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Response mechanism of soil microorganisms to simulated precipitation in the source wetland of Qinghai Lake

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Abstract

Background Changes in precipitation patterns crucially impact soil microbial communities, and the ecosystem in Qinghai-Tibet Plateau (QTP) is highly vulnerable to climate change. However, we do not fully understand how soil microbial communities in the source wetlands of QTP respond to changes in precipitation. In this study, we employed advanced techniques such as high-throughput sequencing and metabolomics to investigate how soil microbial communities in a source wetland of Qinghai Lake respond to changes in precipitation after quadrennial precipitation treatment.

Results Our findings showed that the predominant microbiota in the source wetland was Proteobacteria. Interestingly, alterations in precipitation levels, whether increased or reduced, did not significantly impact the diversity or functional groups of the microbial community. However, the structure of the microbial community did respond notably to changes in precipitation, leading to shifts in the relative abundance of Spirochaetes and Treponema. A notable finding was that reduced precipitation levels (− 25% and − 50%) and mild increases in precipitation (25%) within the region contributed to increased soil carbon content. However, this effect ceased to manifest when precipitation increased by 50%. Additionally, the reduction in precipitation prompted the release of soil metabolites like syringic acid and aldosterone, while enhanced precipitation resulted in a decrease in aldosterone content.

Conclusions Precipitation changes altered the relative abundance of soil microbial communities and metabolites, which was conducive to increasing carbon storage in this alpine wetland.

Keywords Qinghai-Tibet Plateau, Climate change, Precipitation gradient, Carbon and nitrogen cycles, LC/MS

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Introduction

Soil microbes respond rapidly to environmental changes, and changes in their community characteristics are critical for determining whether ecosystem feedbacks will accelerate or slow the rate of climate change (Jansson and Hofmockel 2020; Ochoa-Hueso et al. 2018). As one of the most important ecological factor for biological communities, precipitation largely determines the temporal and spatial variability of soil moisture and its dynamic changes (Cheng et al. 2020; He et al. 2017), which also have important effects on biogeochemical processes and biodiversity in soil ecosystems (Gao et al. 2016). In recent years, against the background of global climate change, the hydrological cycle has intensified, precipitation patterns have changed, precipitation variability has increased, and the frequency and intensity of extreme precipitation and drought events have further increased (IPCC 2007; Sun et al. 2021). Precipitation patterns alter the soil microclimate and significantly alter soil microbial community characteristics (Chen et al. 2019; Harte et al. 1995; Ochoa-Hueso et al. 2018). Previous studies have indicated that microbial communities have different responses to precipitation gradients at different temporal and spatial scales (Averill et al. 2016; Delgado-Baquerizo et al. 2018). A study by Cruz-Martinez et al. (2009) in California found that the response of soil microbial communities to precipitation changes was weak. However, the study of Berard et al. (2015) on grassland precipitation changes in California demonstrated that soil microbial communities responded strongly to precipitation trends. In addition, soil pH is often considered to be the most important factor in constructing soil bacterial communities (Fierer 2017), while soil water content has less impact on soil microbial communities (Zhang et al. 2014; Zhou et al. 2020). However, previous studies may have underestimated the direct and critical effect of precipitation on soil microbial diversity.

As a dynamic ecosystem, wetlands continuously cycle organic matter and nutrients, and their functions are significantly affected by hydrological processes (Chen et al. 2021; McLaughlin and Cohen 2013). The Qinghai-Tibet Plateau, with an average elevation of more than 4000 m (Gu et al. 2021; Xing et al. 2023), is sensitive to global climate change (Liu and Chen 2000). Its wetland area is approximately 13.19×10^4 km², accounting for 20% of the national wetland area (Yan and Qi 2012). Over the past few decades, the Qinghai-Tibet Plateau has become increasingly warm and humid (Liu and Chen 2000; Song et al. 2014). By the end of the 21st century, the average annual precipitation on the Qinghai-Tibet Plateau is expected to increase by 15–21% (Gao et al. 2014). A study by Zhang et al. (2016) on soil microbes on the Qinghai-Tibet Plateau also found that precipitation changes had a greater impact on microbial community diversity. Yang

et al. (2022a) studied the response of soil microbial communities to a precipitation gradient in the alpine wetland of Qinghai Lake basin, and also found that precipitation changes decreased the richness of soil bacterial communities and increased their diversity. However, little research has been conducted on the response mechanism of soil microbial communities to precipitation change in source wetlands on the Qinghai-Tibet Plateau. To determine the impact of precipitation changes on soil microbial community characteristics and soil metabolism in the source wetlands of the Qinghai Lake basin in this alpine wetland, in 2018, at the headwaters of the Shaliu River in Qinghai Lake, with natural precipitation as a control, field control experiments with ±25% and ±50% precipitation variations were conducted. We hypothesized that: (1) species richness and diversity increase with increasing precipitation; (2) increased precipitation alleviates soil microbial water limitations, thereby increasing the relative abundance of microorganisms; and (3) varying degrees of precipitations change have a differential impact on soil microbial community activity patterns and indirectly affect carbon storage.

Materials and methods

Site description and experimental design

The Wayanshan Experimental Station (37°43′ – 37°46′N, 100°01′ – 100°05′E) is located at the headwaters of the Shaliu River on the north bank of Qinghai Lake, which experiences a typical plateau continental climate (Fig. 1). The average altitude of this area is between 3720 and 3850 m, and the temperature difference between day and night is 31.6 °C. The highest average daily temperature in July is 8.35 °C and the lowest in January is −16.8 °C, with a multi-year average temperature of −3.31 °C and a multi-year average precipitation of 420.37 mm with more than 90% occurring from May to September, highest average daily precipitation in August is 8.35 °C and the lowest in January is −16.8 °C. Affected by geographical differentiation of factors, this region has only a single vegetation type, with *Kobresia humilis* as the dominant species (Li et al. 2020). The soil layer of Wayan Mountain is often in a water-logged state, the main soil type is mollic gleysols, and the layer beneath the surface soil consists of alluvial deposits (Wu et al. 2017).

Sample collection

Soil samples were collected in June 2022 (early growing season). Each sample consisted of 5 soil cores, which were collected by the 5-point sampling method using a soil drill (4.5 cm in diameter) to collect 0–10 cm of topsoil. A total of 15 soil samples were collected, with 5 treatments × 3 replicates. The plots were laid in 2018, and the situation of the plots are shown in the figure (Figure S1). We reduced the natural precipitation by installing
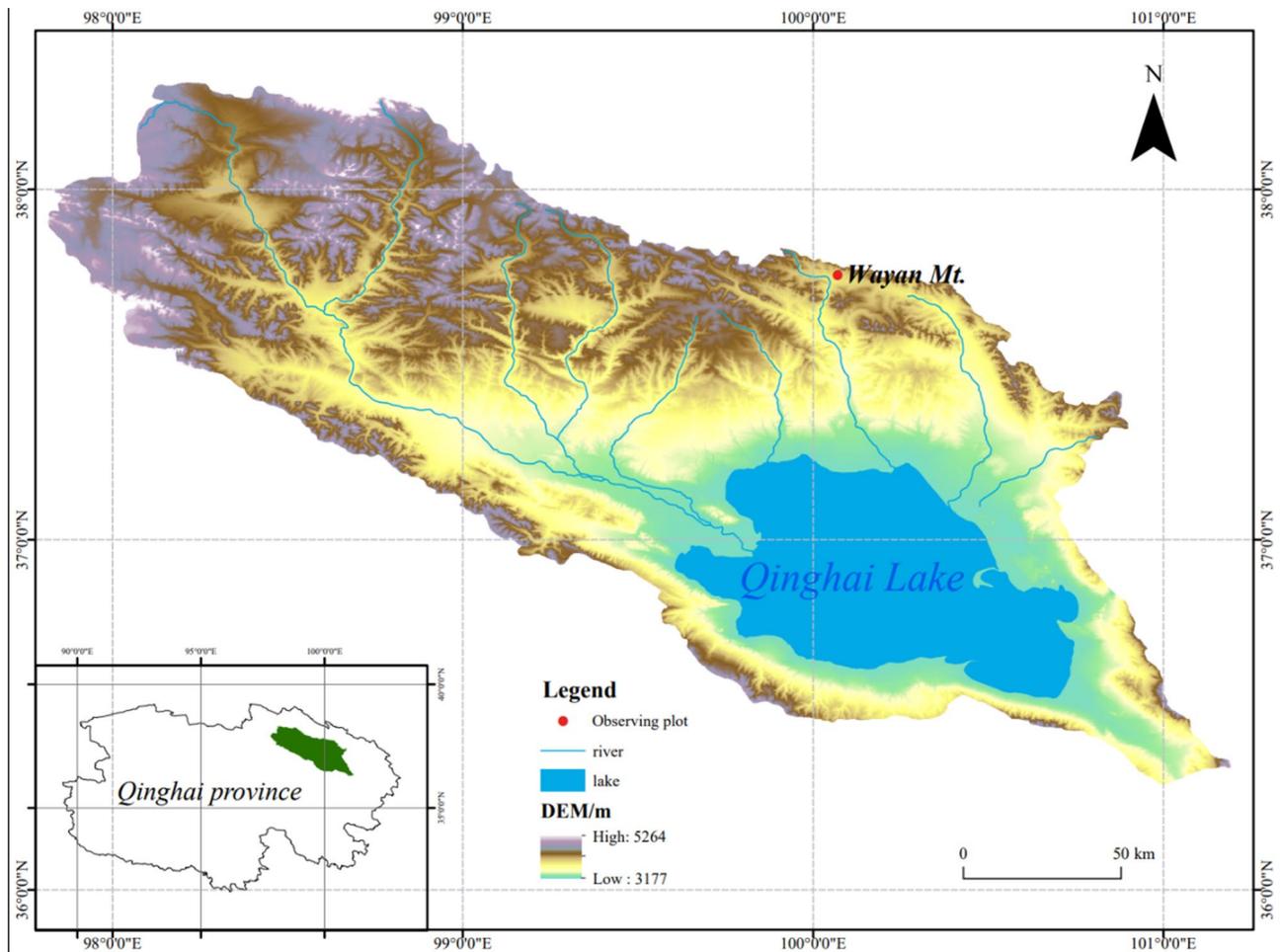
Fig. 1 The location of Qinghai Lake basin and our observation plots in the northeastern Qinghai Province, China

equidistant inclined diversion channels of different areas. The diversion channels collect rainwater into the horizontal tank in the concourse, and increase the natural precipitation through the spray device. The samples were named Wck (natural control), ZA (50% more precipitation), ZB (25% more precipitation), JA (50% less precipitation), and JB (25% less precipitation). All samples were sieved (2 mm aperture) to remove roots, dead branches, and stones, stored in ice packs, and sent back to the laboratory immediately. Some soil samples were stored at −80 °C and used for soil DNA extraction.

Determination of soil physicochemical properties

Soil pH was measured at a fresh soil to water ratio of 1:2.5 using a pH probe (FE20-FiveEasy pH, Mettler Toledo, Germany). Total carbon (TC) and total nitrogen (TN) were measured using an elemental analyzer (Vario EL III, Elemental Analysis System GmbH, Germany). Soil (0–10 cm) water content and temperature were monitored using a TDR-300 soil moisture meter (Spectrum Technologies Inc., Plainfield, Illinois, USA) and an LI-8100 probe (LI-COR Inc., Lincoln, Nebraska, USA).

DNA extraction and polymerase chain reaction (PCR)

Soil DNA was extracted from 0.5 g of fresh soil and quantified by PCR. The V3–V4 hypervariable region of 16S rRNA was amplified with specific primers 341F (5′-CCTAYGGGRBGCASCAG-3′) and 806R (5′-GGAC-TACNNGGGTATCTAAT-3′) (Huse et al. 2008). PCR products were sequenced using the Illumina HiSeq sequencing platform. Amplicon sequencing was performed using Illumina HiSeq platform from Shanghai Ling Biological Co., Ltd. DNA extraction and quantification were performed as described in Yuan et al. (2023).

Untargeted metabolism

Quality control (QC) samples were generated by mixing equal volumes of all samples, and metabolite extraction was performed simultaneously from QC and experimental samples. Liquid chromatography mass spectrometry (LC/MS) analysis was performed using an ultrahigh performance liquid chromatography (UHPLC)-Q-Orbitrap high-resolution mass spectrometry (HRMS®) system (Thermo Fisher Scientific™, USA) and an ACQUITY UPLC bridged ethyl hybrid (BEH®) C18 column

(2.1×100 mm, 1.7 μm, Waters™, USA). The mobile phase was acetonitrile and 0.1% formic acid, and gradient elution was performed according to a previous study (Li et al. 2022).

Statistical analysis

Bioinformatics analysis of microbiome disembarkation data was conducted through a QIIME 2 (2019.4) process (Bolyen et al. 2019). Reads labels and primers were removed from the original sequence data by cutadpt plug-in (Martin 2011), and then DADA2 plug-in was used to obtain error-free biological sequences by quality control, error correction and chimerism removal for sequence noise reduction (Callahan et al. 2016). The Amplicon Sequence Variants (ASVs) obtained after de-duplication were taken as the minimum taxon. Finally, each representative ASV sequence was classified and identified by comparing them with the NR database.

R software (version 4.1.2) was used to organize amplicon sequence variant (ASV) annotation result tables and plots. The MicrobiotaProcess_1.6.2 package was used to calculate the alpha diversity index and the beta diversity index. The significance between groups was calculated by the Wilcoxon rank sum test. The results of NMDS (metaMDS function), ADONIS (adonis2 function) and ANOSIM (anosim function) based on Bray-Curtis distance were calculated using Vegan_2.5-7 packaging to confirm the validity of the grouping; at the same time, redundancy analysis of the data was performed based on a linear model. FAPROTAX was used to predict functional groups corresponding to microorganisms (Liang et al. 2020). The linkET_0.0.2.10 package of R software was used to calculate data correlations and draw correlation network heatmaps. The ropls_1.26.4 package was used to calculate between-group variable importance in projection (VIP) values, and the analysis of variance (aov) function was used to calculate between-group metabolite significance. The psych_2.1.9 package (corr.test function) was used to calculate correlations between data and screen for values with R greater than 0.6 and P less than 0.05.

Results

Response of microbial community diversity to precipitation changes

The amount of sequencing data for each sample was reasonable (Fig. 2a), and the number of sequences obtained in the bacterial community ranged from 31,195 to 41,513 among the 15 samples. It was found that the number of ASVs shared by the 5 groups was 314 and that the numbers of unique ASVs of Wck, JA, JB, ZA, and ZB were 606, 773, 1037, 592, and 844, respectively (Fig. 2b). PCA demonstrated that the soil heterogeneity in the source wetland was relatively large and that the soil microbial community was affected by precipitation changes (Figure S2a). Multiple test results (NMDS, ANOSIM, ADONIS) verified the validity of the grouping ($P<0.05$; Fig. 2c). A 50% increase in precipitation decreased microbial species richness and increased species evenness, while the remaining treatments showed the opposite trend (Fig. 2d). A 25% precipitation change had a greater impact on microbial community diversity than a 50% precipitation change. Overall, there was no statistically significant relationship between the effects of precipitation changes on the species richness index and evenness index.

Response of the microbial community structure to precipitation changes

The predominant phyla of soil bacteria in the source wetland (Fig. 3a) were Proteobacteria (46.11%), Actinobacteria (23.41%), Firmicutes (22.86%), and Spirochaetes (1.83%), accounting for more than 90% of all sequences. Spirochaetes responded significantly to precipitation changes (Fig. 3b), and a 25% increase or decrease in precipitation significantly decreased the relative abundance of this microbiota ($P<0.05$). A precipitation reduction of 50% (JA) decreased the relative abundance of this microbiota, and a 50% precipitation increase (ZA) increased the relative abundance of this microbiota, but these changes were not significant ($P>0.05$). The dominant bacterial genera in the source wetland (Fig. 3c) were *Azospirillum* (41.60%), *Lactobacillus* (20.56%), *Streptomyces* (13.62%), *Cutibacterium* (9.56%), *Treponema* (1.82%), *Klebsiella* (1.71%), *Pararhodospirillum* (1.30%), and *Pelotomaculum* (1.00%), which accounted for more than 80% of all sequences. Among them, the relative abundance of *Treponema* was significantly affected by precipitation changes ($P<0.05$; Fig. 3d), showing the same response trend as the dominant microbiota Spirochaetes at the phylum level.

Response of microbial community functions to precipitation changes

The results of microbial functional classification annotation (Fig. 4a) indicated that the ecological functions of soil microbial communities in the source wetland of Qinghai Lake were classified into 32 functional groups (relative abundance>0.1%). The microbial functions corresponded mainly to chemoheterotrophy (27.03%), aerobic_chemoheterotrophy (19.19%), nitrogen_fixation (13.83%), ureolysis (13.82%), fermentation (8.23%), animal_parasites_or_symbionts (4.44%), human_associated (4.43%), human_pathogens_all (3.95%), human_gut (1.06%), and mammal_gut (1.06%). In addition, statistical analysis results demonstrated that precipitation changes had no significant effect on microbial functional groups ($P>0.05$). There were 14 functional groups related to the
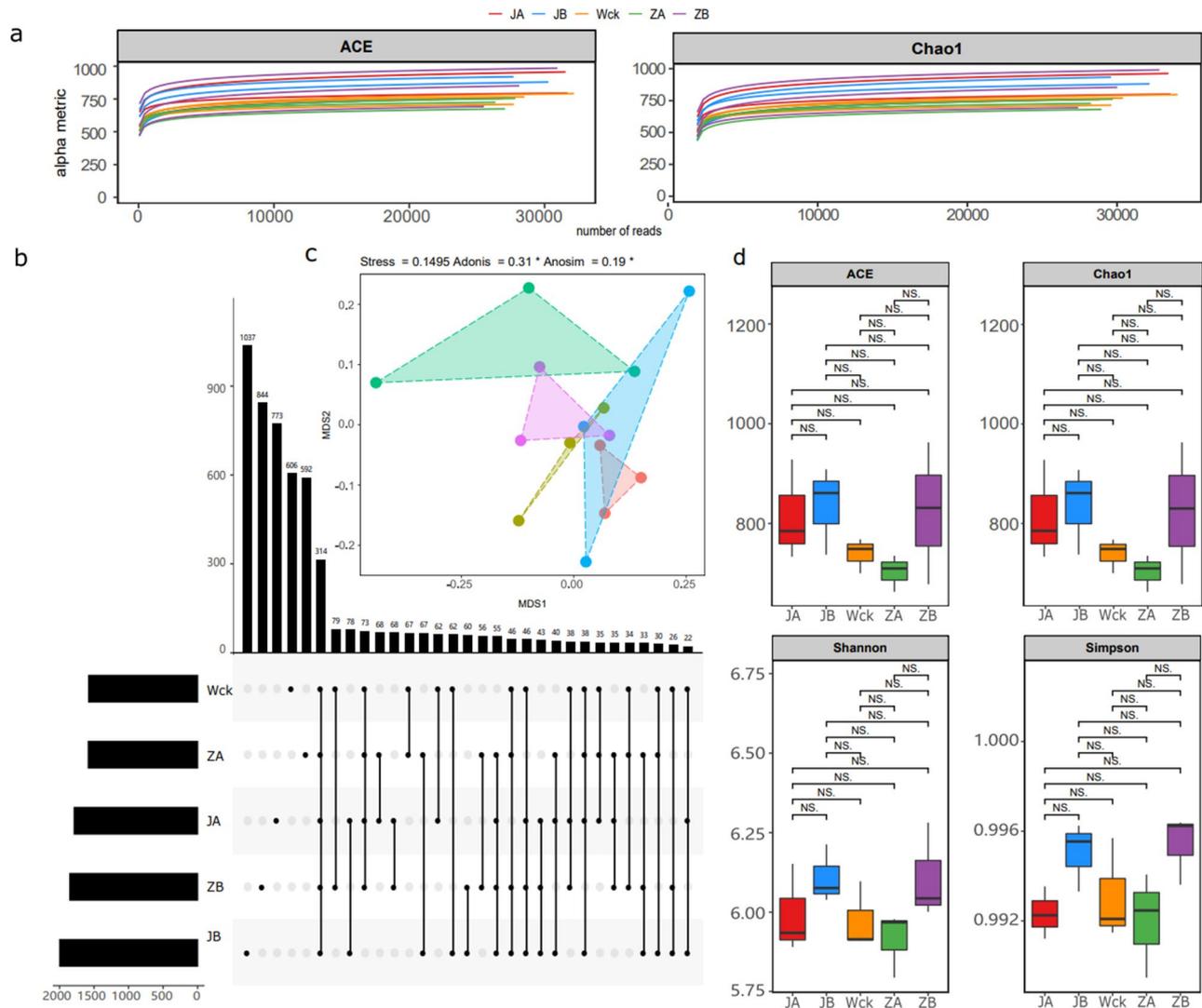
Fig. 2 Sequencing of soil microorganisms after 4 years of simulated precipitation: (**a**) Sample dilution curve; (**b**) ASV distribution map of each group; (**c**) ANOSIM statistical box plot; and (**d**) alpha diversity index. Note: NS denotes that the difference between the 2 groups was not statistically significant ($P > 0.05$)

carbon and nitrogen cycles (Fig. 4b). Reverse localization of microbiota associated with the carbon and nitrogen cycles revealed that 23 genus-level microbiota belonging to 7 phyla were involved mainly in the biochemical cycling process of carbon and nitrogen. Except for *Brucella* of Proteobacteria, which had nitrate reduction as its main functional group, all microbiota had chemoheterotrophy as their main function.

Response of soil physical and chemical factors to precipitation changes

Precipitation changes significantly altered soil moisture and TC content (Fig. 5a), while soil pH, TN, and temperature did not respond significantly to precipitation changes (Figure S2d). After a 50% precipitation enhancement, soil moisture in the source wetland of Qinghai

Lake increased significantly, and the effects of other treatments on soil moisture were not significant. A 50% precipitation reduction and 25% precipitation enhancement significantly increased TC content, while a 25% precipitation reduction and 50% precipitation enhancement did not significantly affect TC content. Further analysis of the correlations in the data revealed that TC and TN were significantly positively correlated ($P < 0.05$), and soil physicochemical properties were associated with major phylum-level microbial communities (relative abundance > 1%) and major soil metabolites (relative abundance > 1%), but without significant relationships (Fig. 5b). Redundancy analysis of genus-level microbiota (top 10) and soil physicochemical properties (Fig. 5c) demonstrated that soil temperature, carbon and nitrogen content were the most important influencing factors
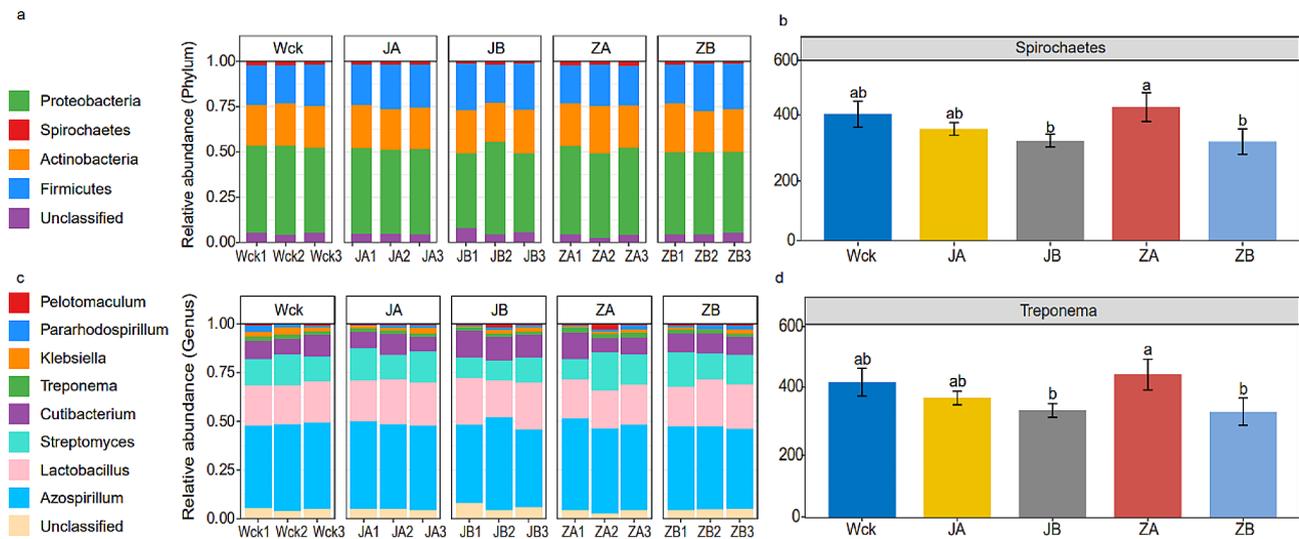
Fig. 3 The microbial community composition of soil samples after 4 years of simulated precipitation: (**a**) Phylum-level community structure; (**b**) phylum-level differential microbiota; (**c**) genus-level community structure; and (**d**) genus-level differential microbiota. Note: (**a**)–(**d**) indicates significance, the same letter indicates no significant difference (*P* > 0.05), and different letters indicate significant differences (*P* < 0.05)

of microbial community, while pH and soil moisture had minor effects on microbial communities.

Responses of soil metabolites to precipitation changes

QC samples were clustered tightly in the PCA results for LC/MS untargeted metabolism (Figure S2b), illustrating the repeatability of the experimental method and the stability of the instrumental analysis system. Partial least squares-discriminant analysis (PLS-DA) revealed differences in the metabolic profiles of each group (Figure S2c) and indicated that the differences between groups were statistically significant and that the difference between the Wck and ZB groups was relatively small. Precipitation changes significantly affected the relative abundances of 2 metabolites: syringic acid and aldosterone (Fig. 5d). Precipitation reduction treatment increased their relative abundance, while precipitation enhancement treatment increased the relative abundance of syringic acid but decreased the relative abundance of aldosterone. The topological relationship between genus-level microbiota (top 10) and differential metabolites (Figure S2e) indicated that syringic acid and aldosterone were positively associated with all 5 microbiota (*Streptomyces*, *Oikopleura*, *Cutibacterium*, *Lactobacillus*, and *Treponema*). In addition, syringic acid was significantly positively correlated with *Pararhodospirillum*, and aldosterone was significantly positively correlated with *Klebsiella*. Among them, *Streptomyces*, *Klebsiella*, *Lactobacillus*, and *Treponema* are carbon-nitrogen cycle-related microbiota. *Azospirillum*, as the most important carbon-nitrogen cycling microbiota, showed a significant negative correlation with differential metabolites.

Precipitation changes affected the relationships between soil microbes

There were some differences in the relationship network of microorganisms in different treatments. Compared with the control group, precipitation changes resulted in decreases in the total numbers of nodes and connections, and the network complexity tended to decrease (Table 1). The numbers of nodes and connections in the JB network decreased substantially, and the differences in the numbers of nodes and connections between the other groups and the control group were small (Table 1). There were differences in the variation trends of topological properties between different treatments (Table 1). JA and JB (50% and 25% reduction in precipitation, respectively) decreased the negative correlations between bacteria, while JB and ZB (25% precipitation enhancement and reduction, respectively) decreased the number of positive connections between bacteria.

Discussion

Precipitation changes slightly affect microbial community diversity

The richness of soil microbial species diversity determines the stability of microbial community structure and function (Wang et al. 2010), and it is also crucial for evaluating the effectiveness of wetland ecological restoration (Li et al. 2021). Studies have demonstrated that microbial communities are highly dependent on water for movement and substrate dispersal; hence, precipitation changes and soil water availability often lead to corresponding responses in species diversity (Harris 1981; Zeglin et al. 2013). The response for the alpha diversity of the microbial community in the source wetland of
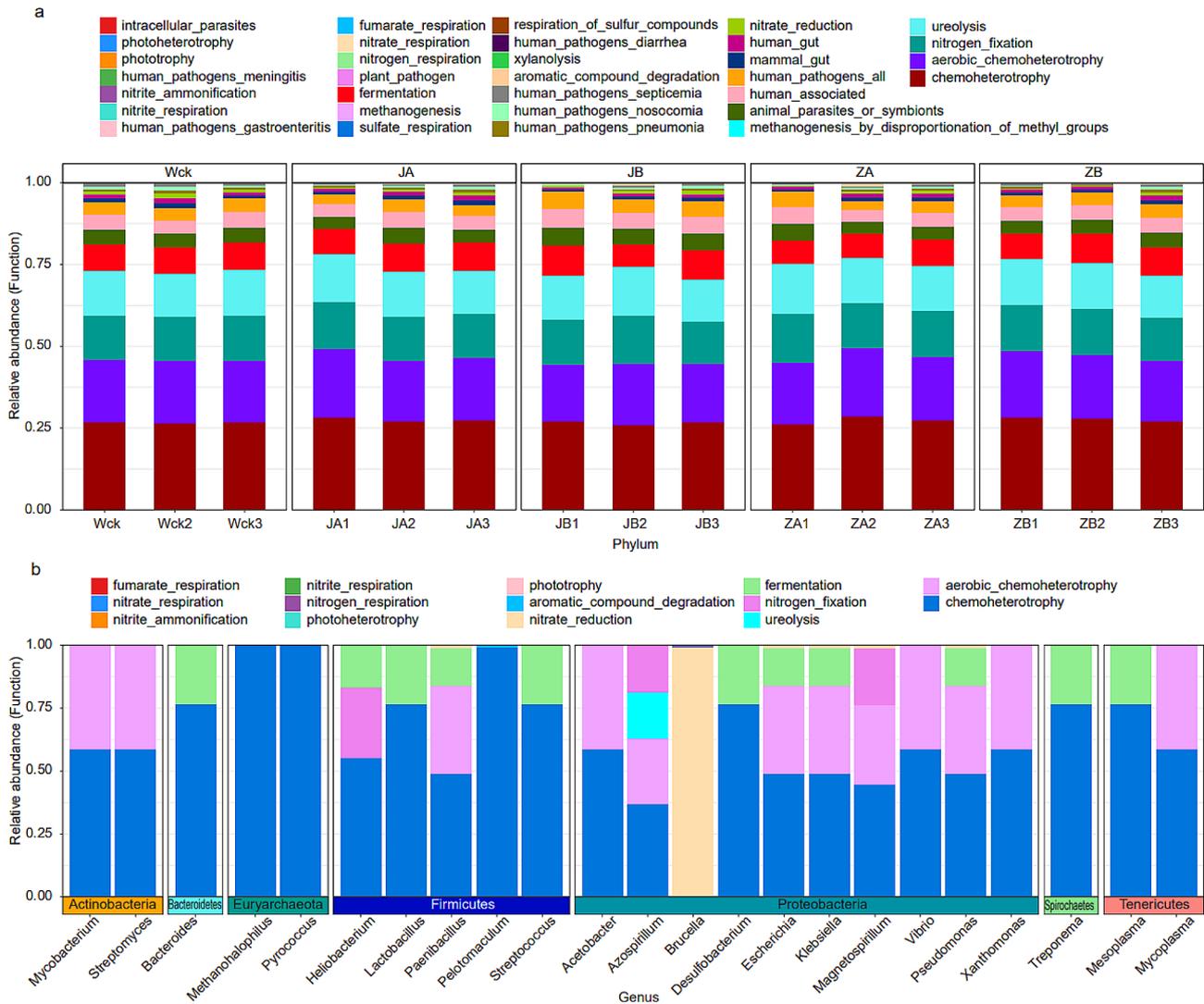
Fig. 4 The microbial functional groups of soil samples after 4 years of simulated precipitation: (**a**) Functional groups with relative abundance greater than 0.01; (**b**) functional groups and microbial microbiota related to the carbon and nitrogen cycles

Qinghai Lake indicated that the microbial species richness and diversity first increased and then decreased with increasing precipitation and showed the same trend with decreasing precipitation, which was inconsistent with the hypothesis. In previous studies, there were also differences in the responses of microbial community diversity to precipitation changes. A 7-year study by Yu et al. (2019) on the Qinghai-Tibet Plateau found that sites with higher precipitation tended to have lower soil microbial richness and uniformity. Kieft et al. (1987) suggested that osmotic stress caused by increased soil moisture leads to a decrease in microbial community diversity. A study by Schimel et al. (2007) also demonstrated that certain species of microorganisms die under water stress; thus, increased precipitation leads to a decrease in soil microbial alpha diversity. Zeglin et al. (2019) reported that decreased precipitation greatly limits the growth of

microorganisms, thereby reducing the alpha diversity of soil microorganisms, which was also confirmed by Nielsen and Ball (2015). In this study, the alpha diversity of the microbial community in the source wetlands of Qinghai Lake was not significantly affected by the precipitation changes, which may be due to the fact that historical precipitation regimes have led to regional adaptations in microbial response to soil moisture, thereby limiting the microbial response to precipitation pattern changes (Averill et al. 2016). A study by Banu et al. (2004) in Australia also revealed that microbial diversity did not respond significantly to precipitation changes.
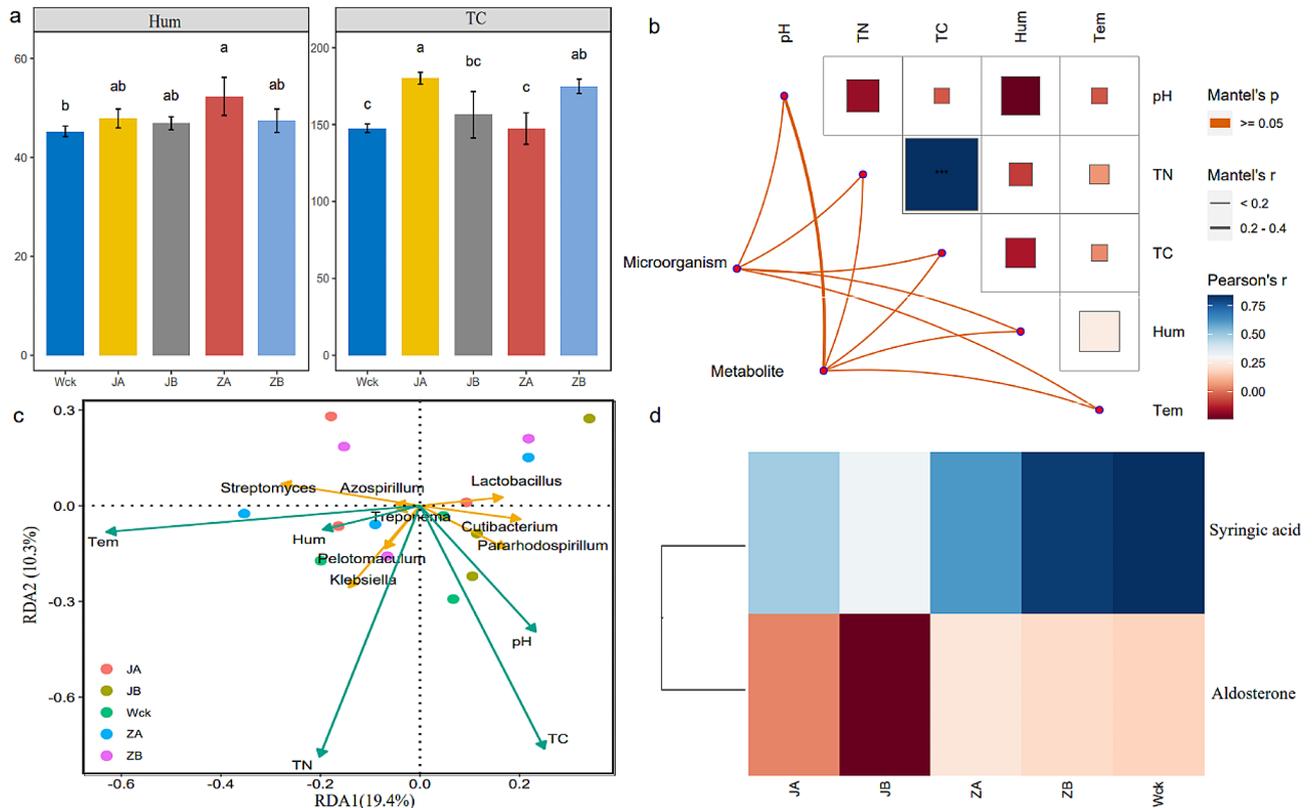
Fig. 5 Physicochemical properties and differential metabolites of soil samples after 4 years of simulated precipitation: (**a**) Physicochemical factors with significant differences; (**b**) correlation network diagram of microorganisms, metabolites, and physicochemical factors; (**c**) redundancy analysis of microorganisms and physicochemical factors; and (**d**) differential metabolite heatmap. *Note* Hum: soil humidity; pH: soil pH; TC: total carbon; Tem: soil temperature; and TN: total nitrogen. (**a**)–(**d**) denotes significance, the same letter indicates no significant difference ($P > 0.05$), and different letters indicate significant difference ($P < 0.05$)

Table 1 Data of the microbiome correlation network in the group

Group	Number of nodes	Number of positive connections	Number of negative connections	Total number of connections
JA	168	1442	1231	2673
JB	150	1218	1239	2457
ZA	155	1481	1461	2942
ZB	168	1372	1439	2811
Wck	170	1516	1483	2999

Precipitation changes significantly affect the structure of microbial community and slightly affect community function

Proteobacteria are considered the most abundant microbiota in soil and are critical for global carbon, nitrogen, iron, and sulfur cycling (Spain et al. 2009). The predominant microbiota in the source wetland of Qinghai Lake is Proteobacteria, which is consistent with the results of previous studies on the Qinghai-Tibet Plateau and alpine wetlands (Costello and Schmidt 2006; Guo et al. 2015). Soil microorganisms have unique physiological characteristics and survival strategies, and they are often very sensitive to changes in soil water availability (Engelhardt

et al. 2018). Therefore, precipitation change patterns tend to affect soil microbial community structures (Ochoa-Hueso et al. 2018), and the responses of microbial community structures under different patterns often differ (Zeglin et al. 2013). The soil microbial community structure in the source wetland of Qinghai Lake responded significantly to precipitation changes, and changes in the precipitation pattern significantly changed the relative abundance of Spirochaetes (phylum) and *Treponema* (genus). Their relative abundance was increased by the 50% precipitation enhancement treatment, which demonstrated the above hypothesis to a certain extent. Research has shown that augmenting precipitation can mitigate water limitations on the structure of the soil microbial community (Kong et al. 2022). This could explain the positive impact of precipitation enhancement treatments on the relative abundance of soil microbial communities.

The present study found that a 25% precipitation enhancement decreased the relative abundance of the microbiota and that precipitation reduction similarly decreased the relative abundance of the significantly altered microbiota. Howard and Howard (1993) reported

that low soil water content inhibits the diffusion of nutrients and carbon substrates in the soil, further limiting the growth and activity of soil microorganisms, which is consistent with the results of this study. Lawlor and Cornic (2002) also demonstrated that when soil moisture decreases, the diffusion of substrates is limited, and the growth and reproduction processes of microorganisms slow down due to insufficient resources, which again provides strong evidence for the response of microbial community structure to precipitation changes. Some studies have demonstrated that the microbial community structure is not affected by precipitation patterns. For example, Taylor et al. (2004) conducted a 2-year precipitation change treatment and found that the soil microbial community composition was not affected by precipitation enhancement or reduction. Che et al. (2002) also found that soil pH value, electrical conductivity and temperature were important factors affecting the composition of microbial community, rather than soil water. Precipitation changes did not have a significant impact on the functional groups of soil microbes in the source wetlands of Qinghai Lake. This is inconsistent with the conclusion drawn by Na et al. (2019), who suggested that changes in precipitation disrupt the ecological functions of soil microbial communities. This discrepancy may be attributed to the low relative abundance of microbiota undergoing significant changes, which does not affect the overall functional taxa. In addition, Proteobacteria are the most important microbiota in the carbon and nitrogen cycling process, which may have an important impact on soil nutrient cycling and even biogeochemical processes (Engelhardt et al. 2018).

Precipitation changes significantly alter soil moisture, carbon content, and soil metabolite content

Carbon and nitrogen are extremely common limiting environmental elements in the ecosystem, and their dynamic changes in the soil have an important impact on the ecosystem (Wang et al. 2014). Precipitation changes can alter soil properties and regulate carbon and nitrogen allocation, thereby affecting soil microbial communities (Manzoni et al. 2014; Toju et al. 2018). Precipitation changes in the source wetlands of Qinghai Lake significantly changed the soil moisture and TC content, consistent with the hypothesis. Previous studies have indicated that increased precipitation alleviates soil water limitations and increases soil carbon content, while decreased precipitation reduces soil carbon mineralization rates. In contrast, the present study found that the precipitation reduction treatment increased soil carbon content, while soil carbon content increased significantly at 25% precipitation enhancement and decreased at 50% precipitation enhancement. Yang et al.'s (2022b) study on the precipitation change of lakeside wetland of Qinghai Lake

found that the total carbon content of soil under precipitation enhancement treatment was lower than that under precipitation reduction treatment, which was consistent with the results of this study. The decrease in soil carbon content due to precipitation enhancement may be because after the soil water holding capacity exceeds 50%, excessive water content is detrimental to microbial activity (Franzluebbers 1999), resulting in a decreased soil mineralization rate. Other studies have demonstrated that precipitation changes mainly drive changes in microbial communities by causing physicochemical changes in soil moisture and pH (Felsmann et al. 2015; Ochoa-Hueso et al. 2018). However, the results of redundancy analysis indicated that soil temperature, carbon and nitrogen content were the most important factors affecting soil microorganisms in the source wetland of Qinghai Lake, while pH and soil moisture had a minor effect on the microbial community. This may be due to the combination of precipitation changes affecting the microenvironment and altering the distribution of carbon and nitrogen. There were no significant relationships between soil metabolites and soil physicochemical factors, but precipitation changes significantly affected the relative abundances of syringic acid and aldosterone, which may further affect carbon storage in source wetlands.

Conclusions

Based on simulated precipitation experiment, this study identified the mechanism via which the microbial community responds to precipitation changes in the source wetland of Qinghai Lake. The microbial diversity response to precipitation changes was not significant, but precipitation changes significantly altered the relative abundances of Spirochaetes and *Treponema*. Precipitation reduction treatment promoted the synthesis of carbon-related organic compounds to a certain extent, while precipitation enhancement treatment decreased the content of aldosterone. In addition, a 50% precipitation enhancement significantly increased soil water content and had little effect on soil carbon storage, while the remaining precipitation treatments increased soil carbon storage. In conclusion, the further increase of precipitation may inhibit the production of organic carbon and reduce soil carbon storage in alpine wetland. This study provides new insights into the mechanism via which precipitation changes regulate microorganisms and metabolism in alpine wetland ecosystems.

Supplementary Information

Supplementary Material 1: Plot layout for rain increase and decrease treatment. Figure S2. Correlations between microorganisms and metabolites

Author contributions
Conceptualization, Xinye Wang and Kelong Chen; Data curation, Desheng Qi and Yuanxi Ma; Investigation, Desheng Qi and Yuanxi Ma; Software, Ni Zhang; Writing – original draft, Xinye Wang; Writing – review & editing, Ni Zhang and Tiexi Chen.

Data availability
The raw data has been uploaded to NCBI, and Its BioProject is PRJNA983962.

Declarations

Ethics approval and consent to participate
Not applicable.

Consent for publication
Not applicable.

Competing interests
The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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