International Journal of Biology and Life Sciences
ISSN: 2957-9511 | Vol. 11, No. 2, 2025

pH and Soil Water Content as Key Drivers of Soil Microbial Community Shifts in the Alpine Wetlands around Qinghai Lake

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Abstract: To understand the variation of soil microbial communities and their key Driving factors across different alpine wetlands in the Qinghai Lake basin, we investigated 11 alpine wetlands around Qinghai Lake, analyzing the composition and diversity of soil bacterial and fungal communities, as well as the soil properties, especially the soil pH and soil water content (SWC). The results showed that: (1) 43 bacterial OTUs (operational taxonomic units) and 3 fungal OTUs were shared among all 11 sites, Proteobacteria dominated the bacterial communities, while Ascomycota was the most dominant fungal phylum. (2) Significant differences ($p < 0.01$) were observed in alpha diversity indices (Chao1, Observed species, and Shannon) for both bacterial and fungal among the different wetlands. (3) Fungal Chao1 and Shannon indices exhibited highly significant negative correlations with pH ($P < 0.01$), as did bacterial Chao1 and Shannon indices. Our findings indicated that both pH and SWC exerted substantial influences on the diversity of bacterial and fungal communities, and highlights the influence of water recharge, lake level, and salinity on the composition and diversity of soil microbial communities in the alpine wetlands surrounding Qinghai Lake.

Keywords: Alpine Wetland; Qinghai Lake; Soil Microbial Communities.

1. Introduction

Wetland ecosystems constitute a distinct natural complex formed by land-water interactions. Characterized by intricate diversity, these ecosystems provide critical habitats for a majority of biological species [1]. alpine wetland represent a significant category of wetlands in China, uniquely defined by brackish interactions between freshwater and saltwater. They effectively mitigate the discharge of terrestrial pollutants into oceans while buffering against seawater intrusion into land areas [2]. As multifunctional and complex ecosystems, they possess exceptional ecological value and resource potential. Although wetlands cover merely 6% of the Earth's surface, their ecosystem service value per hectare surpasses all other ecosystem types [3]. The Qinghai Lake basin is situated in the northeastern Qinghai-Tibet Plateau. The wetland ecosystems within this basin serve as vital geographical units maintaining the ecological equilibrium of the Qinghai-Tibet Plateau region. This area exhibits a distinctive geographical setting and demonstrates heightened sensitivity to climate change [4]. Qinghai Lake's unique physiographic conditions have fostered rich wetland biodiversity. In recent years, however, this biodiversity faces escalating threats from climate change and anthropogenic activities, drawing significant concern regarding its ecological status.

Soil microorganisms constitute a fundamental component of both the structure and function within estuarine wetland ecosystems. They drive essential processes including energy flow, material cycling, ecosystem succession, and biodiversity maintenance – underpinning the normal functioning of the ecosystem – and serve as key indicators for characterizing wetland types [5]. Furthermore, as the most dynamic element of the soil biota, soil microorganisms participate in the decomposition of soil organic matter and the transformation of nutrients. Simultaneously acting as the primary drivers of nutrient element cycling and transformation, they propel the organic cycles of the entire wetland system [6-7].Analysis of microbial community composition and diversity represents a central research focus in wetland microbiology. This analysis pertains to the composition, abundance, and interrelationships of microorganisms within a defined region or habitat. These factors determine the characteristics and intensity of wetland ecological functions, making them crucial elements for realizing ecological functions and serving as markers for environmental change [8]. Investigating the distribution of soil microbial communities and their environmental drivers within the Qinghai Lake estuarine wetland ecosystem is essential for understanding the soil microbial diversity of Qinghai Lake wetlands. This understanding enables the interpretation of the current state of the Qinghai Lake wetland ecosystem, thereby providing a theoretical basis for its enhanced protection. Such research holds significant practical importance for the sustainable management of natural wetland systems and the achievement of coordinated ecological, economic, and social development.

Current research reports on soil microbial communities in Qinghai Lake's alpine wetland primarily focus on aspects such as soil microbial respiration, soil enzyme activities coupled with microbial characteristics, and microbial biomass distribution. However, studies specifically addressing the abundance characteristics of soil microorganisms and their influencing factors in these wetlands remain scarce. Deeper investigation in this area holds substantial reference value for tapping microbial resources, exploring wetland ecosystem structure and function, and informing conservation and restoration strategies. For instance: Bao Han [9] examined different wetland types within the Qinghai Lake basin (marsh, lakeshore, estuarine, and sediment wetlands), employing metagenomic sequencing to study soil enzyme activities and microbial community characteristics. The research identified soil physicochemical properties – primarily influenced collectively by soil water content, pH, total nitrogen, and other factors – as key determinants of microbial community structure. Wang Hengsheng et al. [10] investigated the abundance and distribution patterns of soil microbial groups in Xiaopo Lake wetland (Qinghai Lake basin). Their findings indicated that soil microorganisms are synthetically influenced by vegetation, soil physicochemical properties, and water content, with bacteria numerically dominating across different soil layers.

Therefore, this study targets the alpine wetland within the Qinghai Lake basin. By analyzing the abundance of soil microorganisms across distinct alpine wetland and investigating their spatial variations, we aim to establish a theoretical foundation for understanding the communities, abundance, and influencing factors of soil microorganisms in these wetlands, representative of the Qinghai Lake basin ecosystem.

2. Materials and Methods

2.1. Study Site

The Qinghai Lake basin is situated in the northeastern Qinghai-Tibet Plateau, entirely surrounded by mountains. It exhibits distinctive characteristics of an alpine semi-arid ecosystem. Geographically, it spans latitudes 36°17′N to 38°24′N and longitudes 97°56′E to 101°45′E, encompassing multiple cities and counties, primarily including Gangcha County, Gonghe County, and Haiyan County. The total drainage area is 29,661 km^2. Numerous rivers flow within the basin into Qinghai Lake, with catchment areas of approximately 14,000 km^2. The basin experiences a plateau semi-arid frigid climate, with an average elevation exceeding 3,000 meters above sea level. The mean annual temperature is 1.2°C, and the mean annual precipitation is 360 mm. Precipitation is concentrated primarily from May to September, accounting for over 70% of the total annual rainfall. Wetlands cover approximately 24% of the basin area. These mountains and grasslands form a crucial barrier impeding the eastward expansion of the western deserts. The basin serves as a critical stopover site for rare migratory birds and a vital breeding ground within China's plateau lake region. Furthermore, it provides essential habitat for endemic fish species and endangered animals unique to the Qinghai-Tibet Plateau.

2.2. Experimental Design and Data Collection

In this study, 11 alpine wetland around the Qinghai Lake were selected **Table 1**, at each sampling site, five randomly positioned 1m×1m quadrats were established, with a minimum separation distance of 10 m between adjacent quadrats. Within each harvested quadrat, soil samples were collected using the three-point sampling method with a 5-cm diameter soil auger. Samples were taken from two depth intervals: 0–10 cm and 10–20 cm. Three auger cores were collected per depth interval per quadrat. Soil cores from the same depth interval within a single quadrat were combined to form a homogenized composite sample. Each composite sample was immediately placed into a labeled zip-lock bag, sealed, and transported to the laboratory.

Table 1. Latitude, longitude, elevation, and administrative divisions of the alpine wetlands around the Qinghai Lake

Code	Longitude	Latitude	Elevation	Full name
BHH	99°73'88.48"	37°02'02.18"	3183m	Buha River
LJH	99°61'50.42"	36°96'76.20"	3145m	Laiji River
GRN	99°60'90.06"	36°94'21.47"	3150m	Garina River
ZHL	99°78'72.76"	36°79'83.48"	3154m	Zhehoulong River
ZQH	99°82'71.30"	36°71'46.81"	3206m	Zhengquhu River
ZGRT	100°00'33.30"	36°65'37.00"	3153m	Zhegeritang River
JCG	100°29'78.47"	36°64'30.87"	3165m	Jiangxigou River
DTH	100°70'82.38"	36°54'15.49"	3156m	Daotang River
QJH	100°01'00.53"	37°22'46.93"	3206m	Quanji River
YKWL	100°19'83.13"	37°20'09.82"	3193m	Yikewulan River
HMH	99°78'98.79"	36°72'63.72"	3154m	Heima River

2.3. Soil Microbial Determination

Total soil DNA was extracted using the Omega Bio-tek M5635-02 Soil DNA Kit according to the manufacturer's protocol. The extracted DNA was transported to Shanghai Personal Biotechnology Co. Ltd. for high-throughput sequencing. DNA concentration and quality were assessed via 0.8% agarose gel electrophoresis.

2.4. Data Analysis

One-way ANOVA was used to analyze and compare the differences in microbial composition and diversity among different alpine wetland. Correlation analysis was conducted to explore the relationship between microorganisms and soil nutrients and pH. Statistical analysis was performed using SPSS, and correlation analysis was completed with Origin 2021.

3. Results

3.1. Soil Fungal and Bacterial Community Structure

The top 10 species in terms of relative abundance at the soil bacterial phyla level in the wetlands around the estuary of Qinghai Lake were plotted as a stacked bar chart. As can be seen from the figure, among them, Proteobacteria is the dominant bacterial phylum. Next come the Acidobacteriota, Actinobacteriota, Chloroflexi, Gemmatimonado, Bacteroidota, and Methylomirabi Ten bacterial phyla such as lota, MBNT15, NB1-j, and (Desulfobacterota). The bacterial structure composition of 11 alpine wetland was similar. There was no significant change in the dominant bacterial groups of different alpine wetland, but there were differences in their relative abundances. Among them, the relative abundances of HMH (44.56%), ZQH (40.92%), CJH (40.79%), and QJH (40.79%) were relatively high. The relative abundance of BHH (13.9%) is relatively low. The main dominant bacteria at the soil bacterial genus level in the wetland at the estuary of Qinghai Lake are KD4-96, RB41, Vicinamibacterace, Sphingomonas, Rokubacteriales, MBNT15, Subgroup-7, and N Bacterial genera such as B1-j, SC-I-84, and Ellin6067. The dominant bacterial groups changed in different places. KD4-96, RB41 and Vicinamibacteraceae were the top three most dominant groups in the composition of the microbial community in the estuary wetland of Qinghai Lake. KD4-96 had the highest relative abundance in ZGRT (5.52%) and the lowest in HMH (1.50%). RB41 was the highest in ZHL (5.56%) and BHH (5.55%), and the lowest in GRN (0.35%).

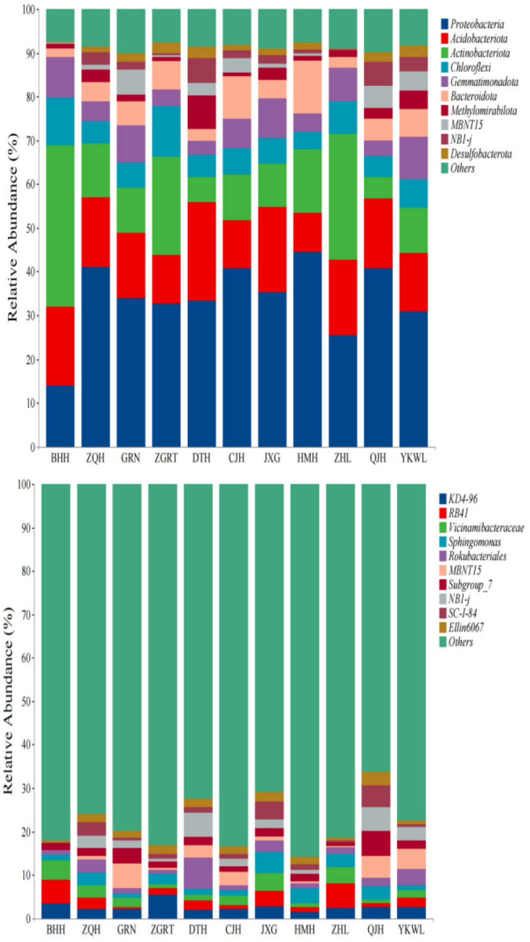


Figure 1. Species abundance at the phylum and genus levels of bacteria

The top 10 species of the relative abundance of the soil fungi phyla in the wetlands around the estuary of Qinghai Lake were plotted as a stacked bar chart species composition. As can be seen from the picture. The top ten species of fungi at the phylum classification level are Ascomycota, Basidiomycota, Rozellomycota, Mortierellomycota, and Aphelidiomycota. There are 10 bacterial phyla, including Mucoromycota, Chytridiomycota, Glomeromycota, Monoblepharomycota, and Entorrhizomycota. Among them, the abundance of Ascomycota was the highest (78.52%), and it was distributed in all estuarine wetland distribution areas.

The relative abundances in the wetlands of ZHL, HMH, JXG, CJH, DTH, ZGRT, GRN, ZQH, BHH, YKWL and QJH were 70.61%, 46.23%, 69.17%, 69.05%, 43.17%, 41.97%, 30.17%, 74.45% and 78.52% respectively. 33.27% and 45.71%. The top ten species at the genus level are Fusarium, Lecythophora, Preussia, Cladosporium, Penicillium, Plectosphaerella, and Archaeor Ten fungal genera, including hizomyces, Hygrocybe, Vishniacozyma, and Halobyssothecium. The dominant bacteria (Lecythophora) of the Qinghai Lake Estuary wetland was the highest at 14.38% in the CJH wetland, but this phylum was not present in the BHH, GRN, ZGRT, DTH and HMH plots. The relative abundance of the Fusarium genus was the highest at 10.84% in the ZGRT wetland. The relative abundance of Fusarium in the YKWL wetland was the lowest at 0.25%.

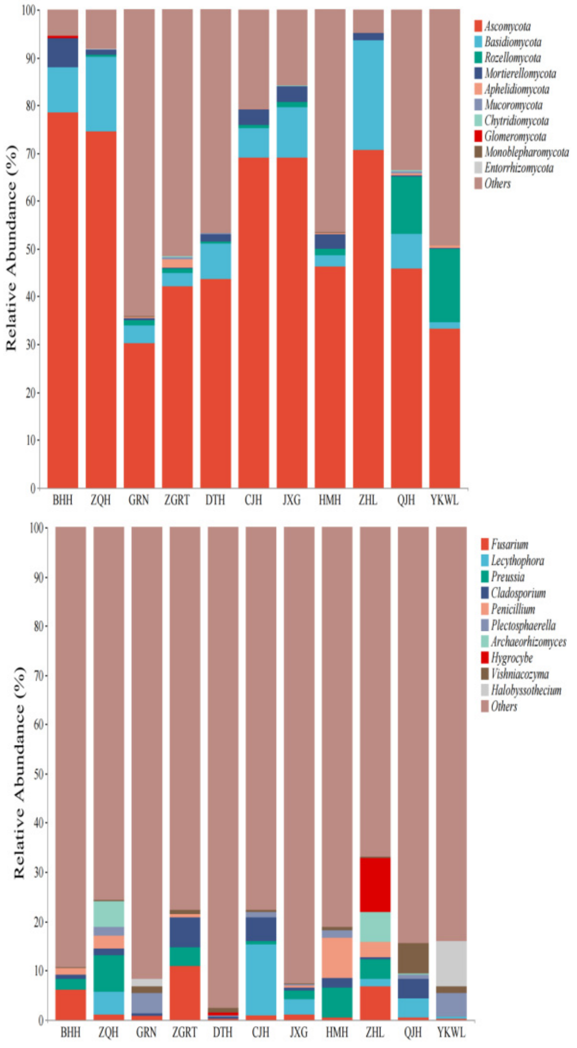
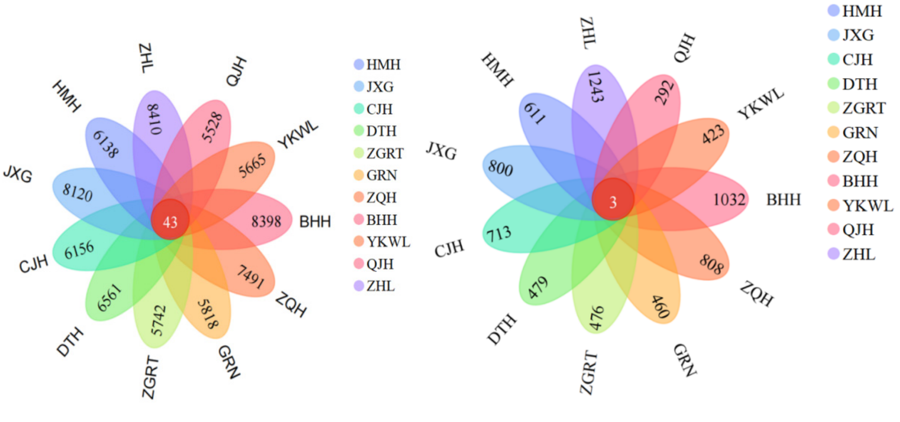


Figure 2. Species abundance at the phylum and genus levels of fungi

3.2. Distribution Patterns of Bacterial and Fungal OTUs

The total number of OTUs in various point bacterial communities is 43. The specific community in the Zhehoulong Estuary wetland is the largest, with 8,410, and that in the Quanji River estuary wetland is the smallest, with 5,528. The proportions are: Zhehoulong 11.35%, Buha River 11.34%, Jiangxiagou 10.96%, Zhengqihu 10.11%, DaoTanghe8.86%, Laiduhe 8.31%, Heima River 8.29%, Garina 7.85%, Zhigeritang 7.75%, Yikewulan 7.65%, Quanjihe 7.46%. It can be seen that the soil of the Zhehoulong

Estuary wetland contains more specific microbial groups. The total number of OTUs in the fungal community is only 3. The number of fungal OTUs in the Zhehoulong Estuary Wetland is the largest, and the number of OTUs in the Quanji Estuary wetland is the smallest. The proportions of the latter are 16.93% > Buha River 14.06% > Zhengqu Hu 11.01% > Jiangxi Gou 10.90% > Lai Du River 9.71% > Hei Ma River 8.32% > DaoTanghe6.53% > Zhi Ge Ri Tang 6.49% > Ga Ri Na 6.27% > Yi Ke Wu LAN 5.76% greater than Quan Ji River 3.98%.



Bacteria **Fungi**

Figure 3. Wayne diagrams of soil fungal community composition in alpine wetland around a lake

3.3. Analysis of Soil Bacterial and Fungal Community Diversity

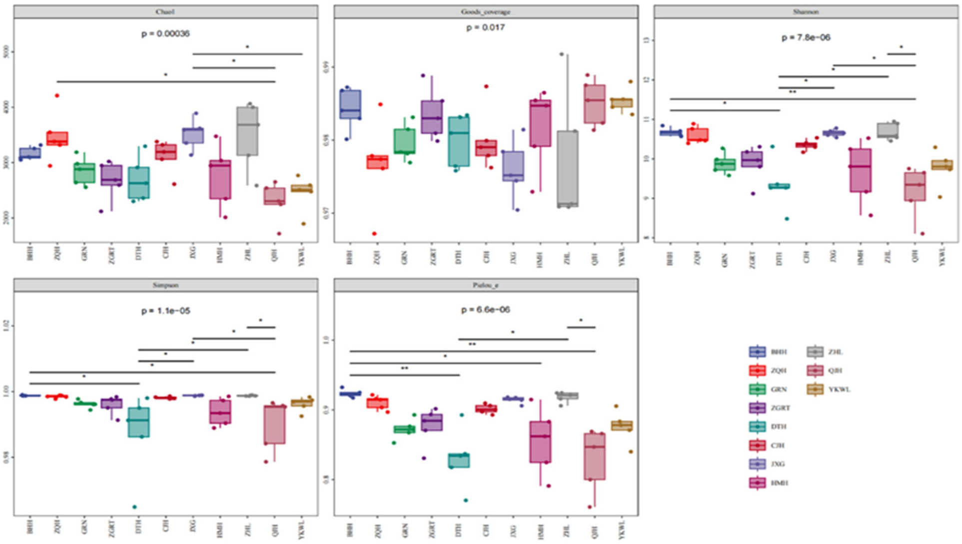


Figure 4. Distribution of soil bacterial α-diversity in the alpine wetland around Qinghai Lake and analysis of the differences

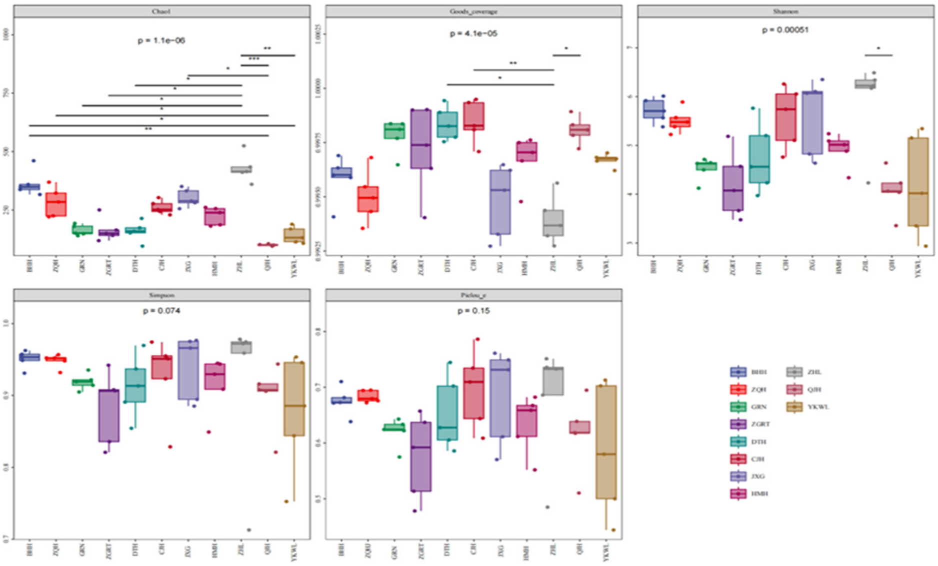


Figure 5. Distribution and differential analysis of soil fungal α-diversity in the alpine wetland around Qinghai Lake

As shown in **Figure 4**, although the diversity of soil bacterial communities in the 11 alpine wetland varies, all reach significant differences. Overall, the variation of the Shannon index of the soil bacterial community in the estuary wetland around Qinghai Lake is as follows: ZHL > ZQH > JXG > BHH > CJH > HMH > ZGRT > GRT > YKWL > DTH. In the Chao1 index, there were significant differences between ZQH and QJH, JXG and QJH, and JXG and YKWL, but no significant differences between them and other alpine wetland. In the Simpson index, there were significant differences between BHH and DTH and QJH, DTH and JXG and ZHL, but no significant differences between them and other alpine wetland. Among all the plots, the ZHL plot has the highest diversity indices of Chao1, Simpson and Shannon. As shown in **Figure 5**, among the fungal diversity indices, the Chao1 index, Shannon index and Simpson index of the ZHL estuarine wetland are the highest among all the plots, and the soil fungal community diversity of the 11 alpine wetland is different. In the Shannon index, there is a significant difference between ZHL and QJH alpine wetland but no significant difference between ZHL and other alpine wetland. In the Chao1 index, there is a significant difference between BHH and QJH and YKWL alpine wetland, and a significant difference between ZQH and QJH. There are significant differences between GRN, ZGRT and DTH and ZHL alpine wetland, and there are also significant differences between ZHL and QJH and YKWL alpine wetland.

3.4. Relationships Between Soil Microbial Diversity and Edaphic Factors

As shown in **Figure 6**, the Chao1 index of fungi has an extremely significant negative correlation with the soil pH value ($P < 0.001$), a significant positive correlation with NO_3^--N and TP, and a significant negative correlation between the Observed index and the soil pH value and soil moisture content ($P < 0.01$). There was a significant negative correlation between Shannon value and pH value ($P < 0.01$), a significant positive correlation with TP, NO_3^--N, TN, AN and AP ($P < 0.01$), and Simpson value had NO significant correlation with each soil environmental factor. The Chao1 value of bacteria had a highly significant negative correlation with the soil pH value ($P < 0.001$), and a positive correlation with TP, AP, AN and NO_3^--N ($P < 0.01$). The Observed value had a highly significant negative correlation with the pH value ($P < 0.001$). The Shannon value showed a highly significant negative correlation with the pH value ($P < 0.001$), a significant negative correlation with SWC ($P < 0.001$), a highly significant positive correlation with the pH value ($P < 0.01$), and a significant negative correlation with TN and SOC ($P < 0.01$). The Pielou value showed a significant negative correlation with pH value and SWC ($P < 0.01$), the Simpson value had an extremely significant positive correlation with NO_3^--N ($P < 0.01$), and a significant negative correlation with NH_4^+-N and soil moisture content ($P < 0.01$).

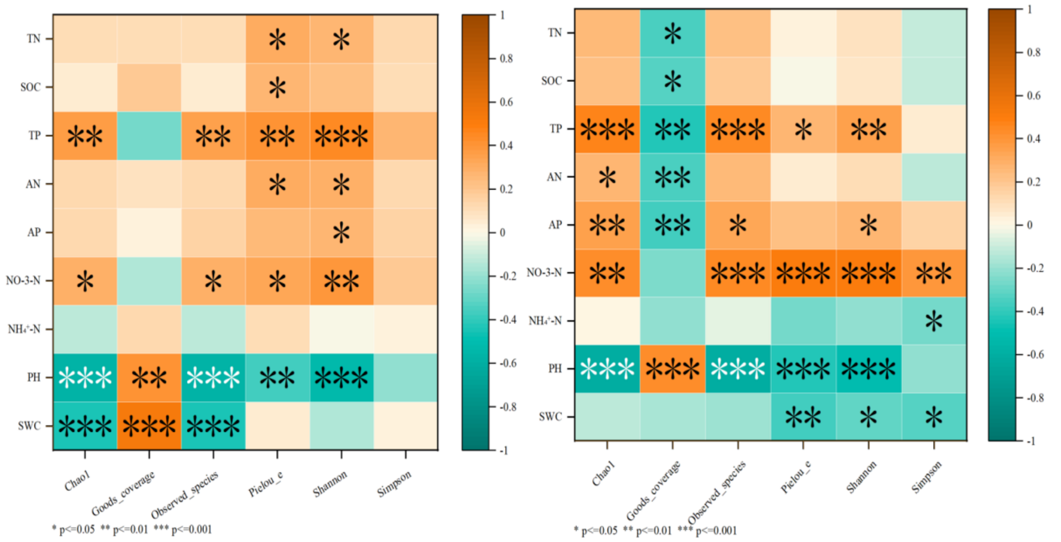


Figure 6. Heat map of correlation between soil bacterial fungi and soil microbial Alpha diversity

3.5. Redundancy Analysis of Soil Microbial Communities Constrained by Edaphic Factors

As shown in **Figure 7**, pH value and SWC have a significant impact on the diversity of fungal communities. pH, SWC, AP, AN, TN, SOC and NH_4^+-N are positively correlated with fungal Observed and Chao1 ($P < 0.01$), while pH, SWC and NH_4^+-N are significantly negatively correlated with the fungal Chao1 index. As shown in the figure (bacteria), there is a significant negative correlation between the Chao1 index and the pH value ($P < 0.01$). There was a significant positive correlation with TN, TP, AN, AP, NO_3^--N and SOC ($P < 0.01$), and 0bserved had a significant negative correlation with NH_4^+-N and SWC ($P < 0.01$).

4. Discussion

4.1. Characteristics of Soil Microbial Communities in Qinghai Lake Alpine Wetland

From each sampling point in the wetland habitat at the estuary of Qinghai Lake, the soil is all alkaline soil. The number of bacterial OTUs in soil microorganisms is greater than that of fungi, indicating that the reproductive capacity of bacteria in the Qinghai Lake area is stronger than that of fungi. The number of OTUs of bacteria and fungi varies at different points. Among them, the number of OTUs of fungi and bacteria in the Zhehoulong Estuary wetland is the largest, while the number of OTUs of fungi and bacteria in the Quanji River estuary wetland is the smallest. Proteobacteria have strong adaptability and contain various species with metabolic functions, and can adapt to the alkaline soil environment in the Qinghai Lake estuary wetland area. Actinomycetes, as an important type of microbial community in the soil, have a significant impact on the carbon and nitrogen material cycles in nature. With a relatively high abundance, they can better adapt to various extreme weather conditions, such as low temperatures and nutrient deficiencies in the ecological environment. Bacteria of other phyla are distributed at all sampling points, but the proportions vary, indicating that the degree of soil bacterial specificity is low in the wetland habitat of the Qinghai Lake estuary. There are unclassified groups at the genus level, indicating that there is potential to discover new fungal species in the soil of the estuary wetland of Qinghai Lake. The relative abundance of Ascomycota in the estuary wetlands of Buha River, Zhengquhu, Laidu River, Jiangxiagou and Zhehoulong is higher than that in the other six sample sites.

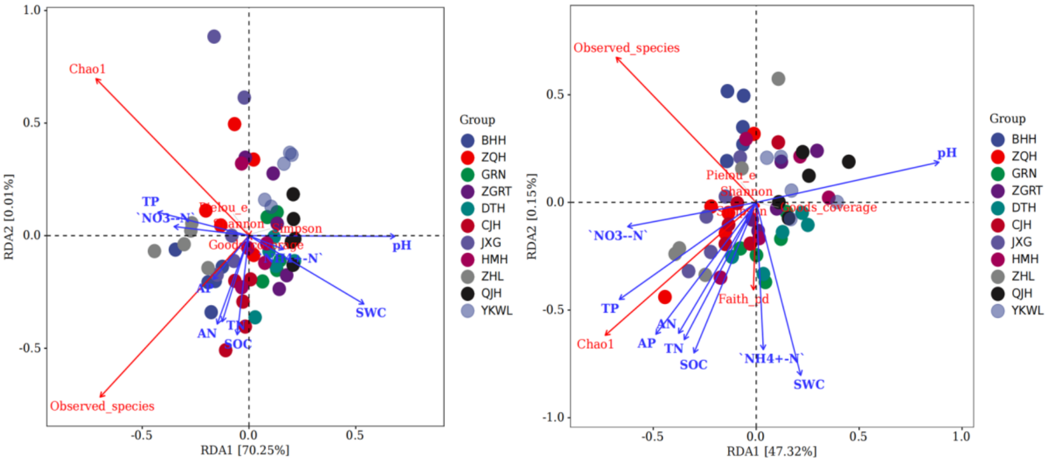


Figure 7. Redundancy analysis of soil bacterial fungal communities with environmental factors

The soil bacterial community at the estuary wetland around Qinghai Lake is mainly composed of Proteobacteria and others at the phylum level, which is consistent with the research results of Song et al. [17] on the bacterial community of coastal wetlands. There are a large number of bacterial groups involved in the carbon, nitrogen and phosphorus material cycle and adapted to the alpine climate in the grassland ecosystem of the Qinghai-Tibet Plateau [11]. The number of sequencing results of the samples is the same as that of Schutte et al. [12]. The dominant bacterial phyla such as Acidobacteria, Chloroflexi, Actinobacteria and Proteobacteria have certain differences in the main bacterial phyla in regions like Tianshuihai on the Qinghai-Tibet Plateau [13-16]. From the perspective of the bacterial community structure, among them, Proteobacteria and Acidobacteriota have the highest relative abundance in all sampling areas and are the dominant bacterial phyla in the alpine wetland around Qinghai Lake. This is consistent with the research results of Crump et al. [18] on rivers. Proteobacteria have a strong adaptability to the environment, which may enable them to have a relatively high growth rate in the surface water environment. Some studies have also shown that the bacteria within the Proteobacteria phylum have a strong effect on nitrogen and phosphorus removal [19].

The main microbiota of soil microorganisms has also been one of the research hotspots in recent years. Studies show that although the overall composition of microbial communities varies greatly under different living conditions, the dominant microbial communities are basically similar. As Shen et al. [20] found in soil microorganisms, Proteobacteria and Acidobacteriota were the main bacterial phyla. Zhang et al. [21] conducted a study on the changes of soil microbial communities, and the results indicated that Acidobacteriota, Proteobacteria, and Actinobacteria were the dominant bacterial phyla. Lu Hui et al. [22] found in their research on soil microorganisms that Proteobacteria, Acidobacteriota, Actinobacteria and Bacteroides are the most important bacterial groups with the highest relative abundance [23].

The increase of soil pH value is regarded as a key driving factor promoting the increase of soil bacterial community diversity and dominates the distribution of bacterial communities in different regions. Similar to the results of previous studies, the contents of SOM, C, N, AP and AK in the soil are the definite factors determining the characteristics of the soil bacterial community. This is because the soil bacterial community changes due to the alteration of soil nutrient conditions, and a good and suitable soil nutrient content is conducive to the growth and reproduction of the soil bacterial community. Soil bacteria are mainly composed of Proteobacteria, Actinobacteria, Chloroflexi, Firmicutes and Acidobacteriota. Proteobacteria, as the largest phylum in the bacterial domain, dominates the soil ecosystem [24]. The growth rate and metabolic rate of Proteobacteria enable it to adapt to complex environments. Proteobacteria have also been confirmed to be the representative phylum of extremely alkaline wetlands. In this study, the correlation analysis between the dominant phylum and the physical and chemical properties of the soil showed that Proteobacteria had significant correlations with soil organic carbon and underground biomass, which was consistent with the existing research conclusions. In this study, the relative abundance of Proteobacteria was the highest. Soil moisture retention reduced the supply of oxygen, which could inhibit the respiration of bacteria and create a suitable growth environment for Proteobacteria. pH value and SWC have a significant impact on the diversity of fungal communities.

4.2. Environmental Drivers of Soil Microbial Community Structure

Both the dynamic succession of vegetation and the heterogeneity of soil physical and chemical properties can have a significant impact on microbial diversity. Plants improve soil nutrient conditions through biomass and root substances, providing energy for the growth and reproduction of soil bacterial communities. Therefore, plant biomass can significantly increase the diversity of soil bacterial communities [26]. The increase of soil pH value is regarded as a key driving factor promoting the increase of soil bacterial community diversity and dominates the distribution of bacterial communities in different regions. Similar to the results of previous studies, the contents of SOM, C, N, AP and AK in the soil are the definite factors determining the characteristics of the soil bacterial community. This is because the soil bacterial community changes due to the alteration of soil nutrient conditions, and a good and suitable soil nutrient content is conducive to the growth and reproduction of the soil bacterial community. Soil bacteria are mainly composed of Proteobacteria, Actinobacteria, Chloroflexi, Firmicutes and Acidobacteriota. Proteobacteria, as the largest phylum in the bacterial domain, dominates the soil ecosystem [27]. The growth rate and metabolic rate of Proteobacteria enable it to adapt to complex environments. Proteobacteria have also been confirmed to be the representative phylum of extremely alkaline wetlands. In this study, the correlation analysis between the dominant phylum and the physical and chemical properties of the soil showed that Proteobacteria had significant correlations with soil organic carbon and underground biomass, which was consistent with the existing research conclusions. In this study, the relative abundance of Proteobacteria was the highest. Soil moisture retention reduced the supply of oxygen, which could inhibit the respiration of bacteria and create a suitable growth environment for Proteobacteria. In this study, Proteobacteria had the highest relative abundance in the Heima River estuary wetland, the lowest relative abundance in the Buha River estuary wetland, and Acidobacteriota had a higher relative abundance in the Daotang river estuary wetland. The analysis results of the top ten dominant bacterial phyla in terms of relative abundance and environmental factors in the results of this study show that pH value and SWC have a significant impact on the diversity of fungal communities. pH, SWC, AP, AN, TN, SOC and NH^+_4-N are positively correlated with the fungal Observed and Chao1 indices. pH, SWC and NH^+_4-N were significantly negatively correlated with the Chao1 index of fungi. This study found that there are correlations among the composition and diversity of fungal communities, pH value and water content in alpine wetland. The structure and diversity of soil fungal communities in alpine wetland around Qinghai Lake are related to various environmental factors.

5. Conclusion

The top 10 bacteria at the soil bacterial phylum level in the wetland at the estuary of Qinghai Lake are Proteobacteria, which are the dominant bacteria. They are followed by Acidobacteriota, Actinobacteriota, etc. The top 10 phyla of fungi are Ascomycota, Basidiomycota, Glomeromycota, Monoblepharomycota and other 10 bacterial phyla. Among the top 10 phyla of fungi, pH value showed a highly significant negative correlation with Ascomycota and Basidiomycota ($P < 0.01$), while among the top 10 phyla of bacteria, pH value was positively correlated with MBNT15 ($P < 0.01$). There was a significant positive correlation with Desulfobacterium (OTA) ($P < 0.01$). Soil moisture content was significantly positively correlated with Proteobacteria, MBNT15, NB1-j, Methylomirabilota and Desulfobacterota ($P < 0.01$); The Chao1 value of fungi was extremely significantly negatively correlated with the soil pH value ($P < 0.001$), the Chao1 index of bacteria was extremely significantly negatively correlated with the soil pH value ($P < 0.001$), and the Shannon value was extremely significantly negatively correlated with the pH value ($P < 0.001$). The Pielou-e value was extremely significantly negatively correlated with pH value and SWC ($P < 0.001$). Through RDA redundancy analysis of the correlation between soil physical and chemical properties and soil fungi and bacteria, the PH value was significantly negatively correlated with Basidiomycota ($P < 0.01$). The pH value was significantly positively correlated with the Ascomycota ($P < 0.01$). The analysis of soil microbial community diversity index and soil physicochemical content showed that the pH value and SWC had a greater impact on the diversity of the fungal community.

Author Contributions

HAN Bitan performed the experiments, analyzed the data, and wrote the initial draft of the manuscript. HUO Lili, CHEN Jinxuan and LI Honglin assisted with data collection. LI Honglin also provided guidance on experimental design and contributed to the revisions of the manuscript.

Data Availability Statement

Data will be made available on request.

Conflicts of Interest

All authors declare no conflict of interest.

Acknowledgments

This study was supported by the “Research and Evaluation of Carbon Sources and Sinks in Rivers, Lakes, and Wetlands of Qinghai Lake” project (2023) and the Central Government-Funded Demonstration and Extension Projects for Forestry Science and Technology (2024-TG).

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