Variations of soil bacterial community structure and function under different habitats of Tamarix ramosissima Ledeb. in the upper reaches of the Tarim River, Northwest China: postprint

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Abstract

Diversity of soil microorganisms in different habitats of arid and semi-arid areas plays an important role in the soil texture and nutrient, promoting the growth of vegetation in those areas. To clarify the response of soil bacterial community diversity to the changes of environmental factors in different habitats, this study collected soil samples under the canopies of Tamarix ramosissima Ledeb. in oasis, transition zone, and desert habitats in the upper reaches of the Tarim River, Northwest China. High-throughput sequencing technology and PICRUSt2 software were used to explore the composition and function of soil bacterial communities in different habitats of T. ramosissima. The results showed that: (1) soil environmental factors under the canopy of T. ramosissima in the three habitats differed significantly, with soil moisture and nutrient conditions being better in the oasis; (2) Proteobacteria, Bacteroidetes, Firmicutes, Actinobacteria, and Gemmatimonadetes were the major bacterial communities in the three habitats; (3) soil bacterial community composition under the canopy of T. ramosissima varied greatly, and the richness was significantly different among the three habitats; (4) redundancy analysis indicated that soil water content and available phosphorous were the most important environmental factors influencing the composition of soil bacterial community; and (5) 6 primary functions and 21 secondary functions were obtained by PICRUSt2 function prediction, with metabolism being the most dominant function. This study revealed the response of soil bacterial community composition to habitat changes and their driving factors in the upper reaches of the Tarim River, which could improve the understanding of ecological sensitivity of soil microorganisms in arid and semi-arid areas, and provide a theoretical foundation for improving soil quality and ecological protection.

Full Text

Preamble

Variations of Soil Bacterial Community Structure and Function Under Different Habitats of *Tamarix ramosissima* Ledeb. in the Upper Reaches of the Tarim River, Northwest China

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Abstract: Diversity of soil microorganisms in different habitats of arid and semi-arid areas plays an important role in soil texture and nutrient dynamics, promoting vegetation growth in these regions. To clarify the response of soil bacterial community diversity to environmental changes across different habitats, this study collected soil samples from beneath *Tamarix ramosissima* Ledeb. canopies in oasis, transition zone, and desert habitats in the upper reaches of the Tarim River, Northwest China. High-throughput sequencing technology and PICRUSt2 software were used to explore the composition and function of soil bacterial communities in these different habitats. The results showed that: (1) soil environmental factors under *T. ramosissima* canopies differed significantly among the three habitats, with better soil moisture and nutrient conditions in the oasis; (2) Proteobacteria, Bacteroidetes, Firmicutes, Actinobacteria, and Gemmatimonadetes were the dominant bacterial communities across all three habitats; (3) soil bacterial community composition under *T. ramosissima* canopies varied considerably, with significant differences in richness among habitats; (4) redundancy analysis indicated that soil water content and available phosphorus were the most important environmental factors influencing soil bacterial community composition; and (5) PICRUSt2 functional prediction revealed six primary functional categories and 21 secondary functions, with metabolism being the most dominant. This study revealed the response of soil bacterial community composition to habitat changes and their driving factors in the upper reaches of the Tarim River, which could improve understanding of the ecological sensitivity of soil microorganisms in arid and semi-arid areas and provide a theoretical foundation for improving soil quality and ecological protection.

Keywords: high-throughput sequencing; soil bacterial community; environmental factors; function prediction; soil nutrients

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1 Introduction

Soil microorganisms serve as a crucial link between above-ground and below-ground ecosystems, playing a dominant role in soil nutrient cycling, ecosystem stability, disturbance resistance, and sustainable resource utilization. They are key factors in maintaining soil health and quality (Zhao et al., 2020). Soil bacteria are the most numerous and diverse microorganisms in soil ecosystems, performing essential ecological functions such as decomposition, mineralization, and promotion of soil material cycling and energy flow (Guo et al., 2020). Their activity and diversity reflect the stability of soil microbial communities and are closely related to stress responses and resource availability (Sun et al., 2020). Because soil bacterial communities are highly responsive to changes in soil environmental factors, they serve as key biological indicators reflecting changes in soil environmental quality and health (Chen et al., 2019).

There exists a complex network of relationships among above-ground vegetation, soil environmental factors, and soil microorganisms. Soil microbial communities are significantly affected by soil chemical properties, especially soil pH, carbon, and nitrogen contents (Wang et al., 2022). Additionally, they are closely related to many other environmental factors such as soil moisture and temperature, nutrients, vegetation types, and may also be influenced by exogenous substances. Studies have shown that soil pH can directly or indirectly affect bacterial diversity through various mechanisms, including altering bacterial nutrient utilization, physiological and metabolic activity, and establishing new inter-population competition relationships (Zhang et al., 2017). Soil temperature changes affect the evaporation and movement of soil water, which in turn influences soil microorganisms' access to water and nutrients (Frindte et al., 2019). Within a certain range, increased soil water content can enhance soil microbial quantity and respiration intensity, while excessive moisture can reduce soil permeability, resulting in decreased richness and biomass of soil microorganisms (Yang et al., 2016). Most studies have demonstrated significantly positive correlations between soil properties and soil microorganisms, particularly for soil organic carbon, total nitrogen, and organic matter (Rousk et al., 2010; Liu et al., 2018). Plants influence soil microorganisms primarily by altering soil physical and chemical properties through root secretions and litter differences, thereby regulating the composition and structure of soil microbial communities and playing an important role in the functional composition of soil bacteria (Landesman et al., 2014). Meanwhile, soil microorganisms can indirectly affect plant community growth and succession by promoting nitrogen fixation and the dissolution of insoluble phosphorus and potassium (Hu et al., 2020).

Soil environmental conditions are heterogeneous across different landscapes. Oasis and desert represent special geographical landscapes in arid areas. Oases are ecosystems dominated by vegetation with primary productivity significantly higher than the surrounding environment, depending on external mountain surface and groundwater (Wang, 2000). Deserts are characterized by low annual precipitation, insufficient soil moisture, sparse vegetation, extensive bare land, and low ecosystem biological productivity. The desert-oasis transition zone lies between desert and oasis, representing an ecological zone where desert and oasis systems interact and transform (Zhao et al., 2016). The transition zone shares similar characteristics with desert habitats, including scarce precipitation, large evaporation, significant water shortage, serious wind erosion and deposition on the surface, and easy formation of biological soil crusts (Zhou et al., 2021). The transition zone also retains some oasis-like characteristics, maintaining a certain degree of fertility that allows drought-, salt-, and wind erosion-resistant desert vegetation to grow and develop normally (Ma et al., 2023). The formation of the desert-oasis transition zone results from gradient changes in water and heat environmental factors from oasis to external desert, leading to transitional characteristics in the comprehensive landscape, including vegetation, soil, and landform (Mu et al., 2013). In summary, oasis, transition zone, and desert have significantly different environmental conditions, which may lead to different characteristics of soil bacterial communities.

The Taklimakan Desert is an ecologically fragile area in Northwest China with a warm temperate continental climate characterized by scarce precipitation, strong evaporation, and large diurnal and seasonal temperature differences. This area is dominated by desert plants such as *Tamarix ramosissima* Ledeb., *Nitraria tangutorum* Bobrov, *Alhagi camelorum* Fisch., *Phragmites communis* Trin., and *Karelinia caspica* (Pall.) Less. Desert vegetation is a critical element in maintaining the stability of deserts, oases, and transition zones. *T. ramosissima*, with its tolerance to drought, salt, and barren conditions, is an excellent species for windbreak and sand fixation in arid areas, playing an important role in curbing ecological degradation and maintaining oasis ecosystem stability (Zheng et al., 2010; Xiao et al., 2021). Therefore, this study used soils beneath *T. ramosissima* canopies in desert, oasis, and transition zone habitats in the upper reaches of the Tarim River as research material, employing high-throughput sequencing technology to reveal soil bacterial community structure and function across different habitats, aiming to provide a scientific basis for sustainable development of soil ecological function in the upper reaches of the Tarim River. The study addresses the following scientific questions: (1) whether there are differences in soil bacterial community characteristics, diversity, and functional genes beneath *T. ramosissima* canopies in different habitats; and (2) what are the main environmental factors determining the soil bacterial community beneath *T. ramosissima* canopies in different habitats?

Materials and Methods

2.1 Study Area

The study area is located in the desert-oasis transition zone of the Tarim River, Northwest China (39°30 -41°15 N, 79°40 -81°53 E; 1012 m a.s.l.). Precipitation is less than 50 mm, while evaporation can reach as high as 2550 mm. The annual mean temperature is 11°C, average annual sunshine duration is about 2814 h, and the frost-free period is about 190–220 d. Soil types include mainly sandy, brownish desert, and saline soils (Meng et al., 2019).

2.2 Sample Collection and Processing

According to the distribution of naturally growing *T. ramosissima* in different habitats (oasis, transition zone, and desert; Fig. 1 [Figure 1: see original paper]), we established three quadrats of 20 m$\times$20 m under similar conditions in each habitat, totaling nine quadrats (Zhang et al., 2023). The characteristics of *T. ramosissima* populations in different habitats are shown in Table 1 . In each quadrat, we selected well-grown *T. ramosissima* samples with similar morphology, removed surface litter near plant roots, and harvested the 0–20 cm surface soil layer using a soil auger and sterile shovel sterilized with 75.00% alcohol. Approximately 10 g of collected soil samples were placed in sterile centrifuge tubes for microbial analysis and stored at -80°C for DNA extraction. Additionally, undisturbed soil samples were collected using ring knives for bulk density determination, and 0–20 cm soil was collected with sterile shovels. After removing plant roots, stones, and other impurities, a portion was placed in aluminum boxes for soil water content determination. The remaining soil samples were dried through a 2-mm sieve and placed in sterile sealed bags for physical and chemical property analysis.

2.3 Measurement of Soil Environmental Factors

Soil physical and chemical properties were measured according to Bao (2000). The pH was determined by potentiometric method using a 1:5 soil:water ratio suspension (PHS—3C, Shanghai Yidian Scientific Instrument Co., Ltd., Shanghai, China). Electrical conductivity (EC) was determined by conductivity method (DDS-307, Shanghai Yidian Scientific Instrument Co., Ltd., Shanghai, China). Soil water content (SWC) was determined by drying method. Soil bulk density (BD) was determined using the ring knife method. Soil organic carbon (SOC) was determined by potassium dichromate volumetric method with external heating. Available phosphorus (AP) was determined by sodium bicarbonate leaching. Available nitrogen (AN) was determined by alkaline diffusion method. Total nitrogen (TN) was determined by Kjeldahl method. Total phosphorus (TP) was determined by molybdenum-antimony colorimetric method. Soil microbial biomass was analyzed according to Wu et al. (2011). Microbial biomass nitrogen (MBN), microbial biomass phosphorus (MBP), and microbial biomass carbon (MBC) were determined by chloroform fumigation-extraction method.

2.4 Soil Bacterial DNA Extraction, Polymerase Chain Reaction (PCR) Amplification, and Gene Libraries

DNA from soil samples of different habitats was extracted using MO BIO’ s PowerSoil DNA Isolation Kit (MO BIO Laboratories, Inc., Carlsbad, USA). DNA concentration was measured using a microplate reader (Synergy HTX, Gene Company Ltd., Beijing, China), and DNA quality was assessed by 1.00% agarose gel electrophoresis. For bacterial communities, the full-length region of the bacterial 16S rDNA gene sequence was amplified using universal bacterial primers 27F (5 -AGRGTTTGATYNTGGCTCAG-3) and 1492R (5 -TASGGHTACCTTGTTASGACTT-3). PCR amplification was performed in a total reaction volume of 30.0 L, containing 10.5 L nuclease-free water, 15.0 L KOD OneTM PCR Master Mix (Toyobo Co., Ltd., Osaka, Japan), 3.0 L barcode primer pairs, and 1.5 L genomic DNA. PCR conditions were as follows: initial denaturation at 95°C for 2 min, 25 cycles of denaturation at 98°C for 10 s, annealing at 55°C for 30 s, extension at 72°C for 90 s, and final extension at 72°C for 2 min. PCR products were purified and quantified, homogenized to obtain the sequencing library, and tagged gene sequences were determined by PacBio Single Molecule Real-Time Sequencing technology (Biomarker Technology Co., Ltd., Beijing, China).

2.5 Processing of Sequencing Data

Raw amplicons were corrected using SMRT-Link v.8.0 software to obtain circular consensus sequencing (CCS) sequences. Lima v1.7.0 software was used to identify CCS sequences from different samples by barcode sequences, and UCHIME v.4.2 software was used to remove chimeras and obtain high-quality CCS sequences. The obtained high-quality sequences were clustered at a 97.00% similarity level using USEARCH v.10.0 software to obtain operational taxonomic units (OTUs). OTUs were taxonomically identified and annotated using the bacterial SILVA (high-quality ribosomal RNA databases) as a reference database, and community composition of each sample at different levels (phylum, class, order, family, genus, and species) was calculated. Sample alpha diversity indices including Chao1 index, Abundance-based Coverage Estimator (ACE) index, Shannon index, and Simpson index were calculated by QIIME v.2.0 software. All sequencing raw data were deposited in the Sequence Read Archive (SRA) of NCBI (National Centre for Biotechnology Information) database with the BioProject ID PRJNA1123075.

2.6 Statistical Analysis

SPSS v.26.0 software (IBM, Chicago, USA) was used to process and analyze soil environmental factor and microbial data. One-way analysis of variance (ANOVA) and least significant difference (LSD) tests were used to analyze differences among habitats ($P<0.05$). Statistical results are presented as mean±standard error. Data processing, statistical analysis, and figure preparation were completed using Excel v.2022, Canoco v.5.0 (CanocoLab, Microsoft, Redmond, Washington DC, USA), and Origin v.2023 (OriginLab, Northampton, USA). Effect size was analyzed by LEfSe (linear discriminant analysis effect size) with LDA score >4 to identify significant differences in biomarkers between groups. Principal coordinate analysis (PCoA) was applied to analyze beta diversity based on Binary-Jaccard distance. Correlations between soil microorganisms and environmental factors were analyzed using the Biomarker Microbial Diversity Analysis Platform (www.biocloud.net). A correlation matrix was constructed to show differences in microbial community structure between groups. Relative abundance of functional genes was obtained by comparing Kyoto Encyclopedia of Genes and Genomes (KEGG) database information with Phylogenetic Investigation of Communities by Reconstruction of Unobserved States (PICRUSt2) software.

Results

3.1 Soil Environmental Factors

Soil environmental factors beneath *T. ramosissima* canopies in different habitats were analyzed by one-way ANOVA. Results showed that SOC, TN, AN, and MBP contents in the oasis were significantly higher than those in the transition zone and desert ($P<0.05$; Table 2). TP and AP contents in the transition zone were significantly lower than those in the oasis ($P<0.05$; Table 2). However, there were no significant differences in soil BD, pH, MBN, or MBC among the three habitats ($P>0.05$; Table 2).

3.2 Soil Bacterial Community Composition

By classifying and annotating the high-throughput sequencing results, we obtained 29 bacterial phyla. For convenience of observation, only the 10 phyla with highest relative abundance were displayed, with remaining species merged as "others" (Fig. 2 [Figure 2: see original paper]). The relative abundance of dominant phyla ranged as follows: Proteobacteria (21.00%-61.00%), Bacteroidetes (16.00%-69.00%), Gemmatimonadetes (0.00%-7.00%), Firmicutes (0.00%-5.00%), Actinobacteria (0.00%-6.00%), Verrucomicrobia (0.00%-4.00%), Deinococcus-Thermus (0.00%-2.00%), Acidobacteria (0.00%-2.00%), Patescibacteria (0.00%-11.00%), and Planctomycetes (1.00%-10.00%). Proteobacteria and Bacteroidetes were the dominant phyla in each habitat.

The LEfSe evolutionary branching diagram revealed 24 bacterial taxa with significant differences among the three habitats, including 8 in the transition zone, 6 in the oasis, and 10 in the desert (Fig. 3 [Figure 3: see original paper]). The number of differential species was higher in the desert than in the oasis, with the number of potential biomarker species increasing as water availability decreased. Bacteroidetes, Sphingomonadaceae, Hymenobacteraceae, Sphingomonadales, Tunicatimonas, and Pontibacter were significantly differentiated bacteria in the oasis. Differential bacterial communities in the transition zone included Acidimicrobiia, Oceanospirillales, Actinomarinales, and uncultured_{bacterium}o_{Actinomarinales}. Differential indicator bacteria in the desert included Alifodinibius, Halofilum, Balneolaceae, Saccharospirillaceae, Balneolales, Ectothiorhodospirales, and Rhodovibrionales. All these bacteria play important roles in structuring community composition differences between soils of different habitats.

3.3 Soil Bacterial Diversity

As shown in Figure 4 [Figure 4: see original paper], ACE and Chao1 indices differed significantly among the three habitats ($P<0.05$). ACE and Chao1 indices of soil bacteria in the oasis were significantly higher than those in the desert ($P<0.01$). The ACE index in the oasis was also significantly higher than in the transition zone ($P<0.05$), though Simpson and Shannon indices showed no significant differences among habitats ($P>0.05$).

Based on the Binary-Jaccard distance algorithm, PCoA was used to analyze soil bacterial community composition beneath *T. ramosissima* canopies in the three habitats (Fig. 5 [Figure 5: see original paper]). The contribution rates of PC1 and PC2 were 43.46% and 19.79%, respectively. Sampling points from the same habitat aggregated together, while those from different habitats were scattered, indicating that soil bacterial community structure and composition were similar within habitats but differed among habitats.

3.4 Relationships Between Dominant Soil Bacteria and Environmental Factors

Relationships between the top 10 bacterial phyla and soil environmental factors are shown in Figure 6 [Figure 6: see original paper]. The first and second ordination axes contributed 56.75% and 17.57%, respectively, with a cumulative contribution rate of 74.32%, effectively explaining the relationship between bacterial community and environmental factors. Results showed that SWC and AP were the most critical environmental factors affecting soil bacterial community structure. SWC was positively correlated with TN, AN, MBP, SOC, and pH, while AP was negatively correlated with EC and SWC. Effects of soil environmental factors varied according to bacterial taxa. Planctomycetes and Acidobacteria were positively correlated with SWC. Bacteroidetes and Deinococcus-Thermus were positively correlated with AP but negatively correlated with SOC, TN, and AN. Gemmatimonadetes and Acidobacteria were positively correlated with SWC and EC but negatively correlated with AP, pH, and SOC.

Monte Carlo permutation test assessed the contribution of all environmental factors to soil bacterial community composition, selecting five soil indicators: SWC, AP, AN, EC, and TP. Based on correlation analysis between environmental factors and microbial taxa, we constructed a correlation network diagram (Fig. 7 [Figure 7: see original paper]). The correlation network complexity between soil microbial species and environmental factors was highest in the oasis, where most bacterial genera were positively correlated with environmental factors, and AP and AN positively promoted all bacterial genera. No significant difference was observed between positive and negative correlations in the transition zone, where SWC and TP had more significant effects on bacterial genera. Most bacterial genera in the desert were negatively correlated with SWC. Across all three habitats, Proteobacteria showed significant responses to environmental factors, followed by Bacteroidetes.

3.5 Prediction of Soil Bacterial Function

Based on characteristic sequences of the 16S rDNA marker gene, PICRUSt2 software was used to predict functions of soil bacterial OTUs beneath *T. ramosissima* canopies in different habitats. Six primary metabolic functional categories were obtained, with relative abundances greater than 1.00% including metabolism, genetic information processing, environmental information processing, cellular processes, human diseases, and organismal systems (Table 3). Except for genetic information processing and human diseases, relative abundances of other functional genes differed significantly among habitats. The relative abundance of metabolism and organismal systems functional genes in the oasis was significantly higher than in the other two habitats ($P<0.05$), while environmental information processing and cellular processes functional genes were significantly lower ($P<0.05$).

Based on secondary KEGG database functions, 21 sub-functional layers were predicted from the six primary functional layers of soil bacteria, with 18 sub-functional layers showing relative abundance above 0.10% (Fig. 8 [Figure 8: see original paper]). Global and overview maps functional genes dominated with a relative abundance of 42.78%. Functional genes differed among habitats at the sub-functional level. Membrane transport functional gene abundance in the transition zone was significantly higher than in the other two habitats ($P<0.05$). In the desert, relative abundances of amino acid metabolism, nucleotide metabolism, and other amino acid metabolism functional genes were significantly higher, while metabolism and membrane transport, and metabolism of cofactors and vitamins were significantly lower than in other habitats ($P<0.05$).

Discussion

4.1 Soil Bacterial Community Composition

Diversity and richness of soil bacteria beneath *T. ramosissima* canopies varied among habitats. Chao1 and ACE indices of soil bacterial communities in the desert were extremely significantly lower than those in the oasis ($P<0.01$), indicating that soil bacteria were highly sensitive to micro-environmental changes (Ma et al., 2020). The oasis provided adequate soil nutrients and better moisture conditions, offering a more suitable living environment for soil bacteria and influencing their growth and reproduction, thus increasing bacterial community richness. However, Shannon and Simpson indices showed no significant differences among the three habitats ($P>0.05$), possibly because soil pH did not differ significantly among habitats. Previous studies have shown that soil pH is the main factor determining soil bacterial diversity and composition (Bahram et al., 2018; Liu et al., 2020). Beta diversity analyses showed that species diversity of soil bacterial communities varied more between different habitats than within the same habitat, further indicating that richness and relative proportions of soil microbial communities changed significantly across habitats, though dominant species remained similar.

In this study, sequencing technology detected a total of 28 phyla, 71 classes, 153 orders, 237 families, and 397 genera. The dominant soil bacterial phyla beneath *T. ramosissima* canopies across different habitats were Proteobacteria, Bacteroidetes, and Firmicutes, consistent with previous research in desert ecosystems (Bahadur et al., 2021). Proteobacteria is widely distributed, and its strong nitrogen-fixing capacity combined with variable morphological and physiological properties provides great competitive advantages in ecological niches (Stevenson and Hallsworth, 2014). This result was supported by RDA analysis, which showed a significant positive correlation between soil TN and Proteobacteria abundance. Proteobacteria and Firmicutes reproduce via spores, possess complete ultraviolet repair mechanisms, and have strong secondary anabolism capabilities, adapting to intense light and dry climate conditions (Ren et al., 2018). No significant difference was observed in phylum composition of soil bacterial communities beneath *T. ramosissima* canopies across habitats in the upper reaches of the Tarim River, though community abundance percentages differed. This could be attributed to discrepancies in soil nutrients among the three habitats, leading to differences in microbial communities and abundances. The relative abundances of Bacteroidetes and Firmicutes in the desert were significantly higher than in the other two habitats. Bacteroidetes and Firmicutes participate in promoting organic matter decomposition and carbon cycling processes (Larsbrink and McKee, 2020; Gavande et al., 2021). Bacteroidetes are main members of polysaccharide degradation pathways, capable of converting complex polysaccharides into utilizable compounds and efficiently utilizing polysaccharide compounds secreted by plant roots, thereby gaining greater competitiveness in drought and low-fertility environments (Gavande et al., 2021). Members of Firmicutes participate in biogeochemical cycles such as nitrogen utilization and stress response in desert soils (Lester et al., 2007; Goswami et al., 2014). Gemmatimonadetes are adapted to grow in soils with low water content and difficulty surviving in acidic soils. Salt-tolerant or halophilic characteristics make them suitable for growth and reproduction in high-salt-content soils (Chen et al., 2022). These soil microorganisms distributed in arid and semi-arid deserts constantly adapt to the arid environment through natural selection under long-term stress, which is also an effective guarantee for normal soil ecosystem function.

4.2 Influence of Environmental Factors on Soil Bacteria

Numerous studies have shown that abundance and community composition of soil microorganisms are closely related to soil physical-chemical properties such as pH, water content, and organic matter content (Cheng et al., 2020; Cui et al., 2020). In this study, RDA analysis revealed that SWC and AP were the most important soil environmental factors causing differences in soil bacterial community composition beneath *T. ramosissima* canopies across habitats, while pH was not the most important influencing factor, inconsistent with conclusions from other studies (Zhao et al., 2019). This may be because the sampling site is located in the oasis-desert transition zone where soil pH ranges from 8.24 to 8.74 (alkaline), with slight overall pH changes that obscure its influence. SWC is key to maintaining normal microbial metabolism, and its changes affect nutrient status, thereby influencing soil microbial community diversity (Wang et al., 2018). In this study, SWC in the oasis was significantly higher than in the transition zone and desert, indirectly confirming that both oasis soil bacterial diversity and abundance were significantly higher. Previous studies have found that microbial biomass and diversity increased with soil moisture content, and diversity of soil bacterial and fungal communities in arid and semi-arid areas showed significantly positive correlation with soil moisture content when SWC ranged from 0.00%–15.00% (Taniguchi et al., 2012). Soil phosphorus content was positively correlated with microbial biomass, and microbial death could significantly increase soil available phosphorus content (Jiang et al., 2021). In the desert, available phosphorus content was significantly higher than in the oasis and transition zone. This may result from high desert temperatures causing death of large numbers of temperature-intolerant strains and creating differences in microbial community structure (Zhang et al., 2021). Meanwhile, phosphorus is easily converted to calcium phosphate and fixed by soil under high saline conditions, damaging the microenvironment for microbial survival and leading to further changes in microbial community structure.

4.3 Prediction of Soil Bacterial Functions

Vegetation impacts on soil bacterial community structure further influence bacterial functional composition (Jin et al., 2019; Liang et al., 2020). Three functional categories in the primary functional layer—metabolism, genetic information processing, and environmental information processing—showed high abundance and play important roles in plant growth. Particularly, the relative abundance of metabolic functional genes in the oasis accounted for more than 80.00%, representing the core bacterial function. Previous studies have found that soil bacteria participate in soil material circulation and transformation through metabolic activities, thereby promoting plant growth and increasing crop yields. Nitrogen fixation and phosphorus solubilization functions increase root absorption of nitrogen and phosphorus nutrients through metabolism (Yang et al., 2020). In the secondary functional layer, the relative abundance of membrane transport functional genes in the transition zone was significantly higher than in the other two habitats. Studies have shown that membrane transport plays an important role in bacterial substance transport and active nutrient uptake (Zeng and Charkowski, 2021). Bacteria can selectively absorb plant-secreted metabolites by regulating membrane transport and establishing interactions with plants (Trivedi et al., 2020). These results indicate that soil bacterial communities in the transition zone have greater potential for plant interactions when membrane transport is the main function. The relative abundances of functional genes for amino acid metabolism, nucleotide metabolism, and other amino acid metabolism in the desert were significantly higher than in other habitats. This occurs because low nutrient content in desert soil accelerates decomposition of organic matter in the humus layer, while enhancing carbohydrate, amino acid, and nucleotide metabolism capabilities, resulting in increased metabolic genes and corresponding functional microorganisms in the desert. This is important for maintaining nutrient availability required for plant growth and reflects the adaptability of soil microorganisms to stressful and disturbed environments (Zhou et al., 2017). Activation of these functions enables soil bacteria to promote their own nutrient uptake and utilization in harsh desert environments. Prediction of soil bacterial function helps verify changes in soil bacterial community structure across habitats and clarifies the important influence of environmental factors on soil microbial community function.

5 Conclusions

This study investigated differences in diversity and function of soil bacterial communities beneath *T. ramosissima* canopies in oasis, desert-oasis transition zone, and desert habitats in the upper reaches of the Tarim River, Northwest China. We found differences in community abundance percentages across habitats. Alpha diversity indices of soil bacteria showed significant differences, with desert soils displaying the lowest diversity and richness indices. Environmental factors —SWC and available phosphorus content—acted as driving factors shaping soil bacterial community structure, diversity, and functional differences. Through functional prediction, we identified six primary functional categories and 21 secondary functions, with metabolic function being the most crucial. Changes in soil bacterial structure and function reflected variations in soil environmental conditions and indicated the adaptability of soil microorganisms to stressful and disturbed environments. These findings deepen understanding of the ecological sensitivity of soil microorganisms in arid and semi-arid areas and advance knowledge of bacterial ecology in desert environments.

Conflict of Interest: 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.

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Note: Figure translations are in progress. See original paper for figures.