fascicle 1, page 187, figures 1-10 (1933). A voucher specimen was prepared in the form of a wax-leaf specimen and deposited in the Herbarium of Xinjiang Institute of Ecology and Geography, Chinese Academy of Sciences. The voucher specimen number is 2022xjkk0503-PS-20029.

Samples were collected from two locations in the upper reaches of the Yili River Valley on the southern slopes of the western Tianshan Mountains in Xinjiang, China: Zhaosu Chahan Wusu Township (80.74° E, 42.85° N; average altitude 1638.45 m; annual mean temperature approximately 3-5 ℃) and Tekec Racecourse (81.97° E, 43.24° N; average altitude 1065 m). Tekec and Zhaosu Counties are characterized by a temperate continental semi-humid climate influenced by the Tianshan Mountains and the Tekec Valley, with mean annual temperatures of 5.5-7.5℃ and mean annual

precipitation of 500-600 mm, which is notably higher than most arid zones of Xinjiang. The region benefits from snowmelt runoff that provides ample water resources during spring and summer; however, in lowland plains and alluvial depressions, shallow mineral-rich groundwater and poor drainage conditions have led to the development of light to moderate soil salinization. Salinity types are predominantly chloride-sulfate salts, with occasional soda-type characteristics, particularly in poorly drained irrigated farmland and lake-margin wetlands. The study area is therefore classified as a typical saline–alkali meadow and river beach ecosystem.

A multi-point mixed sampling strategy was employed in this study. In total, five sampling sites were randomly distributed within the study area, with distances between sites not less than 200 m; three sites were located in Tekec Racecourse, and two sites were selected in Zhaosu Chahan Wusu Township. At each sampling point, 3-5 healthy T. kok-saghyz individuals with similar-sized growth crowns were selected, and rhizosphere soil samples were collected. The soil was excavated to remove the entire root system (approximately 10-40 cm). Loose soil attached to the root system was gently shaken off, and the soil tightly adhering to the root surface (1-3 mm) was retained for analysis.

All samples were collected in sterile plastic bags, placed on dry ice and transported to the laboratory immediately, and divided into at least two parts according to study requirements, one was stored at -80℃ for DNA high-throughput sequencing analysis, and the other was air-dried for physicochemical index detection and analysis.

Soil Physicochemical and Biological Parameters

Soil total nitrogen (TN) was determined using the Kjeldahl digestion method with sulfuric acid and catalyst, followed by analysis on an AA3 continuous flow analyzer (AutoAnalyzer 3, SEAL Analytical, Germany), according to the Chinese standard HJ 717-2014, with reference to the procedure described in Bremner (2015).Soil organic matter (OM) was measured using the potassium dichromate oxidation method with external heating and titration, following the Chinese standard HJ 615-2011, and consistent with the method described by Nelson and Sommers (2015).Available phosphorus (AP) was extracted using the double-acid method and determined by molybdenum–antimony colorimetry with a UV spectrophotometer (UV-2450, Shimadzu, Japan), according to NY/T 1121.7-2014, with reference to Murphy and Riley (1962) and Kovar and Pierzynski (2009). Available potassium (AK), as well as soil potassium (K^+) and sodium (Na^+), were determined by flame photometry (FP6410, Shanghai Yi Dian Analytical Instrument Co., Ltd., China) following NY/T 889–2004, with reference to Helmke and

Sparks (2015). Soil calcium (Ca^{2+}), magnesium (Mg^{2+}), and sulfate (SO_4^{2-}) were measured by EDTA titration according to NY/T 1121.4-2006, in accordance with Sparks (2015). Carbonate (CO_3^{2-}) was determined using a two-indicator acid–base neutralization titration method, and chloride (Cl^-) was analyzed by silver nitrate titration (Mohr method), following NY/T 1121.6-2006, with reference to Rhoades (2015).

DNA extraction and PCR amplification

Total microbial genomic DNA was extracted from soil samples using the E.Z.N.A.® soil DNA Kit (Omega Bio-tek, Norcross, GA, U.S.) according to manufacturer's instructions. The quality and concentration of DNA were determined by 1.0% agarose gel electrophoresis and a NanoDrop2000 spectrophotometer (Thermo Scientific, United States) and kept at -80 ℃ 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'-GGACTACHVGGG TWTCTAAT-3') (Liu et al., 2016) by ABI GeneAmp®9700 (ABI, USA). The PCR reaction mixture including 4 μL 5 × Fast Pfu buffer, 2 μL 2.5 mM dNTPs, 0.8 μL each primer (5 μM), 0.4 μL Fast Pfu polymerase, 10 ng of template DNA, and ddH_2O to a final volume of 20 μL. For fungal community, the ITS sequences were amplified using the primers ITS1F (CTTGGTCATTTAGAGGAAGTAA) and ITS2R (GCTGCGTTCTTCATCGATGC) by ABI GeneAmp®9700 (Chen et al.,2018).The PCR reaction mixture including 2 μl 10× Buffer, 2 μl 2.5 mM dNTPs, 0.8μl Forward Primer (5 μM), 0.8μl Reverse Primer(5 μM), 0.2 μl rTaq Polymerase, 0.2 μl BSA, 10 ng Template DNA, and ddH_2O to a final volume of 20 μL. PCR amplification cycling conditions were as follows: initial denaturation at 95 ℃ for 3 min, followed by 27 cycles of denaturing at 95 ℃ for 30 s, annealing at 55 ℃ for 30 s and extension at 72 ℃ for 45 s, and single extension at 72 ℃ for 10 min, and end at 4 ℃.

Illumina sequencing and Data Records

Purified amplicons were pooled in equimolar amounts and paired-end sequenced on an Illumina Nextseq2000 platform (Illumina, San Diego,USA) according to the standard protocols by Majorbio Bio-Pharm Technology Co. Ltd. (Shanghai, China).

Data processing

Raw FASTQ files were de-multiplexed using an in-house perl script, and then quality-filtered by fastp version 0.19.6 (Chen et al., 2018) and merged by FLASH version 1.2.7 (Magoč &Salzberg,

2011) with the following criteria: (i) the reads were truncated at any site receiving an average quality score of <20 over a 50 bp sliding window, and the truncated reads shorter than 50 bp were discarded, reads containing ambiguous characters were also discarded; (ii) only overlapping sequences longer than 10 bp were assembled according to their overlapped sequence. The maximum mismatch ratio of overlap region is 0.2. Reads that could not be assembled were discarded; (iii) Samples were distinguished according to the barcode and primers, and the sequence direction was adjusted, exact barcode matching, 2 nucleotide mismatch in primer matching. Then the optimized sequences were clustered into operational taxonomic units (OTUs) using UPARSE 7.1 with 97% sequencesimilarity level. The most abundant sequence for each OTU was selected as a representative sequence.The taxonomy of each OTU representative sequence was analyzed by RDP Classifier version 2.2 (Wang et al., 2007) against the 16S rRNA gene database (eg. Silva v138) using confidence threshold of 0.7. The metagenomic function was predicted by PICRUSt2 (Phylogenetic Investigation of Communities by Reconstruction of Unobserved States) based on OTU representative sequences. PICRUSt2 is a software containing a series of tools as follows: HMMER was used to aligns OTU representative sequences with reference sequences. EPA-NG and Gappa were used to put OTU representative sequences into a reference tree. The castor was used to normalize the 16S gene copies. MinPath was used to predict gene family profiles, and locate into the gene pathways. Entire analysis process was accord to protocols of PICRUSt2.

Results and discussion

Soil physicochemical properties

The soil physicochemical properties are summarized in Supplementary Table 1. The five sampling sites differed markedly in their edaphic conditions, but all of them showed saline-alkaline characteristics, with TS > 6.5g kg^{-1} and pH > 8.0. The higher TS values at Zhaosu than at Tekes suggest that the Zhaosu habitats impose stronger salt stress on rhizosphere biota. Previous studies have shown that salinity and pH are key determinants of microbial community assembly and activity in salt-affected soils, and thus the site-specific differences observed here likely contributed to the distinct microbial patterns detected in this study. (Dong et al., 2022; Zhang et al., 2023; Husson, 2013)

The relatively higher TN and OM values in Zhaosu may indicate a comparatively greater nutrient supply in these soils. Since nitrogen is central to microbial metabolism and soil organic matter can

provide available carbon sources and modify the soil microenvironment, both variables may be associated with shifts in rhizosphere microbial composition. Nevertheless, this study did not directly test the mechanistic links among TN, OM, and the diversity of salt-tolerant microorganisms. Accordingly, the relationship should be interpreted cautiously as an association rather than a confirmed causal effect. (Geisseler et al., 2010; Philippot et al., 2023)

Analysis of abundance and diversity of bacterial and fungal communities

A total of 1,105,574 high-quality valid 16S rRNA gene sequences were obtained from the 15 soil samples after sequence quality control. The ACE and Chao1 indices are commonly used to estimate community richness, and higher values generally indicate a greater number of taxa, including rare taxa that may not have been completely sampled (Shi et al. 2024). As shown in Table 1, the ACE and Chao1 indices differed among samples. The richness of the bacterial communities was ranked as TK-5 > TK-1 > ZS-1 > ZS-2 > TK-3. This pattern was generally consistent with the variation in soil salinity across the two regions, suggesting that bacterial richness tended to decline under higher salt stress. Similar trends have been reported in saline soils and rhizosphere systems, where salinity acts as an environmental filter that reshapes microbial communities and often reduces prokaryotic richness in the rhizosphere, although the magnitude and direction of the response can vary with soil type, plant effects, and the intensity of salinization. In this context, the present results support an association between higher salinity and lower bacterial richness, but they do not by themselves demonstrate a direct causal relationship. In addition, salt stress is not determined by total salinity alone; elevated concentrations of specific ions, especially Na^+ and associated sodicity, can further constrain microbial growth and select for salt-tolerant taxa. Accordingly, although some bacterial groups are inhibited under saline-alkaline conditions, other microorganisms with high salt tolerance may persist or even become enriched in high-salt environments (Bao et al. 2024).

Principal coordinate analysis (PCoA), utilizing distance matrices, provides an intuitive visualization of the similarities and differences among soil microbial communities.The PCoA analysis distinctly revealed the variations among all individual samples and groups (Fig 2). It was observed that the 5 five samples from different areas were grouped in a certain space, which explained 40 % and 16.37 % of the total variations for bacteria, 23.21% and 18.57% of the total variations for fungi. Accourding to the PCoA plot tekec soil and Zhaosu soil were significantly different in bacterial community composition (mainly reflected in PC2). Meanwhile, there is a clear gradient along PC1

within the TK group, with TK_5 being the most distinctive. There is also a significant difference between ZS_1 and ZS_2. Overall, the groups are well separated and consistent within themselves.

Analysis of Microbial Community Composition

Bacterial communities. Based on the results of species annotation statistics, a total of 43 Phyla, 147 Classes, 373Orders, 634 Families and 1213 genera were affiliated in all samples. Actinobacteriota, Proteobacteria, Chloroflexi, Firmicutes, Acidobacteriota were the common dominant phyla. Soil bacteria comprised of less dominant phyla (relative abundance >1%) and more nondominant phyla (Fig3A).The sample TK-1,TK-3 and TK_5 seems to have a more homogenous community dominated by Firmicutes and Proteobacteria, while ZS_1 and ZS_2 show a broader diversity of phyla.There may be environmental factors contributing to the shifts in phylum composition between the samples. Many studies have reported that many types of Firmicutes and Proteobacteria each play distinct roles in the plant root system. The former primarily enhances plant growth performance through mechanisms such as growth promotion, disease resistance, and nitrogen fixation, while the latter contributes to plant health through nitrogen fixation, pathogen suppression, and the secretion of plant growth hormones (Wahab et al. 2024). Their interactions within the rhizosphere microbial community jointly help plants better adapt to complex environmental changes; as as they can fix atmospheric N, solubilize phosphate, produce siderophores and auxin, and possess ACC deaminase activity (Rafique et al. 2024).

Genus-level analysis of the bacterial communities revealed that Bacillus was the dominant genus across all five samples (TK_1, TK_3, TK_5, ZS_1, ZS_2), with relative abundance often exceeding 50% and peaking at over 60% in TK_3 and TK_5. The TK-series samples showed a more extreme Bacillus enrichment compared with the ZS-series, where several other genera contributed more substantially to the community structure. Secondary taxa included Actinomarinales and Geminicoccaceae, which maintained low but stable abundances (<10%) across all sites (Fig3B). Notably, Vicinamibacterales was more prevalent in ZS_1 and ZS_2, suggesting environmental conditions in these samples favor taxa adapted to oligotrophic niches, consistent with previous reports of their association with low-nutrient soils (Qi et al. 2025; Delgado et al. 2018). The lower evenness and higher dominance observed in TK samples indicate a bacterial community shaped by strong selection pressures, whereas ZS samples reflect a more balanced assemblage with potential for greater functional redundancy .

Fungal communities. At the phylum level, the fungal communities were overwhelmingly dominated by Ascomycota, generally exceeding 80% of the total reads and reaching >90% in TK_3

and TK_5 (Fig 4A). This pattern was consistent across samples, though ZS_1 and ZS_2 showed a markedly higher proportion of Basidiomycota (~10 – 15%) compared to TK samples (<5%). Mortierellomycota occurred in all samples, peaking at nearly 5% in ZS_2, while remaining <2% in other samples. Low-abundance phyla such as Chytridiomycota, Glomeromycota, and Rozellomycota were sporadically detected, with slightly higher representation in the ZS-series. The predominance of Ascomycota aligns with global soil fungal surveys showing its ability to utilize diverse plant-derived carbon sources and persist under varied nutrient regimes (Egidi et al. 2019; Manici et al. 2025). Enrichment of Basidiomycota in ZS-series samples may be linked to increased presence of lignin-rich organic matter, given their lignocellulose-degrading capacity (Kohler et al. 2015). The elevated Mortierellomycota in ZS_2 suggests microhabitat conditions—such as higher soil moisture or organic nutrient availability—that promote their rapid saprotrophic growth (Liao et al. 2021).

At the genus level, Mortierella dominated most fungal profiles, frequently surpassing 50% relative abundance and reaching maxima in TK_1 and ZS_2. TK_5 and ZS_1, however, exhibited greater diversity, with increased proportions of Metarhizium, Fusarium, and Alfaria (Fig 4B). TK_3 combined high Mortierella presence with notable unclassified_f__Nectriaceae. The enrichment of Metarhizium and Fusarium in TK_5 and ZS_1 suggests environmental conditions conducive to plant-associated or insect-pathogenic fungi (Iwanicki et al. 2021). Fusarium’s rise in ZS_1 may indicate higher organic matter from plant residues, consistent with its known saprotrophic and pathogenic strategies (Bottalico et al., 2002). The appearance of Alfaria and Emericellopsis in moderate abundance suggests that soil microhabitat heterogeneity could influence recruitment patterns (Qi et al. 2025). Minor genera such as Plectosphaerella, Articulospora, and Preussia were sporadic but may maintain specialized decomposition roles (Nilsson et al. 2019).

In both bacterial and fungal domains, TK-series soils were characterised by strong dominance of single taxa (Bacillus, Ascomycota, often Mortierella), resulting in lower taxonomic evenness. ZS-series soils maintained higher representation of secondary taxa, indicating greater community balance and potential functional redundancy. These patterns suggest that TK soils are shaped by environmental filtering and competitive exclusion, whereas ZS soils may reflect more heterogeneous resources and niche partitioning (Bahram et al., 2018; Stegen et al., 2015). Functional analyses—metagenomics, enzymatic assays—are needed to determine whether these compositional differences translate into variation in ecosystem processes such as nutrient cycling or pathogen suppression.

Correlation analysis between microbial community structure and soil properties

Bacterial Community Structure and Environmental Drivers. Redundancy analysis (RDA) of the bacterial community (Figure 5A) revealed that environmental variables collectively explained 42.39% of the total compositional variance (RDA1: 30.01%; RDA2: 12.38%). Salinity-related ions, particularly SO_4^{2-}, Na^+, and Cl^-, exerted the strongest influence, driving the clustering of TK_1 and TK_3 groups toward the positive side of RDA1. This suggests that bacterial assembly in these sample groups is largely shaped by saline–alkaline conditions, potentially originating from seawater intrusion, evaporation, or anthropogenic inputs (Chaieb et al. 2018).

Conversely, ZS_1 and part of ZS_2 grouped along the negative side of RDA1, showing strong positive associations with organic matter (OM), total nitrogen (TN), and total sulphur (TS). These nutrient-rich, lower-salinity conditions likely promote copiotrophic bacteria capable of rapid organic matter degradation, in agreement with observations from estuarine sediments and agricultural soils (Arndt et al., 2018). TK_5 samples occupied intermediate positions, suggesting transitional environments with balanced salinity–nutrient gradients.

Redundancy analysis (RDA) revealed that several environmental variables showed significant associations with community distribution patterns. Among them, sodium (Na^+) exhibited the highest explanatory power (r2=0.659, P=0.008), followed by chloride (Cl^-, r^2=0.527, P=0.014) and readily available phosphorus (RAP, r^2=0.523, P=0.023). Total nitrogen (TN), total solids (TS), bicarbonate (HCO^{3-}), and magnesium (Mg^{2+}) also showed relatively high coefficients (r^2 between 0.47 and 0.49) and were statistically significant (P<0.05P < 0.05P<0.05). Organic matter (OM) accounted for 40.5% of the variation (P=0.039), indicating a moderate but significant influence.In contrast, available phosphorus (AP), calcium (Ca^{2+}), and sulfate (SO_4^{2-}) displayed low explanatory values (r^2<0.23) and lacked statistical significance (P>0.2). Overall, dissolved ion composition, particularly Na^+ and Cl^-, was more influential in shaping community structure compared with some nutrient-related parameters such as AP and Ca^{2+}（table 2）.

Spearman correlation analysis of the dominant bacterial taxa (Figure 5B) revealed two major ecological guilds. Bacillus, 67-14, and JG30-KF-CM45 showed strong positive correlations ($\rho > 0.45$, $p < 0.05$) with each other and co-located in the high-salinity region of the RDA plot, suggesting shared tolerance and potential metabolic complementarity under osmotic stress. In contrast, KD4-96 exhibited significant negative correlations with Victivallales and Euzebyaceae, corresponding to their RDA

separation along nutrient-rich gradients, indicative of niche segregation between oligotrophic and copiotrophic strategies. In conclusion, the soil indices exerting major effects on the fungal community structure were as follows: TN (r^2=0.46976, P<0.05), OM (r^2=0.40458, P<0.05), RAP (r^2=0.52278, P<0.05), TS (r^2=0.48869, P<0.05), Na^+ (r^2=0.65918, P<0.01), Cl^- (r^2=0.5268, P<0.05) and HCO^{3-} (r^2=0.47155, P<0.05) (Table 2).The Envfit results illustrate how multiple physicochemical factors are associated with bacterial community patterns along the RDA axes. Most variables such as TN, OM, RAP, TS, Na^+, and Cl^-show significant correlations (P < 0.05), indicating that they act as major drivers shaping community structure.

These coupled patterns from ordination and correlation imply that bacterial community structuring results from both abiotic filtering by environmental gradients and biotic interactions such as competition and cooperation (Wang et al. 2023).

Fungal Community Structure and Environmental Drivers . RDA of the fungal community (Fig. 6A) explained 26.31% of the variance (CCA1: 13.98%; CCA2: 12.33%). Fungal assemblages were primarily influenced by Ca^{2+}, SO_4^{2-}, Mg^{2+}, and HCO_3^-. TK_3 samples aligned with Ca^{2+} and SO_4^{2-} vectors, consistent with environments influenced by gypsum dissolution or evaporative mineral concentration (Han et al., 2021). ZS_1 and ZS_2 correlated with Mg^{2+} and HCO_3^-, indicative of carbonate-buffered, moderately alkaline conditions possibly derived from dolomitic lithology (Fussmann et al. 2020). TK_1 samples clustered near the ordination origin, suggesting relatively stable ionic environments.

Canonical correspondence analysis (CCA) identified several environmental variables with significant associations to community variation (Table 3). Among them, bicarbonate (HCO3−) showed the strongest explanatory power (r^2=0.721, P=0.001), followed by chloride (Cl^-, r^2=0.632, P=0.007) and sulfate ($SO4^{2-}$, r^2=0.582, P=0.002. Total nitrogen (TN), total solids (TS), and organic matter (OM) also explained a substantial portion of the variation (r^2 ranging from 0.526 to 0.574), with high statistical significance (P≤0.01). Readily available phosphorus (RAP), sodium (Na^+), and magnesium (Mg^{2+}) were likewise significant contributors (r^2≈0.52–0.55). By contrast, pH and potassium (K^+) exhibited weaker correlations (r^2=0.347 and 0.289, respectively), and their effects did not reach significance. Calcium (Ca^{2+}) showed only limited explanatory capacity (r^2=0.186, P=0.286), while available phosphorus (AP) had minimal influence (r^2=0.030, P=0.829).

Overall, the results indicate that bicarbonate, chloride, sulfate, and major nutrient variables such as

TN, TS, and OM were the dominant drivers of community variation, whereas AP and Ca^{2+}had little explanatory value.

Spearman correlations between dominant fungal taxa and environmental factors (Fig. 6B) revealed that Metarhizium and Fusarium were positively associated with pH, electrical conductivity (EC), and total organic carbon (TOC), suggesting tolerance to saline–alkaline, carbon-rich soils. Conversely, Plectosphaerella and Emericellopsis correlated negatively with these variables, indicating adaptation to acidic, low-salinity conditions (Grum-Grzhimaylo et al. 2016; Yang et al. 2020). These associations directly align with fungal RDA results, supporting the importance of pH–ion chemistry as a primary fungal niche axis. In conclusion, the soil indices exerting major effects on the fungal community structure were as follows: TN (r^2=0.57374, P<0.05), OM (r^2=0.52636, P<0.05), RAP (r^2=0.52278, P<0.05), TS (r^2=0.55743, P<0.01), Na^+ (r^2=0.54655, P<0.05), Cl^- (r^2=0.63212, P<0.01), HCO^{3-} (r^2=0.72104, P<0.01), .Mg^{2+} (r^2=0.54655, P<0.05) and SO_4^{2-}(r^2=0.58176, P<0.01) (Table 3). The envfit results indicate that TN, OM, RAP, TS, Na^+ and Cl^- are the primary environmental drivers of the fungal community, as shown by their high r^2 values and significant P-values. Variables such as AP and Ca^{2+}exhibit weak or nonsignificant correlations, suggesting limited influence on community variation. This pattern is consistent with established findings that nutrient availability and ionic composition strongly shape microbial assemblages in soils.

The bacterial and fungal RDA ordinations with their respective correlation networks reavealed that，environmental filtering is taxon-specific. Bacterial communities are most strongly structured by salinity – nutrient gradients (SO_4^{2-}, Na^+, Cl^-，OM, TN, TS), whereas fungal communities respond more to mineral ion chemistry and carbonate buffering (Ca^{2+}, Mg^{2+}, HCO_3^-) and pH. This reflects partially overlapping but distinct ecological niches for bacteria and fungi.High-salinity habitats harbor osmolyte producers, sulphate reducers, and alkali-tolerant decomposers, potentially driving sulphur and carbon cycling. Nutrient-enriched, low-salinity environments support fast-growing copiotrophs and plant-associated fungi, accelerating organic matter mineralization but also increasing vulnerability to eutrophication.

Conclusion

This study provides a comprehensive characterization of the rhizosphere microbial communities associated with Taraxacum koksaghyz Rodin (TKS) inhabiting extreme saline–alkaline soils of tekec and Zhaosu, Xinjiang, China. The results demonstrate that the structure and diversity of these microbial

assemblages are strongly governed by both salinity-related ions and nutrient availability. Sodium (Na^+), chloride (Cl^-), and sulfate (SO_4^{2-}) emerged as the principal environmental drivers shaping bacterial communities, whereas calcium (Ca^{2+}), magnesium (Mg^{2+}), bicarbonate (HCO_3^-), and organic matter predominantly influenced fungal distributions. The observed enrichment of halotolerant bacterial taxa, particularly Bacillus, and stress-resistant fungi such as Mortierella and Metarhizium, suggests that these microbes play synergistic roles in promoting plant resilience under osmotic and alkaline stress.

These findings highlight the intricate interplay between ionic composition, nutrient status, and microbial community assembly in the TKS rhizosphere, revealing that TKS's remarkable salt tolerance may, in part, derive from its capacity to recruit and sustain a specialized consortium of halophilic and stress-adapted microorganisms. The ecological differentiation between tekec and Zhaosu soils further underscores the influence of local edaphic conditions in driving microbial selection and adaptation.

From a broader perspective, the identified microbial consortia represent valuable biological resources for the development of bioinoculants and bioremediation strategies tailored to saline–alkaline agriculture. Future research should integrate metagenomic and metabolomic analyses to elucidate the functional pathways underlying microbe–plant interactions and to explore the potential of key taxa in enhancing stress tolerance and nutrient cycling across degraded saline ecosystems.

Author Contributions Tuhanguli T conceived and designed the experiments, performed the experiments, analyzed the data, contributed reagents/materials/analysis tools, prepared figures and/or tables, and authored or reviewed drafts of the paper. Zheng LP analyzed the data, authored or reviewed drafts of the paper, and approved the final draft. Yan QQ, Zhang Y,Tang LS, Cao JM, Ayijamali A conceived and designed the experiments, analyzed the data, Gao Q and Xu L authored or reviewed drafts of the paper, and approved the final draft. All authors read and approved the final manuscript.

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Declarations

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.

Ethical Approval Not applicable.

Consent for publication: Not Applicable.

Competing interests The authors have no relevant financial or nonfinancial interests to disclose.

Data availability

The datasets generated and analysed during the current study are available in the NCBI Sequence Read Archive (SRA) repository (Accession Number: SRR35936403-432, private reviewer link:https://dataview.ncbi.nlm.nih.gov/object/PRJNA1356636?reviewer=h3e1rj1152ftvb972a2c6lqeql).

References

1. Abuqamar, S. F.et al. Halotolerant plant growth-promoting rhizobacteria improve soil fertility and plant salinity tolerance for sustainable agriculture - a review. *Plant Stress*,12(000);10.1016/j.stress. 2024.100482 (2024).
2. Acharya, B. R., Gill, S. P., Kaundal, A., & Sandhu, D. Strategies for combating plant salinity stress: the potential of plant growth-promoting microorganisms. *Front Plant Sci*. 15, 14069 13;10.3389/fpls.2024.1406913(2024).
3. Arndt, S., Larowe, D. E. Organic matter degradation and preservation. Springer International Publishing, pp 1-6;(2018).
4. Bao, Y.et al. The impact of salinization on soil bacterial diversity, yield and quality of Glycyrrhiza uralensis. Fisch Frontiers in Microbiology, 15:1448301; 10.3389/fmicb.202 4.1448301(2024).
5. Bahram, M. et al. Structure and function of the global topsoil microbiome. Nature, 560, 233–237; 10.1038/s41586-018-0386-6(2018).
6. Bottalico, A., &Perrone, G. Toxigenic Fusarium species and Mycotoxins Associated with Head Blight in Small-Grain Cereals in Europe. *Eur J Plant Pathol.* 108(7):611-624;10.1023/A:102063 5214971(2002) .
7. Bremner, J.M. Nitrogen—Total. In: Sparks, D.L. (Ed.), Methods of Soil Analysis, Part 3. ASA and SSSA (2015).
8. Chaieb, G., Abdelly, C.& Michalet, R. Interactive effects of climate and topography on soil salinity and vegetation zonation in North-African continental saline depressions. *J VEG SCI.* 30(2),312-321; 10.1111/jvs.12693(2018).
9. Chen, S. et al. fastp: an ultra-fast all-in-one FASTQ preprocessor. *Bioinformatics*. 34(17):i884-i890;10.1093/bioinformatics/bty560 (2018).
10. Delgado B.M.et al. A global atlas of the dominant bacteria found in soil. *Science*. 359(6373), 320–325;10.1126/science.aap9516(2018).
11. Dong, Y.et al. Microbial Community Composition and Activity in Saline Soils of Coastal

Agro-Ecosystems. *Microorganisms*. 10(4), 835;10.3390/microorganisms10040835 (2022).

12. Egidi, E. et al. A few Ascomycota taxa dominate soil fungal communities worldwide. Nat. Commun. 10, 2369;10.1038/s41467-019-10373-z (2019).

13. Fussmann, D.et al. Authigenic formation of Ca–Mg carbonates in the shallow alkaline Lake Neusiedl, Austria. *Biogeosciences.* 17(7):2085-2106;10.5194/bg-17-2085-2020 (2020) .

14. Grum-Grzhimaylo, A.A., Georgieva, M.L., Bondarenko, S.A., Debets, A.J.M., Bilanenko, E.N. On the diversity of fungi from soda soils. *Fungal Divers.* 77, 289-303. 2;10.1007/ s13225-015-0320-2(2016).

15. Han, D., Currell, M. J.& Guo, H. Controls on distributions of sulphate, fluoride, and salinity in aquitard porewater from the North China Plain: Long-term implications for groundwater quality. *J Hydrol*, 603(Pt.A),126828;10.1016/j.jhydrol.2021.126828(2021).

16. Helmke, P. A.& Sparks, D. L. Alkali metals. In: Methods of Soil Analysis, Part 3 (2015).

17. Husson, O. Redox potential (Eh) and pH as drivers of soil/plant/microorganism systems: a transdisciplinary overview pointing to integrative opportunities for agronomy. *Plant Soil.* 362, 389–417;10.1007/s11104-012-1429-7 (2013).

18. Ilangumaran, G.& Smith, D. L. Plant growth promoting rhizobacteria in amelioration of salinity stress: a systems biology perspective.*Front Plant Sci*. 8:1768;10.3389/fpls.2017.01768(2017).

19. Iwanicki, N., Botelho, A.B., Klingen, I.& Lysoe, E. Genomic signatures and insights into host niche adaptation of the entomopathogenic fungus metarhizium humberi.*G3*.12(2):jkab416; 10.1093/g3journal/jkab416(2021).

20. Geisseler, D., Horwath, W. R., Joergensen, R. G. &Ludwig B. Pathways of nitrogen utilization by soil microorganisms - A review. *Soil Biol Biochem*. 42(12), 2058–2067; 10.1016/j.soilbio. 2010.08.021(2010).

21. King, W. L.et al. Soil salinization accelerates microbiome stabilization in iterative selections for plant performance. *New Phytol*. 234 (6):2101–10;10.1111/nph.17774(2022).

22. Kohler, A. et al. Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists.*Nat. Genet*. 47, 410–415;10.1038/ng.3223(2015).

23. Kovar J L, Pierzynski G M. Methods of phosphorus analysis. SERA-IEG(2009).

24. Li, H., La, S., Zhang, X., Gao, L.&Tian, Y. Salt-induced recruitment of specific root-associated bacterial consortium capable of enhancing plant adaptability to salt stress.*The ISME Journal*, 15:

2865–2882;10.1038/s41396-021-00974-2(2021).

25. Wang, X. et al. Bacterial diversity and community structure in the rhizosphere of four Ferula species. *Sci Rep*. 8, 5345;10.1038/s41598-018-22802-y (2018).

26. Liao, H. L. The Plant-Growth-Promoting Fungus, Mortierella elongata: Its Biology, Ecological Distribution, and Growth-Promoting Activities. *EDIS*. 2021(2); 10.32473/EDIS-SS679-2021 (2021).

27. Liu, C., Zhao, D., Ma, W., Guo, Y., Lee, D. J. Denitrifying sulfide removal process on high-salinity wastewaters in the presence of Halomonas sp. *Appl Microbiol Biotechnol*. 100(3): 1421-1426;10.1007/s00253-015-7039-6(2016).

28. Liu, Y.et al. Rhizosphere microbes enhance plant salt tolerance: Toward crop production in saline soil. *Comput Struct Biotec*. 20, 6543–6551;10.1016/j.csbj.2022.11.046 (2022).

29. Manici, L.M.et al. Ascomycota and Basidiomycota as key drivers of soil microbial stability under extreme soil moisture and temperature fluctuations.Arch Agron Soil Sci. 7(1):1-13;10.1080/ 03650340.2025.2550629 (2025).

30. Nan, L., Guo, Q., Cao, S. & Zhan, Z. Diversity of bacterium communities in saline-alkali soil in arid regions of northwest china. *BMC Microbiology*. 22(1), 11;10.1186/s12866-021-02424-7 (2022).

31. Nelson, D. W., Sommers, L. E. Organic matter. In: Methods of Soil Analysis (2015).

32. Nilsson, R. H.et al.Taxonomic reliability of DNA sequences in public sequence databases: a fungal perspective.*PLoS ONE*1.e59.10.1371/ journal.pone.0000059(2006)..

33. Philippot, L., Chenu, C., Kappler, A., Rillig, M. C.&Fierer, N. The interplay between microbial communities and soil properties. *Nat. Rev. Microbiol*. 22,pages226–239; 10.1038/s41579-023-00980-5 (2024).

34. Qi, X.et al. Diversity of fungal communities in the rhizosphere soil of Tamarix chinensis in saline-alkaline wetland. *Environ Dev Sustain*. 27, 8693–8709;10.1007/ s10668-023-04250-5 (2025).

35. Ranjitha, K., Prathap, M. A critical Review on Plant Growth Promoting Rhizobacteria. *J Plant Pathol Microbiol*. 06(04);10.4172/2157-7471.1000266 (2015).

36. Rafique, N.et al. A comprehensive evaluation of the potential of plant growth-promoting rhizobacteria for applications in agriculture in stressed environments.*Pedosphere.* 35(1),229-248;

509 10.1016/j.pedsph.2024.02.005(2025).
510 37. Rhoades, J. D. Salinity methods. In: Methods of Soil Analysis (2015).
511 38. Salehi, M., Cornish, K., Bahmankar, M.& Naghavi, M. R. Natural rubber-producing sources,
512 systems, and perspectives for breeding and biotechnology studies of *Taraxacum kok-saghyz*. Ind.
513 Crops Prod., 170, 113667; 10.1016/j.indcrop.2021.113667 (2021).
514 39. Stegen, J.C., Xueju, L., Fredrickson, J.K.& Konopka, A.E. Estimating and mapping ecological
515 processes influencing microbial community assembly. Front. Microbiol. 6, 370; 10.3389/fmicb.
516 2015.00370 (2015).
517 40. Shi, B.et al. Changes and driving factors of microbial community composition and functional
518 groups during the decomposition of Pinus massoniana deadwood. *Ecol Evol*. 14(4); 10.1002/
519 ece3.11210 (2024).
520 41. Sparks D L (Ed.). Methods of Soil Analysis, Part 3. ASA and SSSA (2015).
521 42. Magoč, T., Salzberg, S. L. FLASH: fast length adjustment of short reads to improve genome
522 assemblies. *Bioinformatics*. 2011 Nov 27(21):2957-2963; 10.1093/bioinformatics/btr507
523 (2011).
524 43. Uteulin, K., Suleimenov, B.& Pachikin, K. The Soils of Natural Coenopopulations of Taraxacum
525 kok-saghyz L.E. Rodin in Kazakhstan. *Agronomy.* 13, 2737; 10.3390/agronomy13112737(2023).
526 44. Wahab, A. et al. Plant growth-promoting rhizobacteria biochemical pathways and their
527 environmental impact: a review of sustainable farming practices. *Plant Growth Regul*. 104, 637–
528 662; 10.1007/s10725-024-01218-x (2024).
529 45. Wang, Y.et al. Effects of microbial communities during the cultivation of three salt-tolerant plants
530 in saline-alkali land improvement. *Front. Microbiol.* 15:1470081; 10.3389/fmicb.2024.14700
531 81(2024).
532 46. Wang, Y. et al. Rhizosphere microorganisms mediate ion homeostasis in cucumber seedlings: a
533 new strategy to improve plant salt tolerance. *BMC Plant Biol.* 25(1); 10.1186/s12870-
534 025-06699-0 (2025)
535 47. Wang, Q., Garrity, G., Tiedje, J. & Cole, J. R. Naive bayesian classifier for rapid assignment
536 of RNA sequences into the new bacterial taxonomy. *Appl Environ Microb*, 2007, 73;
537 10.1128/AEM.00062-07 (2007).
538 48. Xu, D. et al. Diversity of nitrogen-fixing bacteria in suaeda salsa rhizosphere during reproduction

539 in the yellow river delta. *IScience*. 27(12):111267; 10.1016/j.isci.2024.111267(2024).
540 49. Yang, C. et al. Soil Salinity Drives the Distribution Patterns and Ecological Functions of Fungi in
541 Saline-Alkali Land in the Yellow River Delta, China. *Front. Microbiol*. 11, 594284;
542 10.3389/fmicb.2020.594284(2020).
543 50. Zhang, G. et al. Microbial diversity and functions in saline soils: a review from a biogeochemical
544 perspective. *J. Adv. Res*. 59, 129-140; 10.1016/j.jare.2023.06.015 (2024).
545 51. Zhang, J. et al. Distribution and Potential Metabolic Functions of Soil Actinobacteria in Degraded
546 Alpine Grassland on the Northern Tibetan Plateau. *Microorganisms.* 13(10), 2230;
547 10.3390/microorganisms13102230 (2025).
548 52. Zhang, S et al. Salt-tolerant and plant-growthpromoting bacteria isolated from high-yield paddy
549 soil. *Can. J. Microbiol*. 64:968–78;10.1139/cjm-2017-0571 (2018).
550 53. Zhang, X.Y. et al. Dominant plant species and soil properties drive differential responses of fungal
551 communities and functions in the soils and roots during secondary forest succession in the
552 subalpine region.Rhizosphere, 21:100483;10.1016/j.rhisph.2022.100483 (2022).
553 **Chinese standards:**
554 54. HJ 717–2014. Soil quality—Determination of total nitrogen—Kjeldahl method. Ministry of
555 Ecology and Environment of China.
556 55. HJ 615–2011. Soil—Determination of organic carbon—Potassium dichromate oxidation method.
557 56. NY/T 1121.4–2006. Soil testing—Part 4: Determination of exchangeable calcium and magnesium.
558 Ministry of Agriculture of China.
559 57. NY/T 1121.6–2006. Soil testing—Part 6: Determination of carbonate and bicarbonate.
560 58. NY/T 1121.7–2014. Soil testing—Part 7: Determination of available phosphorus.
561 59. NY/T 889–2004. Soil testing—Determination of available potassium.

Fig1.The map of sampling site for collecting rhizosphere soil of *Taraxacum kok-saghyz* Rodin.

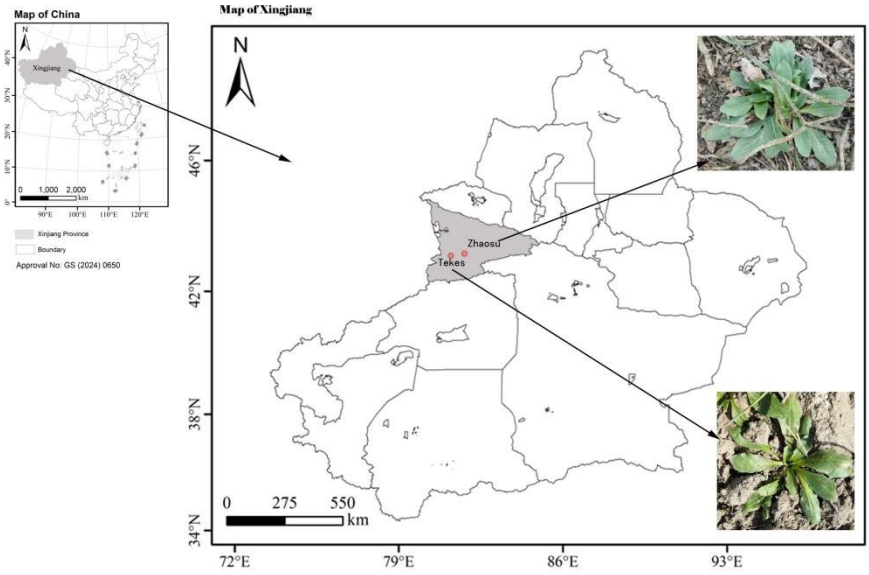


Fig2. Principal co-ordinates analysis (PCoA) plot depicting the Bray-Curtis distance of bacterial (A) and fungal (B) communities.TK and ZSrepresented the rhizosphere soil of Tekec and Zhaosu, numbers represented the different sample area.

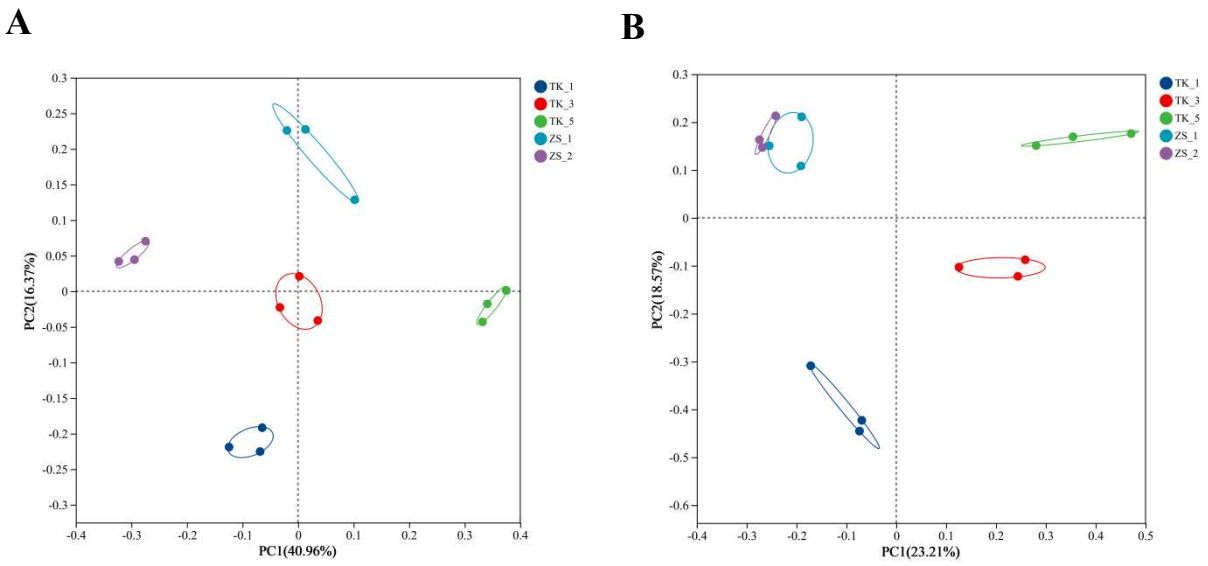


Fig3.The relative abundances of bacteria at the phylum level (A) and the genus level (B). TK and ZSrepresented the rhizosphere soil of Tekec and Zhaosu, numbers represented the different sample area.

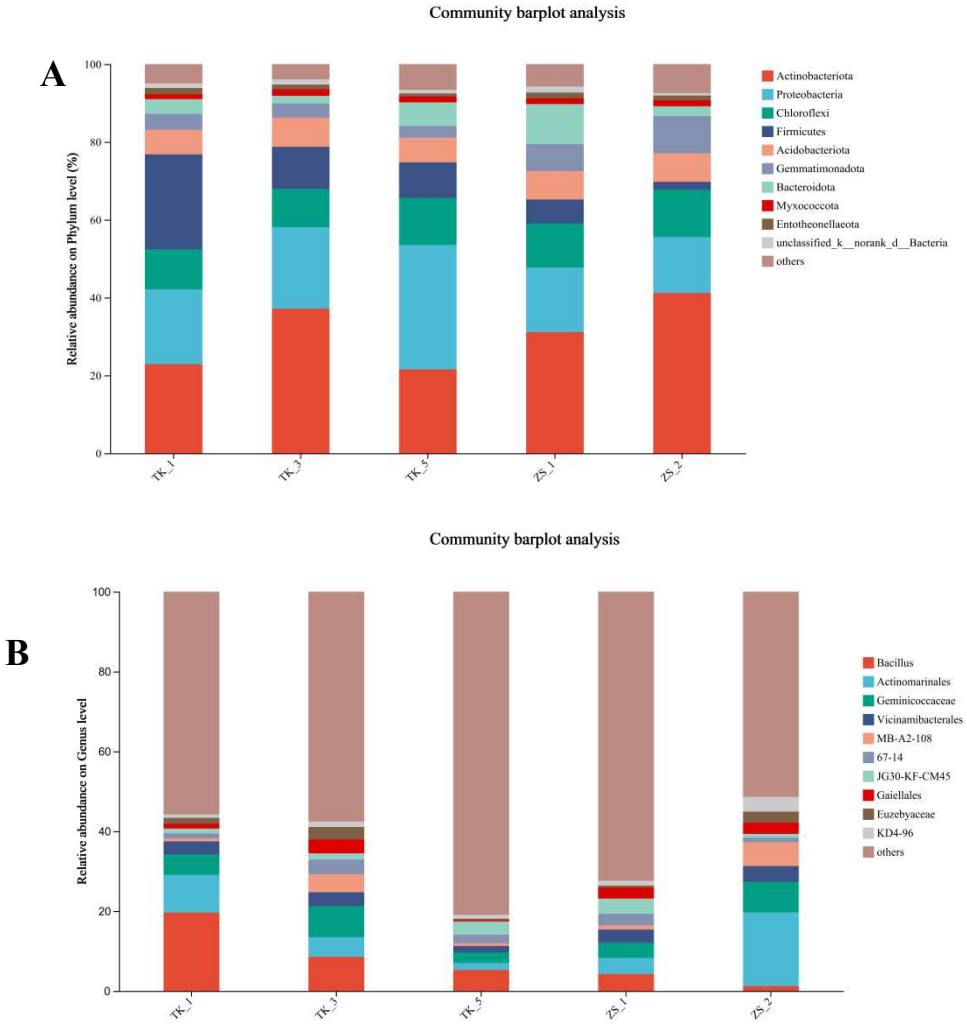


Fig4. The relative abundances of fungal community at the phylum level (A) and the genus level (B) . TK and ZSrepresented the rhizosphere soil of Tekec and Zhaosu, numbers represented the different sample area.

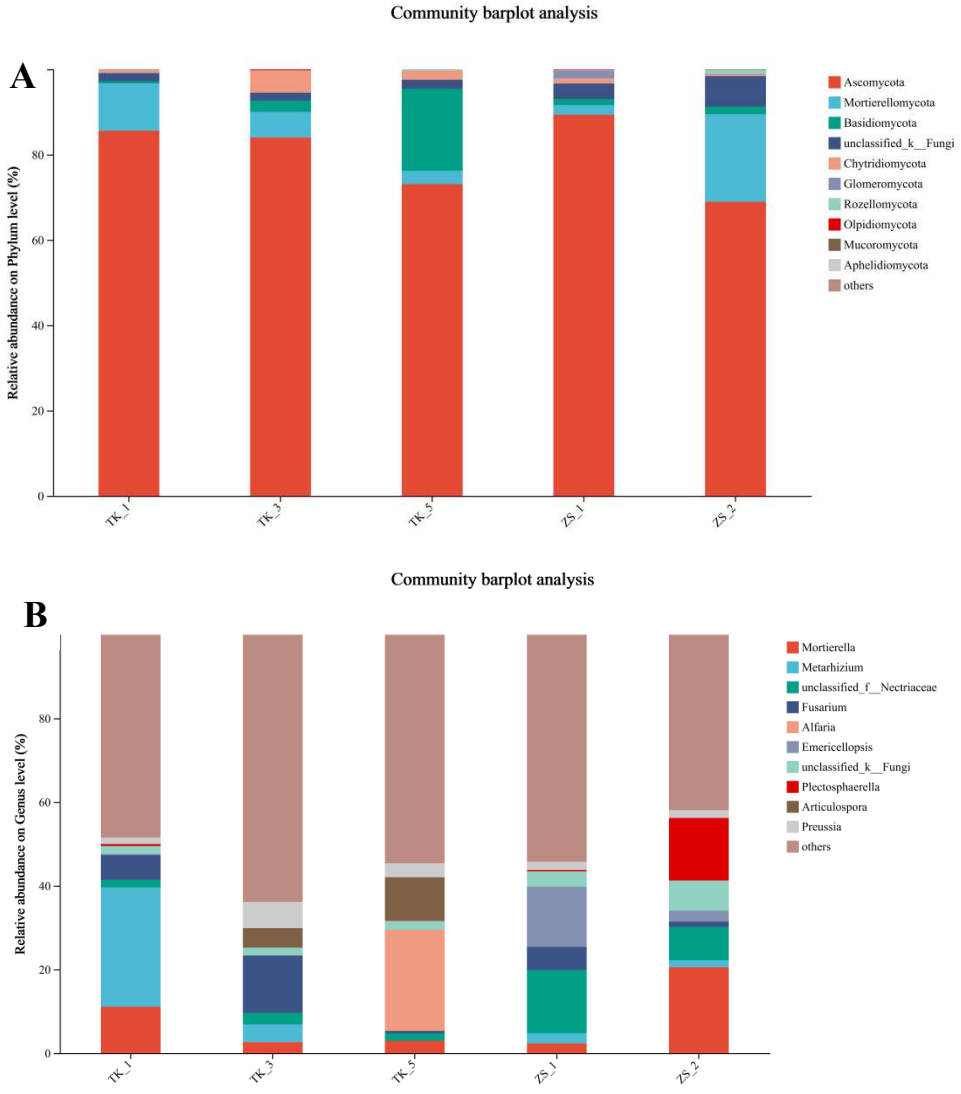
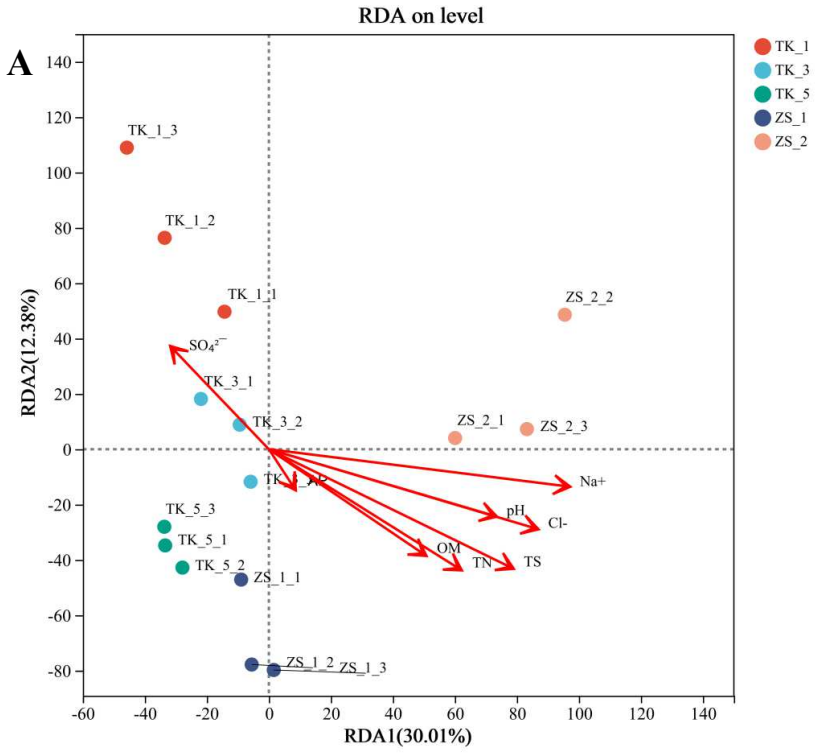


Fig5. RDA analysis(A) and of Spearman correlation heatmap (B) between the bacterial genera and environmental factors. TK and ZSrepresented the rhizosphere soil of Tekec and Zhaosu, numbers represented the different sample area.



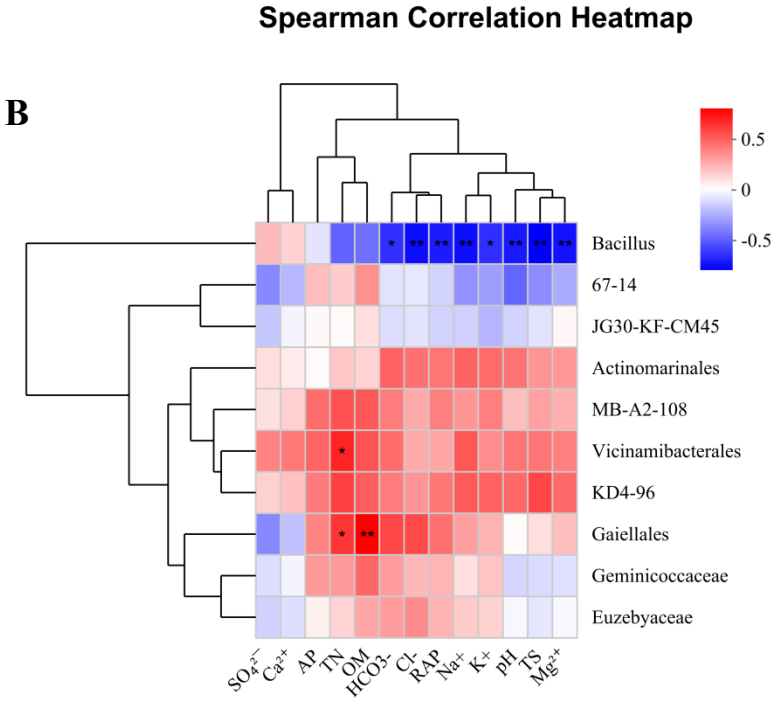
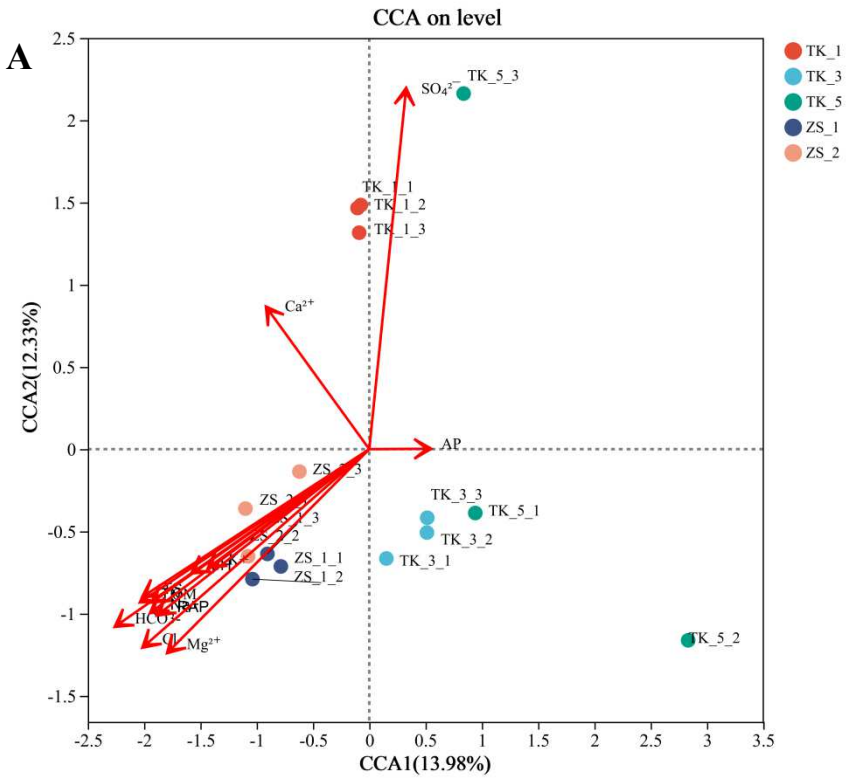


Fig6. RDA analysis (A) and of Spearman correlation heatmap (B) between the fungal genera and environmental factors. TK and ZSrepresented the rhizosphere soil of Tekec and Zhaosu, numbers represented the different sample area.


A
CCA on level
TK_1
TK_3
TK_5
ZS_1
ZS_2
TK_5_3
SO4 2−
TK_1_1
TK_1_2
TK_1_3
Ca2+
AP
TK_3_3
TK_5_1
TK_3_2
TK_3_1
ZS_1_1
ZS_1_2
HCO3−
Cl
Mg2+
TK_5_2
CCA2(12.33%)
CCA1(13.98%)

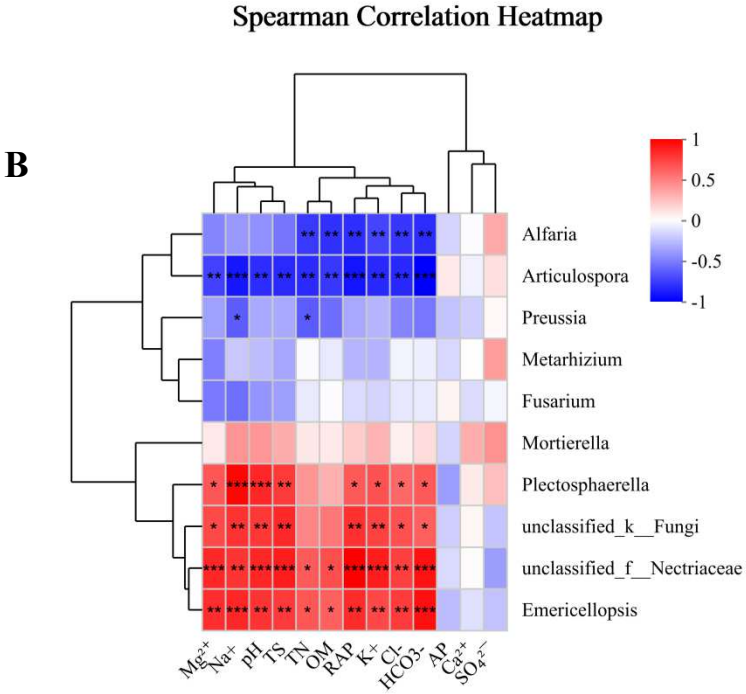

B
Spearman Correlation Heatmap
Alfaria
Articulospora
Preussia
Metarhizium
Fusarium
Mortierella
Plectosphaerella
unclassified_k__Fungi
unclassified_f__Nectriaceae
Emericellopsis
Mg2+
Na+
pH
TS
TN
OM
RAP
K+
Cl-
HCO3-
AP
Ca2+
SO4 2−
1
0.5
0
-0.5
-1

Table 1 .Statistic amplitor sequenc and alpha diversity analysis of the bacteria and fungal community

	Sample name	OTUs amount	Seq amount	ACE index	Chao index	shannon index	simpson index	sobs index	coverage
Bacteria	TK_1	2583.00	44638.00	3152.52±269.44ab	2985.20±243.07ab	5.67±0.35bc	0.03±0.02a	2573±247.05ab	0.98
	TK_3	2489.67	44638.00	2956.07±114.51b	2820.18±98.78b	6.00±0.13ab	0.009±0.002bc	2493.33±73.92c	0.99
	TK_5	2839.00	44638.00	3348.17±151.28a	3244.57±105.09a	6.42±0.07a	0.006±0.0006c	2828.67±124.31a	0.99
	ZS_1	2551.00	44638.00	2973.98±123.67b	2835.31±61.61b	6.19±0.07a	0.0064±0.0004c	2546±104.48ab	0.99
	ZS_2	2382.00	44638.00	2966.57±175.67b	2815.73±178.36b	5.39±0.40c	0.024±0.01ab	2360.33±143.77c	0.98
fungal	TK_1	325	76389	334.45±19.47a	334.66±20.32a	3.12±0.18a	0.13±0.04a	325±14.73a	1.00
	TK_3	272	76389	275.97±16.34ab	276.206±16.22ab	3.55±0.50a	0.08±0.07a	272±16.52ab	1.00
	TK_5	273.67	76389	277.13±88.63ab	280.07±86.94ab	3.01±1.25a	0.21±0.25a	273.67±90.74ab	1.00
	ZS_1	222	76389	227.4±10.01bc	226.25±10.58bc	3.28±0.21a	0.096±0.02a	222±12.29bc	1.00
	ZS_2	167.33	76389	168.34±15.65c	168.06±15.89c	3.11±0.31a	0.14±0.06a	167.33±15.95c	1.00

Table 2 .Envfit function test of environmental factors for the bacterial community

Parameter	RDA1	RDA2	r2	P_value
TN	0.98462	-0.1747	0.46976	0.021
OM	0.98889	-0.14867	0.40458	0.039
AP	-0.46137	-0.88721	0.07118	0.632
RAP	0.99306	-0.11763	0.52278	0.023
pH	0.99465	-0.10333	0.40118	0.06
TS	0.9753	-0.22089	0.48869	0.02
K+	0.9929	-0.11895	0.33135	0.084
Na+	0.99977	0.02164	0.65918	0.008
Cl-	0.99658	-0.08262	0.5268	0.014
HCO3-	0.99301	-0.11805	0.47155	0.02
Ca^{2+}	0.96003	0.27989	0.01839	0.897
Mg^{2+}	0.97325	-0.22976	0.48465	0.029
SO_4^{2-}	-0.40487	0.91437	0.22428	0.204

Table 3 .Envfit function test of environmental factors for the fungal community

parameter	CCA1	CCA2	r2	P_value
TN	-0.91329	-0.40731	0.57374	0.008
OM	-0.9045	-0.42648	0.52636	0.01
AP	0.99985	-0.01744	0.03032	0.829
RAP	-0.88431	-0.4669	0.52278	0.015
pH	-0.90602	-0.42323	0.34701	0.078
TS	-0.91733	-0.39813	0.55743	0.008
K+	-0.89648	-0.44309	0.28949	0.125
Na+	-0.89355	-0.44897	0.54655	0.017
Cl-	-0.86018	-0.50999	0.63212	0.007
HCO3-	-0.90599	-0.4233	0.72104	0.001
Ca^{2+}	-0.72156	0.69235	0.18554	0.286
Mg^{2+}	-0.82366	-0.56708	0.5443	0.011
SO_4^{2-}	0.12513	0.99214	0.58176	0.002

Supplementary Files

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- SupplementaryTable.docx