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Effects of Land Use Conversion on the Soil Microbial Community Composition and Functionality in the Urban Wetlands of North-Eastern China

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Abstract: Urban wetlands are undergoing intensive conversion from natural wetlands to farmlands, woodlands, and even alkaline land. This study aimed to determine the effects of land conversion on soil microbial communities of urban wetlands in the hinterland of Songnen Plain, Northeastern China. Soil samples were collected from various sites of Longfeng wetland, including swamp wetland (SW), meadow wetland (MW), woodland (WL), farmland (FL), and alkaline land (AL). High-throughput sequencing followed by bioinformatic analysis was conducted to evaluate the structure, composition, and function of soil bacterial and fungal communities. The most dominant bacterial and fungal phylum among the land-use types were Proteobacteria and Ascomycota, respectively. In addition, the bacterial diversity and functions varied significantly across different land-use types. However, no remarkable differences in fungal communities were observed under various land-use types. Edaphic parameters, including exchange sodium percent (ESP) and total nitrogen (TN), remarkably influenced the abundance and diversity of soil microbial communities. These results show that land-use type shapes various aspects of soil microbial communities, including soil physicochemical properties, microbial taxa structure, potential functional genes, and correlation with environmental factors. This study provides reliable data to guide land use management and supervision by decision-makers in this region.

Keywords: land-use types; soil microbial community; urban wetland; soil properties; Illumina sequencing

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1. Introduction

Wetlands reserve about 20%–30% of soil carbon and play a key role in the global carbon cycle. Urban wetlands offer ecosystem services for millions of people and other organisms living in the area, including regulated flow, water supply, and flood control. However, human activities, such as rapid urbanization and agricultural production, have dramatically altered about half of the wetlands worldwide [1]. Soil ecosystem services are tightly associated with sustainable development goals published by the United Nations [2]. In-depth understanding and quantification of land-use conversion are crucial in regulating the soil ecosystem and should be well managed to achieve sustainable development goals. Previous studies have shown that land-use conversion exerts massive and prolonged influences on soil biodiversity-ecosystem functioning [3–5]. Therefore, optimizing land-use management in the urban wetland is essential for maintaining a balance between urban development and wetland functions. Urban wetlands offer multiple ecosystem services, including water resource provision, nutrient retention, and water-heat balance. Increasing human interventions such as urbanization and intensive agriculture [6] have reduced wetland areas by converting them into artificial woodland, farmland, and diverse land-use types, exerting lasting impacts on soil structure [7], soil pH [8], and soil nutrient contents [9], thereby affecting soil microbial communities [10,11]. This has ultimately resulted in threats to wetland function and ecological stability [12]. Soil parameter variability influences soil microbial communities [13]. Compared with soil characteristics, soil microorganisms are strongly associated with soil chemical reactions and play a key role in soil quality and vegetation biomass [14].

Moreover, soil microorganisms facilitate soil organic matter disintegration [15], energy flow in wetland ecosystems [16], maintenance of ecosystem function [17], and global biogeochemical processes [18]. For instance, Guo et al. [19] found that wetland conversion to farmland can cause remarkable changes in the soil bacterial community diversity, composition, and functional diversity. Lauber et al. [20] revealed that the ratio of soil fungi to soil bacteria is usually higher following land conversion from wetland to grassland. In addition, soil bacterial taxa and function differed between alpine meadow and farmland that reported long-term land-use patterns; bacterial community composition was largely driven by changes in pH and soil texture, while fungal community composition was most strongly related to soil nutrient availability [21]. Liu et al. [22] revealed that land conversion directly affects functional genes related to potential assimilatory nitrate reduction (ANR) and related metabolic processes in soil microorganisms. Therefore, examining the influence of interactions between soil physicochemical properties and soil microbial community structure under wetland conversion could uncover new insights for managing the wetland ecosystem.

Longfeng urban wetland is located in the Western Songnen Plain in China and is considered a microcosm of wetland degradation in northeast China. Human activities, including urban construction, agricultural development, and Daqing petroleum field exploitation, have led to the degradation of the wetland [23]. Anthropogenic activities strongly affect the ecological security of the urban ecosystem. Although soil bacterial communities can be driven by changes in environmental conditions and spatial factors, there is limited progress in understanding what are the key factors that manipulate the soil bacterial communities in urban wetlands. Previous work has demonstrated how wetland submerged vegetation affected the functional capacity of microbial communities [24]. Yi et al. [25] indicated that urbanization could directly or indirectly affect environmental variables that are responsible for changes in bacterial communities. In addition, land use changes have been considered to be an important competitive element that drives microbial community changes in Sanjiang plain, northeastern China [26]. Therefore, it is crucial to elucidate the effects of land conversion on soil microbial communities in urban wetlands.

In this study, we examined five land-use types in the Longfeng nature reserve, including woodland (WL), swamp wetland (SW), farmland (FL), meadow wetland (MW), and alkaline land (AL), to (1) determine the response of soil microbial community composition and diversity to land conversion; (2) investigate the changes in predicted genes of metabolic pathways in soil microbial communities under land conversion; (3) explore soil factors influencing soil microbial communities under land conversion. The findings of this study will improve our understanding of microbial response to wetland degradation and support efforts geared towards optimizing urban wetland conservation management.

2. Materials and Methods

2.1. Study Area and Soil Sampling

This study was performed in the Longfeng wetland (125°04′59.1′′–125°14′05.6′′ E; 46°26′50.3′′–46°32′00.3′′ N) located in Daqing, Heilongjiang Province, western Songnen Plain, China. Longfeng wetland is one of the largest urban wetlands in China. It has a continental monsoon climate with a mean annual temperature of 4.5 °C and annual precipitation of 435 mm. In the past decades, swamp wetlands have been converted into degraded wetlands and other forms of land use due to increased agricultural activities and overgrazing [27]. In this study, the experimental sites representing five land-use types were randomly divided into three technical replicates. The five land-use types included: (a) woodland, WL; (b) swamp wetland, SW; (c) farmland, FL; (d) meadow wetland, MW; and (e) alkaline land, AL. The woodland fields were covered by *Populus simoni*, whereas swamp wetland was predominated by *Phragmites communis* and *Carex lasiocarpa*. The main crops in the farmland were soybean (*Glycine max*), which were fertilized by nitrogen, phosphorus, and potassium. The meadow wetland and alkaline land fields were planted with *Leymus chinensis* and *Suaeda glauca*, respectively.

The soil was collected randomly using a spade and a soil auger (10 cm deep × 5 cm diameter). In all plots, five specimens were uniformly taken and combined into a composite sample. In total, 15 samples (five levels × 3 repetitions) were collected in plastic bags and sieved to remove residual vegetative tissues using a sieve with 2 mm mesh, then kept at −20 °C in an icebox before further processing for subsequent DNA extraction.

2.2. Measurement of Soil Physicochemical Properties

After sieving, 15 samples (five levels × 3 repetitions) were stored at 4 °C for the initial soil physicochemical analysis. Soil moisture content (MC) was measured by oven-drying the soil at 105 °C for 48 h [28]. Soil pH and electrical conductivity (EC) were determined from the supernatant (1:5; soil: water) using a pH meter (Hach Company, Loveland, CO, USA). The SOM content was measured using the potassium dichromate oxidation heating method [29]. Total nitrogen (TN, g kg^{-1}) was determined using a C/N analyzer (Elementar, Langenselbod, Germany) [30]. Total phosphorus (TP, g kg^{-1}) and total potassium (TK, g kg^{-1}) were determined using a spectrophotometer (7200, UNICO, Franksville, WI, USA) and atomic absorption spectrometer (IRIS Advantage-ER, Thermo Jarrell Ash Corporation) after digestion with H_2SO_4-$HClO_4$ and Na_2CO_3 solution, respectively [31,32]. The exchange sodium percent (ESP) was calculated as the percentage of exchangeable sodium divided by the cation exchange capacity [33].

2.3. DNA Extraction and Sequencing

The DNA was extracted from 0.5 g of each soil sample using a DNA Extraction Kit (D5625-01) (Omega Bio-Tek, Norcross, GA, USA) according to the manufacturer's instructions. The integrity and quality of the extracted DNA were assessed by agarose gel electrophoresis and NanoDrop spectrophotometer (ND-1000, Thermo Fisher Scientific, Waltham, MA, USA). The primers used to bacterial DNA were 338F and 806R, targeting the V3-V4 region [34]. Meanwhile, the primers for amplifying fungal DNA were ITS1F and ITS2F, targeting the ITS region [35]. Finally, equal amounts of the PCR amplicons were sequenced on the Illumina MiSeq platform at Personal Biotechnology Co. Ltd. (Shanghai, China). After sequencing, the merged reads were processed for quality control and imported into QIIME2 following the user manual (http://docs.qiime2.org/2019.4/tutorials, accessed on 13 October 2020), with slight modification. The raw data were stored in the NCBI database under the Sequence Read Archive (SRA), accession number PRJNA748990.

2.4. Statistical Analysis

Soil physicochemical parameters and microbial community taxa were compared using a one-way analysis of variance (ANOVA) followed by the Least Significant Difference (LSD) test ($p < 0.05$) in SPSS 22.0 software (SPSS, Chicago, IL, USA). Tukey's HSD was used to determine significant differences at $p < 0.05$. Spearman's correlation analysis of environmental factors and dominant bacteria and fungi was performed in R (v3.2.0) [36]. Alpha diversity indices, including Shannon diversity and Chao1 richness index, were evaluated using QIIME2. Beta diversity was detected by hierarchical clustering and principal coordinate analysis (PCoA). The Bray–Curtis distance was used to estimate the differences in bacterial and fungal community structure among different land-use types [37]. LDA effect size (LEfSe) technique was performed to identify significantly differing biomarkers between groups. Redundancy analysis (RDA) of the soil physicochemical properties and the dominant microbial community was executed on CANOCO 5.0 software (Microcomputer Power, Ithaca, NY, USA) [38]. Variance partitioning analysis (VPA) was conducted by R using the "vegan" package to explore the contributions of soil variables to the composition of the soil microbial community. Phylogenetic investigation of microbial communities by the reconstruction of unobserved states 2 (PICRUSt2) and FUNGuild was used to categorize and predict bacterial and fungal functions [39]. All the variables were tested for normality and homoscedasticity before analysis, and log transformations were applied to meet these criteria where necessary.

3. Results

3.1. Effect of Land-Use Type on Soil Physicochemical Properties

Significant differences in soil physicochemical properties were observed between the various land-use types (Figure 1, $p < 0.05$). The highest value of MC (67%) was observed in the soil samples from SW, followed by WL (31%) and MW (24%). Meanwhile, SW held a SOM content of 23.12 g kg^{-1}, which was significantly higher than other land-use types ($p < 0.05$). The highest soil pH, EC, and ESP (8.96, 1780.56 µs cm^{-1}, and 45.32%) were observed in AL and were significantly higher than those in the other land-use types ($p < 0.05$). The soil pH of various soil samples indicated that Longfeng wetland soil was slightly to moderately alkaline. The order of the mean value of soil pH of the four land-use types was as follows: AL > FL > MW > SW > WL. Compared with other land-use types, FL had the highest TN, TP, and TK of 1.82, 0.71, and 22.65 g kg^{-1}, respectively (Figure 1).

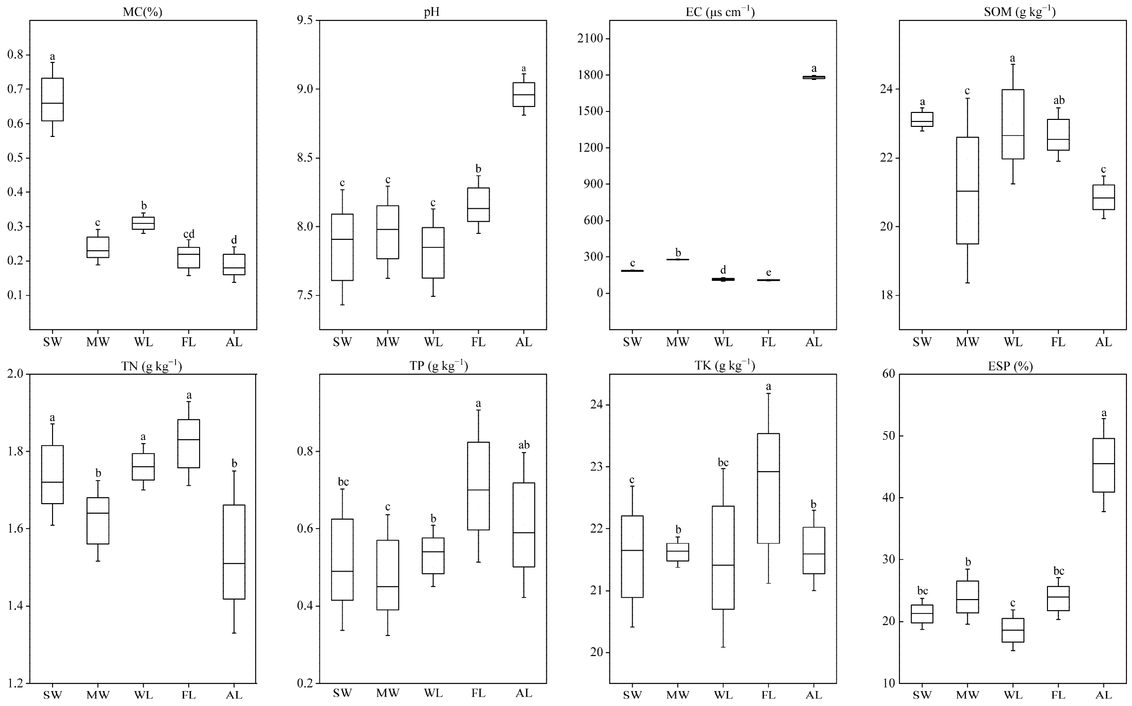

Figure 1. Soil characteristics under different land-use types. Different letters indicate a significant difference among different treatments ($p < 0.05$). MC, moisture content; SOM, soil organic matter; TN, total nitrogen; TP, total phosphorus; TK, total kalium; ESP, exchange sodium percent. SW, swamp wetland; MW, meadow wetland; WL, woodland; FL, farmland; AL, alkaline land.

3.2. Diversity of Soil Microbial Communities under Different Land-Use Types

A total of 1,791,556 bacterial and 1,812,377 fungal sequences were obtained after quality-filtering. Alpha diversity index represents species diversity in the samples, while

Shannon and Chao1 indices describe the diversity and richness of species in the soil microbial community. Shannon and Chao1 indices were used to determine the complexity of microbial communities among the various samples (Figure 2a,b). Significant differences in bacterial diversity and richness were observed between different land-use types ($p < 0.05$). AL had the lowest value of bacterial Shannon and Chao1 indices, while WL had the highest value among different land-use types. However, no significant difference was observed in the fungal Shannon index ($p > 0.05$). Notably, the maximum value of the fungal Chao1 index was observed in WL.

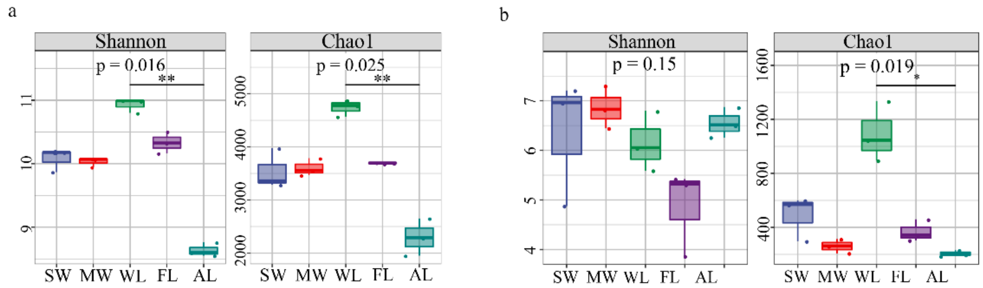

Figure 2. Diversity of soil microbial communities. (**a**) Bacterial and (**b**) fungal community α-diversity index in different land-use types. SW, swamp wetland; MW, meadow wetland; WL, woodland; FL, farmland; AL, alkaline land. * correlation significant at 0.05 level. ** correlation significant at 0.01 level.

Furthermore, PCoA analysis was used to reflect soil bacterial and fungal community beta-diversity, which showed that the first two dimensions explained 52.9% and 33.6% of the total variance, respectively. Adonis analysis of the 16 S rRNA gene and ITS data using the Bray–Curtis distance method revealed that the bacterial and fungal community structures and compositions were significantly different across various land-use types (Figure S1a,b). Interestingly, soil bacterial and fungal communities showed a clear separation from other land-use types.

3.3. Composition of Soil Microbial Community under Different Land-Use Types

At the phylum level, 48 bacterial phyla and 14 fungal phyla were identified among the soil samples tested (Figure 3). Proteobacteria (23.17%–48.05%) was the most predominant bacterial phyla (>5%), followed by Actinobacteria (7.36%–26.76%), Chloroflexi (10.67%–15.9%), Acidobacteria (5.63%–11.03%), Gemmatimonadetes (3.68–16.05%), and Bacteroidetes (3.81%–11.14%) (Figure 3a). On the other hand, Rokubacteria (0.1%–3.99%), Planctomycetes (0.76%–1.97%), Firmicutes (0.55%–3.51%), and Patescibacteria (0.37%–4.13%) were the least abundant (>0.1% but <5%). Specifically, Proteobacteria was the most predominant bacterial phylum in WL (48.05%) and the lowest (23.17%) in AL but exhibited no significant difference in SW (44.25%). SW showed the highest relative abundance of Bacteroidetes but the lowest abundance of Actinobacteria. Notably, the relative abundance of Gemmatimonadetes and Firmicutes significantly increased in AL, while Proteobacteria decreased. At the genus level, the bacterial community composition differed significantly across the soil samples (Figure S2a). For example, the most abundant bacterial genus in FL and MW was *Subgroup_6* (4.67%, 4.99%), while *Thiobacillus* was the most abundant in WL and SW at 5.6% and 3.98%, respectively. Moreover, *PAUC43f* exhibited the highest abundance (6.48%) in AL. Compared with the other land-use types, AL significantly decreased the relative abundance of *Subgroup_6*, *BIrii41*, *MND1*, *Haliangium*, and *Gaiella* while increasing the relative abundance of *Aquabacterium*. Furthermore, LEfSe analysis was used to confirm whether land conversion can significantly alter bacterial and fungal communities, particularly the effect of various land-use types on bacterial and fungal communities. The results revealed that Bacteroidetes were enriched in SW while Acidobacteria were enriched in MW. Proteobacteria were enriched in WL, while Actinobacteria and Gemmatimonadetes were enriched in AL (Figure 4a).

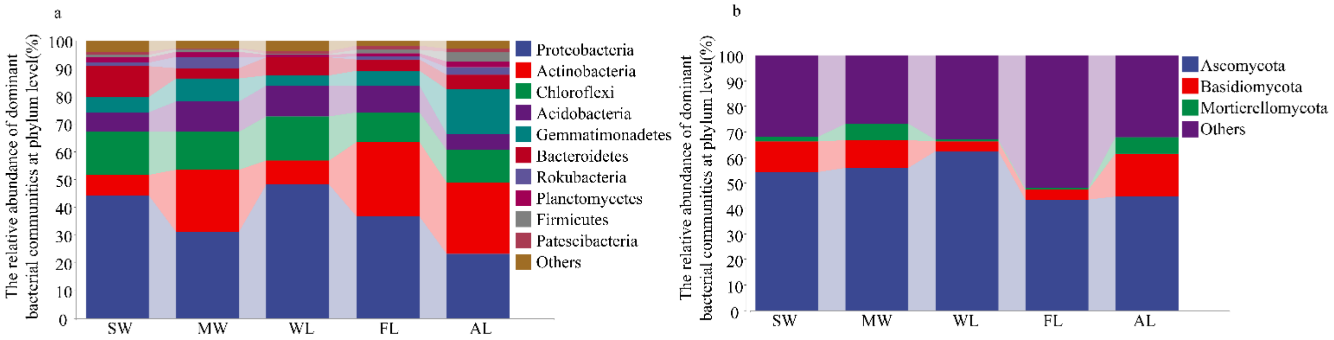

Figure 3. Microbial community composition at the phylum level. (**a**) Bacterial community abundance; (**b**) fungal community abundance. Different colors indicate different microorganisms at the phylum level. SW, swamp wetland; MW, meadow wetland; WL, woodland; FL, farmland; AL, alkaline land.

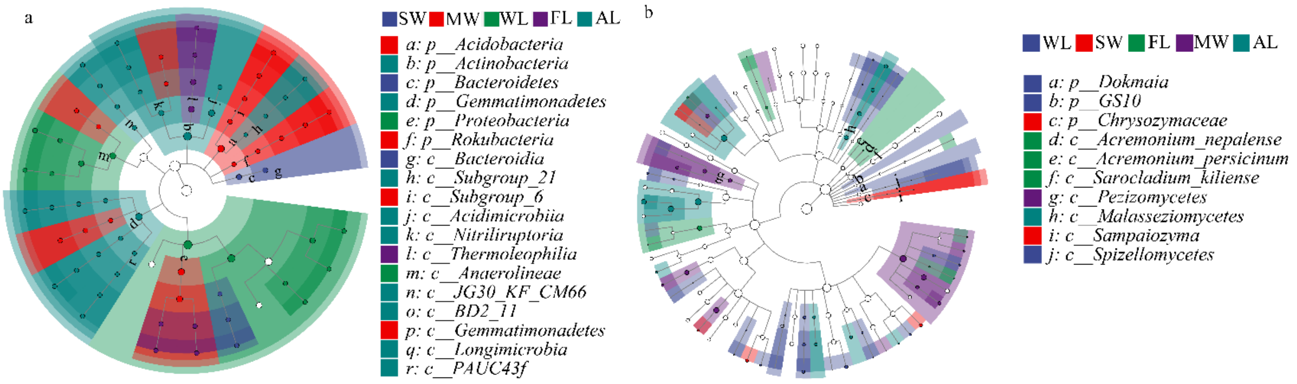

Figure 4. Cladogram of soil microbial abundance in different treatments identifies the significantly different abundant taxa. (**a**) Bacterial community abundance; (**b**) fungal community abundance. SW, swamp wetland; MW, meadow wetland; WL, woodland; FL, farmland; AL, alkaline land.

Predominant fungal phyla were Ascomycota, Basidiomycota, and Mortierellomycota, accounting for 52.07%, 9.42%, and 3.27% of the total fungal communities, respectively (Figure 3b). Ascomycota was the most predominant fungal phylum in WL (62.41%) and the lowest (43.36%) in FL. However, no significant differences in the dominant fungal phyla were found among the different study sites. In total, 13 genera (*Phoma*, *Mortierella*, *Plectosphaerella*, *Didymella*, *Malassezia*, *Humicola*, *Acremonium*, *Pichia*, *Phialemoniopsis*, *Aspergillus*, *Tingoldiago*, *Echria*, *Trichoderma*) exhibited >1% abundance (Figure S2b). Concerning the genus level, the relative abundance of *Malassezia* and *Aspergillus* decreased significantly in SW. However, a significant increase in *Phoma* abundance was observed in WL. Furthermore, LEfSe analysis showed that *GS10* was enriched in WL, while *Sclerostagonospora* and *Malasseziomycetes* were enriched in SW and AL, respectively (Figure 4b).

3.4. Associations between Microbial Communities and Soil Physicochemical Properties under Different Land-Use Types

Spearman's analysis showed that SOM and TN were the key drivers of soil bacterial and fungal diversity (Figure 5b). RDA analysis was employed to determine the relationship between microbial phylum composition and soil physicochemical parameters (Figure 5c,d). Two axes explained 90.3% of the bacterial community variations in RDA1 (46.3%) and RDA2 (21.7%) (Figure 5c). Here, ESP, pH, EC, SOM, TN, and MC were the dominant drivers of soil bacterial community composition. VPA analysis was used to analyze the comprehensive contribution of soil physicochemical parameters to the soil bacterial community. Based on the results, the ESP value explained the high variability of 40.6%, while MC, SOM, EC, pH, TN, TP, and TK alone explained 19.6%, 12.1%, 8.1%, 4.1%, 3.2%, 1.4%, and 1.3%, respectively (Figure S3a). Regarding the fungal communities, RDA1 and RDA2 accounted for 64.4% and 6.5% of the variations in the results (Figure 5d). TN and SOM were the major factors affecting the fungal community. The influence of soil physicochemical parameters on soil fungal community structure decreased in the order of TN > ESP > SOM > MC > pH > EC > TP > TK (Figure S3b). Specifically, Spearman's rank correlations illustrated that SOM and TN were positively correlated with Proteobacteria abundance, while soil pH and ESP were positively associated with the abundance of Actinobacteria and Acidobacteria (Figure 5a). For fungi, SOM was positively associated with Basidiomycota and Mortierellomycota (Figure 5a).

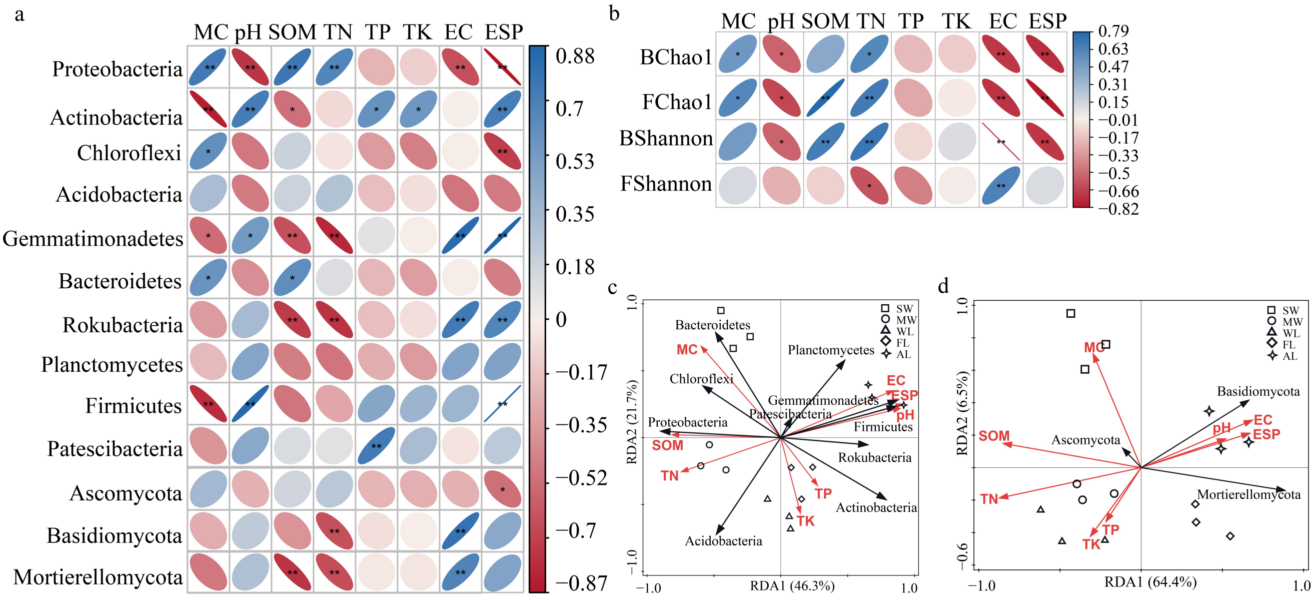

Figure 5. Spearman correlation analyses between soil characteristics and (**a**) dominant microbial phyla and (**b**) microbial community alpha diversity and redundancy analysis (RDA) on soil dominant (**c**) bacteria and (**d**) fungi at the phylum level constrained by soil characteristics variables. MC, moisture content; SOM, soil organic matter; TN, total nitrogen; TP, total phosphorus; TK, total kalium; ESP, exchange sodium percent. SW, swamp wetland; MW, meadow wetland; WL, woodland; FL, farmland; AL, alkaline land. * correlation significant at 0.05 level. ** correlation significant at 0.01 level.

3.5. Microbial Functional Responses to Different Land-Use Types

The PICRUSt2 metagenomic was used to predict the functions of the bacterial community at level 2 KEGG orthologues (KOs). Specifically, the level 1 KO groups included metabolism, organismal systems, human diseases, environmental information processing, cellular processes, and genetic information processing (Figure 6). The top 10 functions were analyzed in level 2. Among the functions, amino acid metabolism had the highest proportion, followed by carbohydrate metabolism and the metabolism of cofactors and vitamins. The genes associated with glycan biosynthesis and metabolism were more abundant in SW than in other land-use types. In addition, cofactors and vitamins were significantly higher in AL than in other study sites, while Xenobiotics biodegradation and metabolism were highest in FL.

FUNGuild analysis was conducted for functional prediction of fungal communities under land conversion. The results revealed that undefined saprotroph, animal pathogen, endophyte, and plant pathogen were the dominant functional guilds (Figure 7). Notably, significant differences in functions were observed under different land-use types. For instance, animal pathogen and plant pathogen were enriched in AL (37.46%, 35.85%), while undefined saprotroph mainly existed in MW (30.55%). In addition, Ectomycorrhizal was predominant in WL (51.98%). Wetland conversion increased the relative abundance of pathogenic fungi.

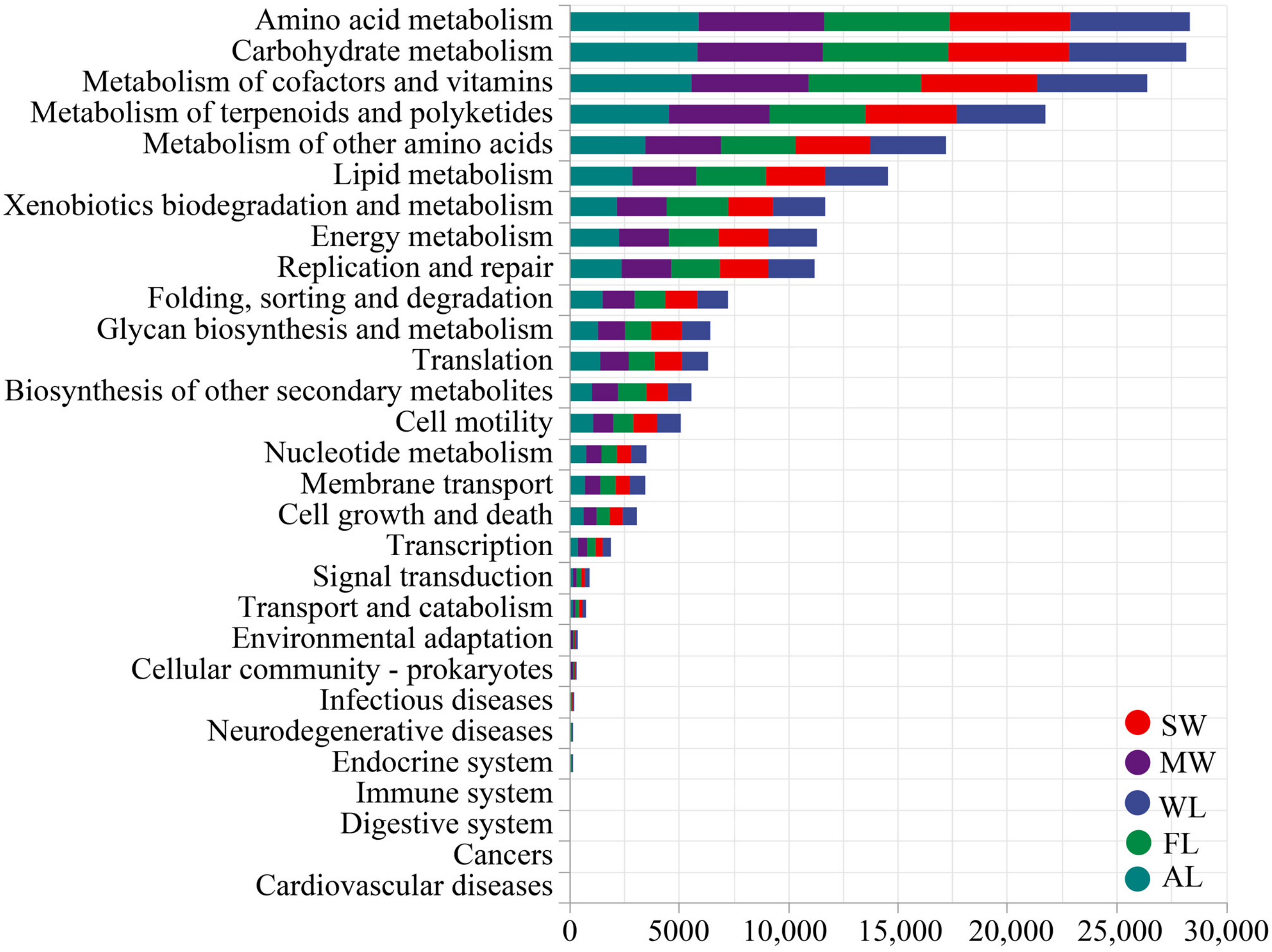

Figure 6. Relative abundance of bacterial metabolic pathways predicted by PICRUSt2. SW, swamp wetland; MW, meadow wetland; WL, woodland; FL, farmland; AL, alkaline land.

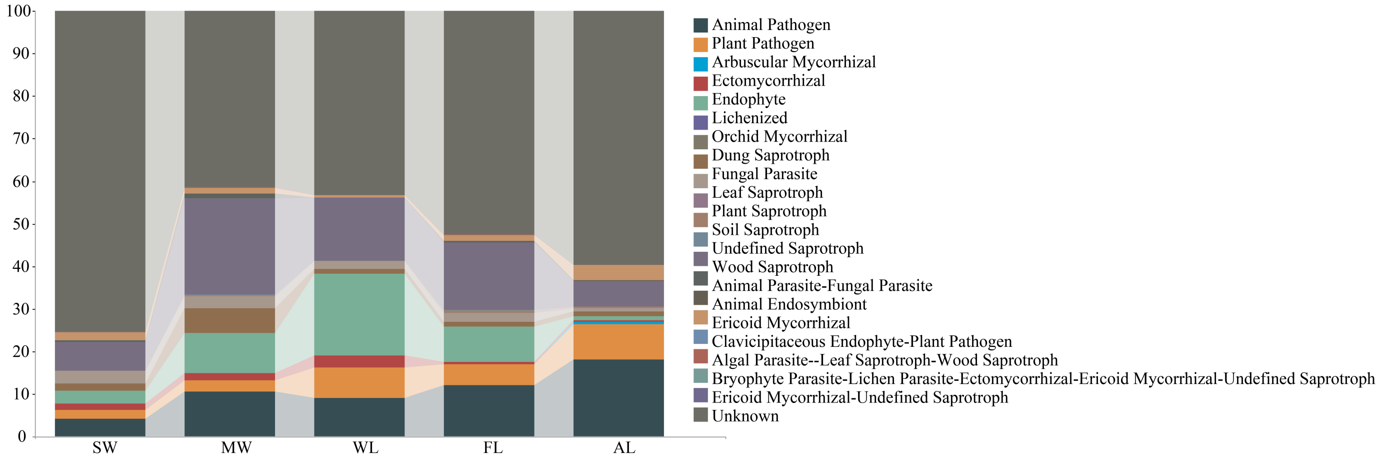

Figure 7. Variations in the composition of fungal functional groups inferred by FUNGuild. SW, swamp wetland; MW, meadow wetland; WL, woodland; FL, farmland; AL, alkaline land.

4. Discussion

4.1. Land-Use Type Influence Soil Physicochemical Properties

Recent studies have shown that land use pattern conversion affects soil physicochemical properties either directly or indirectly [40]. In this study, the soil pH of all the sites was alkaline (7.81–8.96), while the nutrient concentrations of the alkaline soils differed among the land-use types. AL had the highest pH (Figure 1), consistent with Wang et al. [8], who revealed that soil pH increases with the salinization level. Meanwhile, many studies have suggested that saline-alkali soil has the lowest SOM content mainly because of poor vegetation growth [32], which is consistent with the results of this study to some extent. In contrast, high SOM contents were observed in SW soil, similar to previously reported findings [41,42]. Compared to SW, other land-use types had lower soil organic carbon (Figure 1). A previous study showed that vegetation in a natural wetland was gradually replaced by a meadow or other degradation plants as the groundwater levels declined [43]. Natural wetland is usually converted to different land-use types, including farmland, meadow wetland, and saline-alkaline land, resulting in carbon losses [44]. Meanwhile, SW soil had the highest level of MC, while AL had the lowest. Moisture content is a key indicator of urban wetland degradation [45]. In this study, EC and ESP were significantly higher in AL than in other land-use types, consistent with the previous studies [8], suggesting that EC and ESP could influence saline-alkaline land. Land-use conversion significantly affects soil physicochemical properties, which remarkably influence soil microbial diversity [16]. Overall, these results illustrate that soil physicochemical properties play a crucial role in stabilizing the soil ecosystem [46].

4.2. Land-Use Type Influence on the Composition and Structure of Soil Microbial Community

Land-use pattern conversion influences soil microbial communities by affecting the soil physicochemical properties needed to maintain ecosystem functions [47]. Human activities in the wetland ecosystems are the main factors shaping the soil microbial community [48]. In this study, all the indices of bacterial alpha diversity, including the Shannon and Chao 1 indices, were highest in WL and lowest in AL (Figure 2a). These results agree with previous studies, which reported limited access to soil nutrients in AL soil due to low cation exchange capacity, resulting in the lowest bacterial community diversity. Intriguingly, the Chao1 index of the fungal community was highest in WL, while the Shannon index did not differ significantly among the various land-use types (Figure 2b). Soil fungal richness has been shown to reduce as primary wetland or forest sites are converted to other land-used types [49]. This might be due to changes in soil properties and nutrient supply caused by land conversion. As previously stated, vegetation diversity, biomass, and abiotic factors in farmland can reduce the richness of the fungal community [46]. The NMDS analysis revealed differences in the soil microbial communities across various land-use types (Figure 2a,b), which agrees with a previous study [50].

In this study, the predominant bacterial phyla included Proteobacteria, Actinobacteria, Chloroflexi, Acidobacteria, Gemmatimonadetes, and Bacteroidetes (Figure 3a). These bacterial phyla are highly adapted to land conversion and are key drivers of those ecosystems [51]. For instance, Proteobacteria typically occur in high abundance in most land-use types because they utilize diverse carbon sources and exhibit fast growth [10], which is consistent with our results. Moreover, Gemmatimonadetes and Firmicutes were enriched in AL, consistent with the recent findings, indicating that Gemmatimonadetes are tolerant to saline conditions [11]. Furthermore, Firmicutes are considered ideal for probing halophilic enzymes and metabolic pathways of saline soils [8]. Additionally, the abundance of certain bacterial taxa varied between various land-use types. For example, Acidobacteria were the indicator group in SW and exhibited high specificity in other habitats (Figure 5a). Acidobacteria have been shown to flourish in acidic soils [42]. However, we still found a large portion group in SW with a pH of 7.9. Ascomycota and Basidiomycota exert different effects on soil properties. They are the dominant phyla in most land-use types with significant roles in determining the fungal community structure [52]. Notably, Ascomycota belongs to the saprotrophic fungi, which can degrade lignocellulose and soil carbon fractions [53]. Compared with the other land-use types, WL has more lignin content, thus promoting the growth of Ascomycota relative to other fungal phyla (Figure 3b). Thus, WL supported K-selected saprotrophic fungi.

4.3. Correlation between Soil Microbial Communities and Soil Variables under Different Land-Use Types

Recent research demonstrates that soil properties play a crucial role in determining the diversity and composition of soil microbial communities [54]. In this study, ESP, pH, EC, SOM, TN, and MC were the pivotal drivers of soil bacterial community (Figure 5c), consistent with Bradley and Martiny [55], while TN and SOM could influence soil fungal community strongly (Figure 5d), which concurs with Gao et al. [56]. VPA showed that ESP was the key factor in the abundance of soil bacterial communities while TN was vital for the fungal communities (Figure S2), indicating that TN and ESP mainly limited soil microbial community abundance under land-use conversion. Consistent with previous studies, the bacterial community alpha index decreased significantly with the increase in ESP [33]. The accumulation of salts in the soil can lead to death or dormancy of microbial communities not adapted to salt stress environments. Likewise, Lu et al. [42] showed that TN plays a primary role in regulating the soil microbial community [8]. Other studies have also postulated that TN could contribute to the microbial utilization of substrates, thereby enhancing enzyme activity [57]. The present study found that pH was the second most influential factor affecting the soil bacterial community (Figure 6a), similar to previous findings [58]. Soil pH is an excellent predictor of soil microbial community patterns and could shape soil microbial communities under various forms of land use [50].

At the phylum level, Proteobacteria was positively correlated with SOM and TN, consistent with the conclusions by Delgado-Baquerizo et al. [59]. Proteobacteria prefer eutrophic soil with high contents of C and N [59]. Other studies have shown that the abundance of Actinobacteria and Acidobacteria decreases with a rise in soil pH [8]. This is because Acidobacteria is oligotrophic bacteria that prefer acidic soil [60]. Indeed, soil factors are directly correlated to soil pH variations [61]. Therefore, Actinobacteria are sparse under nutritionally deficient conditions because they need nutrients for heterotrophic or chemoautotrophic reasons [62]. Like bacteria, land use alters the availability of soil nutrients by regulating soil enzyme activities [57]. Previous studies indicated that land-use type shifts the input of C and N [4]. This change influences the abundance of Basidiomycota, thereby decreasing the transcription of gene encoding enzymes that depolymerize cell wall lignin [52]. Similar results were obtained in this study, indicating that land-use type significantly influences the abundance and composition of soil microbial communities.

4.4. Prediction of Metabolic Functions of Soil Bacteria under Different Land-Use Types

In this study, the metabolic functions of soil bacteria differed across various land-use types (Figure 7). The major metabolic functions in the microbiomes included carbohydrate, amino acid cofactors, and vitamin metabolisms, consistent with previous studies [19,63]. Compared to the other four land-use types, the predicted abundance of xenobiotic metabolism was significantly enriched in FL, which is in agreement with Grandy and Neff [64]. This could be because farmland requires more nutrients, resulting in a greater abundance of genes involved in xenobiotic biodegradation and metabolism [19]. Meanwhile, glycan metabolism was highest in SW, which can be attributed to SW holding the highest SOM [65]. In addition to accelerating glycan metabolism, the high SOM in SW also enhances cell viability. The present study also revealed high membrane transport in AL relative to other soil types (Figure 1). This could be because salinity and alkali stresses facilitated membrane transport, in particular, soil microbes [50].

Various functional characteristics of the fungal community revealed that the enriched pathogenic fungi abundances accounted for the largest proportion in the land-use types except for SW. Another possible explanation for this is the interference of human activities and foreign substances under land-use conversion; this is consistent with a previous study that postulated that an increased proportion of pathogenic fungi might be linked to the degraded patches in the degraded meadow [66]. Pathogenic fungi produce substances that attack and destroy the structure and function of host cells. The weakened physiological defense function of host cells causes sub-health or even deterioration of the soil environment. This can affect the ecological environment and agricultural productivity, spread through the food chain, and threaten human and livestock health [67]. Meanwhile, another important finding of the present study is that Ectomycorrhizal fungi were enriched in WL, which agrees with previous studies that showed that Ectomycorrhizal fungi ubiquitously exist in woodland soil [68]. However, due to the limitations of PICRUSt2 and FUNGuild prediction analysis, metagenomic profiling should be conducted in the future to validate the findings of this study. Further research should determine the correlation between the soil microbial community and functions to investigate the link between wetland conversion and ecological processes.

5. Conclusions

This study reveals the impacts of land-use type on various aspects of the soil microbial community. Our results show that land conversion can reduce the soil quality and nutrients of a natural wetland. Woodland had the highest bacterial alpha diversity and fungal community richness index. The most dominant bacterial and fungal phyla were Proteobacteria, Actinobacteria, and Ascomycota. More importantly, land conversion affected bacterial community composition at the phylum level, while the fungal community did not change significantly. ESP can predict bacterial community, whereas TN is the key factor influencing the soil fungal community in this study. In addition, the relative abundance of bacterial and fungal functional groups also changed significantly under wetland conversion. This study provides new insights into understanding the mechanism of microbial variation under land conversion and offers guidelines for sustainable soil development.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/f13071148/s1. Figure S1: The nonmetric multidimensional scaling ordinations based on bruy-cuits distance of (a) bacterial and (b) fungal communities in different land-use types. SW, Swamp wet-land; MW, Meadow wetland; WL, Woodland; FL, Farmland; AL, Alkaline land; Figure S2: Soil (a) bacterial and (b) fungal community composition at the genus level. Different colors indicate different microorganisms at the levels. SW, Swamp wetland; MW, Meadow wetland; WL, Woodland; FL, Farmland; AL, Alkaline land; Figure S3: Variance partitioning analysis (VPA) showing the effects of soil factors on soil microbial community. (a) Bacterial community; (b) fungal community. SW, Swamp wetland; MW, Meadow wetland; WL, Woodland; FL, Farmland; AL, Alkaline land. MC, moisture content; SOM, soil organic matter; TN, total nitrogen; TP, Total Phosphorus; TK, Total Kalium; ESP, Exchange sodium percent; Table S1: The relative abundance (>1%) of the total metabolic pathways at level 2; Table S2: Relative abundance (%) of fungal functional group (guild) from selected soil samples inferred by FunGuild.

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References

1. Smith, P.; House, J.; Bustamante, M.; Sobocká, J.; Harper, R.; Pan, G.-X.; West, P.; Clark, J.; Adhya, T.; Rumpel, C.; et al. Global change pressures on soils from land use and management. *Glob. Chang. Biol.* **2016**, *22*, 1008–1028. [CrossRef] [PubMed]
2. Keesstra, S.; Mol, G.; De Leeuw, J.; Okx, J.; Molenaar, C.; Cleen, M.; Visser, S. Soil-related sustainable development goals: Four concepts to make land degradation neutrality and restoration work. *Land* **2018**, *7*, 133. [CrossRef]
3. Wang, Y.; Jia, Y.; Li, Z.; Tao, J.; Lin, L.; Chen, K.; Zhenyuan, L.; Tan, X.; Zhang, Q. Trophic structure in response to land use in subtropical streams. *Ecol. Indic.* **2021**, *127*, 107746. [CrossRef]
4. Mganga, K.; Razavi, B.; Kuzyakov, Y. Land use affects soil biochemical properties in Mt. Kilimanjaro region. *Catena* **2016**, *141*, 22–29. [CrossRef]
5. Bai, Y.; Wong, C.; Jiang, B.; Hughes, A.; Wang, M.; Wang, Q. Developing China's ecological redline policy using ecosystem services assessments for land use planning. *Nat. Commun.* **2018**, *9*, 3034. [CrossRef]
6. Zedler, J.; Kercher, S. Wetland resources: Status, trends, ecosystem services, and restorability. *Annu. Rev. Environ. Resour.* **2005**, *15*, 39–74. [CrossRef]
7. Camacho, V.; Tello-Alcaide, E.; Wootton, A.; Valencia-Barrera, E. Land use change and urban ecosystem services: A case study of urban wetlands in a rapidly sprawling city in the highlands of Chiapas, Mexico. *J. Manag. Sustain.* **2019**, *9*, 67. [CrossRef]
8. Wang, S.; Sun, L.; Ling, N.; Zhu, C.; Chi, F.; Li, W.; Hao, X.; Zhang, W.; Bian, J.; Chen, L.; et al. Exploring soil factors determining composition and structure of the bacterial communities in saline-alkali soils of Songnen Plain. *Front. Microbiol.* **2020**, *10*, 2902. [CrossRef]
9. Xu, S.; Liu, X.; Li, X.; Tian, C. Soil organic carbon changes following wetland restoration: A global meta-analysis. *Geoderma* **2019**, *353*, 89–96. [CrossRef]
10. An, J.; Liu, C.; Wang, Q.; Yao, M.; Rui, J.; Zhang, S.; Li, X. Soil bacterial community structure in Chinese wetlands. *Geoderma* **2019**, *337*, 290–299. [CrossRef]
11. Guan, Y.; Jiang, N.; Wu, Y.; Yang, Z.; Bello, A.; Yang, W. Disentangling the role of salinity-sodicity in shaping soil microbiome along a natural saline-sodic gradient. *Sci. Total Environ.* **2020**, *765*, 142738. [CrossRef] [PubMed]
12. Bacani, V.; Sakamoto, Y.; Quénol, H.; Vannier, C.; Corgne, S. Markov chains–cellular automata modeling and multicriteria analysis of land cover change in the Lower Nhecolândia subregion of the Brazilian Pantanal wetland. *J. Appl. Remote Sens.* **2016**, *10*, 016004. [CrossRef]
13. Wu, Y.C.; Tan, L.; Liu, W.; Wang, B.; Cai, Y.; Lin, X. Profiling bacterial diversity in a limestone cave of the western Loess Plateau of China. *Front. Microbiol.* **2015**, *6*, 244. [CrossRef] [PubMed]
14. Kang, E.; Li, Y.; Zhang, X.; Yan, Z.; Wu, H.; Li, M.; Yan, L.; Zhang, K.; Wang, J.; Kang, X. Soil pH and nutrients shape the vertical distribution of microbial communities in an alpine wetland. *Sci. Total Environ.* **2021**, *774*, 145780. [CrossRef]
15. Bardgett, R.; Putten, W. Belowground biodiversity and ecosystem functioning. *Nature* **2014**, *515*, 505–511. [CrossRef]
16. Sheng, Y.; Wang, H.; Wang, M.; Li, H.; Li, X.; Pan, F.; Chen, X.; Shen, X.; Mao, Z. Effects of soil texture on the growth of young apple trees and soil microbial community structure under replanted conditions. *Hortic. Plant J.* **2020**, *6*, 123–131. [CrossRef]
17. Sleator, R.D.; Shortall, C.; Hill, C. Metagenomics. *Lett. Appl. Microbiol.* **2008**, *47*, 361–366. [CrossRef]
18. Tiwari, S.; Singh, C.; Boudh, S.; Rai, P.K.; Gupta, V.K.; Singh, J.S. Land use change: A key ecological disturbance declines soil microbial biomass in dry tropical uplands. *J. Environ. Manag.* **2019**, *242*, 1–10. [CrossRef]
19. Guo, Y.; Chen, X.; Wu, Y.; Zhang, L.; Cheng, J.; Wei, G.; Lin, Y. Natural revegetation of a semiarid habitat alters taxonomic and functional diversity of soil microbial communities. *Sci. Total Environ.* **2018**, *635*, 598–606. [CrossRef]
20. Lauber, C.; Strickland, M.; Bradford, M.; Fierer, N. The influence of soil properties on the structure of bacterial and fungal communities across land-use types. *Soil Biol. Biochem.* **2008**, *40*, 2407–2415. [CrossRef]
21. Guan, X.; Wang, J.; Zhao, H.; Wang, J.; Luo, X.; Liu, F.; Zhao, F. Soil bacterial communities shaped by geochemical factors and land use in a less-explored area, Tibetan Plateau. *BMC Genom.* **2013**, *14*, 820. [CrossRef] [PubMed]
22. Liu, Y.; Ren, Z.; Qu, X.; Zhang, M.; Yu, Y.; Zhang, Y.; Peng, W. Microbial community structure and functional properties in permanently and seasonally flooded areas in Poyang Lake. *Sci. Rep.* **2020**, *10*, 4819. [CrossRef] [PubMed]
23. Lee, K.H.; Wang, Y.F.; Li, H.; Gu, J.D. Niche specificity of ammonia-oxidizing archaeal and bacterial communities in a freshwater wetland receiving municipal wastewater in Daqing, Northeast China. *Ecotoxicology* **2014**, *23*, 2081–2091. [CrossRef] [PubMed]
24. Wang, B.; Zheng, X.; Zhang, H.; Yu, X.; Lian, Y.; Yang, X.; Yu, H.; Hu, R.; He, Z.; Xiao, F.; et al. Metagenomic insights into the effects of submerged plants on functional potential of microbial communities in wetland sediments. *Mar. Life Sci. Technol.* **2021**, *3*, 405–415. [CrossRef]
25. Yi, X.; Ning, C.; Feng, S.; Gao, H.; Zhao, J.; Liao, J.; Peng, Y.; Zhao, S.; Liu, S. Urbanization-induced environmental changes strongly affect wetland soil bacterial community composition and diversity. *Environ. Res. Lett.* **2022**, *17*, 014027. [CrossRef]
26. Sui, X.; Zhang, R.; Frey, B.; Yang, L.; Li, M.H.; Ni, H. Land use change effects on diversity of soil bacterial, Acidobacterial and fungal communities in wetlands of the Sanjiang Plain, northeastern China. *Sci. Rep.* **2019**, *9*, 18535. [CrossRef]
27. Dong, C.; Shi, Y.; Wang, J.; Zeng, H.; Wang, W. Divergent responses of the soil bacteria community to multi-level nitrogen enrichment in temperate grasslands under different degrees of degradation. *Land Degrad. Dev.* **2021**, *32*, 3524–3535. [CrossRef]
28. Rao, D.; Meng, F.; Yan, X.; Zhang, M.; Yao, X.; Kim, K.S.; Zhao, J.; Qiu, Q.; Xie, F.; Zhang, W. Changes in soil microbial activity, bacterial community composition and function in a long-term continuous soybean cropping system after corn insertion and fertilization. *Front. Microbiol.* **2021**, *12*, 638326. [CrossRef]

29. Lu, R. *Soil and Agro-Chemical Analytical Methods*; China Agricultural Science and Technology Press: Beijing, China, 1999.
30. Rayment, G.; Higginson, F. *The Australian Handbook of Soil and Water Chemical Methods*; Inkata Press: Melbourne, Australia, 1992; Volume 63.
31. Jackson, M. *Soil Chemical Analysis*; Prentice-Hall: New York, NY, USA, 1958; Volume 46.
32. Adeloju, S.; Bond, A.; Briggs, M. Critical evaluation of some wet digestion methods for the stripping voltammetric determination of selenium in biological materials. *Anal. Chem.* **1984**, *56*, 2397–2401. [CrossRef]
33. Paliwal, K.V.; Maliwal, G.L. Prediction of exchangeable sodium percentage from cation exchange equilibria. *Geoderma* **1971**, *6*, 75–78. [CrossRef]
34. Kemp, P.; Aller, J. Bacterial diversity in aquatic and other environments: What 16S rDNA libraries can tell us. *FEMS Microbiol. Ecol.* **2004**, *47*, 161–177. [CrossRef]
35. Nilsson, R.H.; Ryberg, M.; Kristiansson, E.; Abarenkov, K.; Larsson, K.-H.; Kõljalg, U. Taxonomic reliability of DNA sequences in public sequence databases: A Fungal Perspective. *PLoS ONE* **2006**, *1*, e59. [CrossRef] [PubMed]
36. R Development Core Team. *R: A Language and Environment for Statistical Computing*; R Foundation for Statistical Computing: Vienna, Austria, 2012.
37. Zuur, A.F.; Ieno, E.N.; Smith, G.M. Principal coordinate analysis and non-metric multidimensional scaling. In *Analysing Ecological Data*; Springer: New York, NY, USA, 2007; pp. 259–264.
38. Morris, C. Multivariate analysis of ecological data using Canoco 5, 2nd Edition. *Afr. J. Range Forage Sci.* **2015**, *32*, 1–2. [CrossRef]
39. Nguyen, N.; Song, Z.; Bates, S.; Branco, S.; Tedersoo, L.; Menke, J.; Schilling, J.; Kennedy, P. FUN-Guild: An open annotation tool for parsing fungal community datasets by ecological guild. *Fungal Ecol.* **2015**, *20*, 241–248. [CrossRef]
40. Douglas, G.; Maffei, V.; Zaneveld, J.; Yurgel, S.; Brown, J.; Taylor, C.; Huttenhower, C.; Langille, M. PICRUSt2: An improved and extensible approach for metagenome inference. *bioRxiv* **2019**, 672295. [CrossRef]
41. Wu, Y.; Xu, N.; Wang, H.; Li, J.; Zhong, H.; Zong, C. Variations in the diversity of soil microbial community and structure under various categories of degradation wetland in Sanjiang Plain, northeastern China. *Land Degrad. Dev.* **2021**, *32*, 2143–2156. [CrossRef]
42. Lu, M.; Ren, Y.; Wang, S.; Tian, K.; Sun, X.; Peng, S. Contribution of soil variables to bacterial community composition following land use change in Napahai plateau wetlands. *J. Environ. Manag.* **2019**, *246*, 77–84. [CrossRef]
43. Ma, Q.; Cui, L.; Song, H.; Gao, C.; Hao, Y.; Luan, J.; Wang, Y.; Li, W. Aboveground and belowground biomass relationships in the Zoige peatland, Eastern Qinghai–Tibetan Plateau. *Wetlands* **2017**, *37*, 461–469. [CrossRef]
44. Liu, X.; Liu, Y.; Sun, L.; Sun, T. Effects of grassland degradation on vegetation and soil properties in the middle of the Songnen Plain. *Pratacultural Sci.* **2018**, *35*, 2347–2353. (In Chinese)
45. Pan, C.; Li, Y.; Xiaoya, Y.; Ren, S. Drivers of soil bacterial diversity in sandy grasslands in China. *Sci. Rep.* **2021**. [CrossRef]
46. McKinley, V.L. Effects of land use and restoration on soil microbial communities. In *Understanding Terrestrial Microbial Communities*; Springer: Cham, Switzerland, 2019; pp. 173–242.
47. Lauber, C.L.; Ramirez, K.S.; Aanderud, Z.; Lennon, J.; Fierer, N. Temporal variability in soil microbial communities across land-use types. *ISME J.* **2013**, *7*, 1641–1650. [CrossRef] [PubMed]
48. Dang, C.; Kellner, E.; Martin, G.; Freedman, Z.; Hubbart, J.; Stephan, K.; Kelly, C.; Morrissey, E. Land use intensification destabilizes stream microbial biodiversity and decreases metabolic efficiency. *Sci. Total Environ.* **2021**, *767*, 145440. [CrossRef] [PubMed]
49. Asmelash, F.; Bekele, T.; Belay, Z.; Kebede, F. Soil physicochemical property and arbuscular mycorrhizal fungi resilience to degradation and deforestation of a dry evergreen Afromontane forest in central Ethiopia. *Land Degrad. Dev.* **2021**, *32*, 3338–3350. [CrossRef]
50. Feng, H.; Wang, S.; Gao, Z.; Wang, Z.; Ren, X.; Hu, S.; Pan, H. Effect of land use on the composition of bacterial and fungal communities in saline–sodic soils. *Land Degrad. Dev.* **2019**, *30*, 1851–1860. [CrossRef]
51. Kraychenko, A.N.; Guber, A.K.; Razavi, B.S.; Koestel, J.; Quigley, M.Y.; Robertson, G.P.; Kuzyakov, Y. Microbial spatial footprint as a driver of soil carbon stabilization. *Nat. Commun.* **2019**, *10*, 10. [CrossRef]
52. Zhao, F.; Ren, C.; Zhang, L.; HHan, X.; HYang, G.; Wang, J. Changes in soil microbial community are linked to soil carbon fractions after afforestation: Soil microbial community affects carbon fractions. *Eur. J. Soil Sci.* **2018**, *69*, 370–379. [CrossRef]
53. Hanson, C.; Allison, S.; Bradford, M.; Wallenstein, M.; Treseder, K. Fungal taxa target different carbon sources in forest soil. *Ecosystems* **2008**, *11*, 1157–1167. [CrossRef]
54. Dong, H.; Kong, C.; Wang, P.; Huang, Q. Temporal variation of soil friedelin and microbial community under different land uses in a long-term agroecosystem. *Soil Biol. Biochem.* **2014**, *69*, 275–281. [CrossRef]
55. Bradley, D.; Martiny, J. Patterns of fungal diversity and composition along a salinity gradient. *ISME J.* **2010**, *5*, 379–388. [CrossRef]
56. Gao, W.; Gao, K.; Guo, Z.; Liu, Y.; Jiang, L.; Liu, C.; Liu, X.; Wang, G. Different responses of soil bacterial and fungal communities to 3 years of biochar amendment in an alkaline soybean soil. *Front. Microbiol.* **2021**, *12*, 630418. [CrossRef]
57. Shahariar, S.; Helgason, B.; Soolanayakanahally, R.; Bedard-Haughn, A. Soil enzyme activity as affected by land-use, salinity, and groundwater fluctuations in wetland soils of the prairie pothole region. *Wetlands* **2021**, *41*, 31. [CrossRef]
58. Rousk, J.; Bååth, E.; Brookes, P.; LLauber, C.; Lozupone, C.; Gregory Caporaso, J.; Knight, R.; Fierer, N. Soil bacterial and fungal communities across a pH gradient in an arable soil. *ISME J.* **2010**, *4*, 1340–1351. [CrossRef] [PubMed]

59. Delgado-Baquerizo, M.; DBardgett, R.; MVitousek, P.; Maestre, F.; AWilliams, M.; JEldridge, D.; Lambers, H.; Neuhauser, S.; Gallardo, A.; García-Velázquez, L.; et al. Changes in belowground biodiversity during ecosystem development. *Proc. Natl. Acad. Sci. USA* **2019**, *116*, 201818400. [CrossRef]
60. Fierer, N.; Bradford, M.A.; Jackson, R.B. Toward an ecological classification of soil bacteria. *Ecology* **2007**, *88*, 1354–1364. [CrossRef] [PubMed]
61. Waldrop, M.; Holloway, J.; Smith, D.; Goldhaber, M.; Drenovsky, R.; Scow, K.; Dick, R.; Howard, D.; Wylie, B.; Grace, J. The interacting roles of climate, soils, and plant production on soil microbial communities at a continental scale. *Ecology* **2017**, *98*, 1957–1967. [CrossRef]
62. Ait Barka, E.; Vatsa, P.; Sanchez, L.; Vaillant-Gaveau, N.; Jacquard, C.; Klenk, H.-P.; Clément, C.; Ouhdouch, Y.; Wezel, G. Taxonomy, physiology, and natural products of Actinobacteria. *Microbiol. Mol. Biol. Rev.* **2015**, *80*, 1–43. [CrossRef]
63. He, H.; Miao, Y.; Gan, Y.; Wei, S.; Tan, S.; Rask, K.A.; Wang, L.; Dai, J.; Chen, W.; Ekelund, F. Soil bacterial community response to long-term land use conversion in Yellow River Delta. *Appl. Soil Ecol.* **2020**, *156*, 103709. [CrossRef]
64. Grandy, S.; Neff, J. Molecular C dynamics downstream: The biochemical decomposition sequence and its impact on soil organic matter structure and function. *Sci. Total Environ.* **2008**, *404*, 297–307. [CrossRef]
65. Rath, K.; Maheshwari, A.; Bengtson, P.; Rousk, J. Comparative toxicities of salts on microbial processes in soil. *Appl. Environ. Microbiol.* **2016**, *82*, 2012–2020. [CrossRef]
66. Li, Y.M.; Wang, S.P.; Jiang, L.L.; Zhang, L.R.; Cui, S.J.; Meng, F.D.; Wang, Q.; Li, X.N.; Zhou, Y. Changes of soil microbial community under different degraded gradients of alpine meadow. *Agric. Ecosyst. Environ.* **2016**, *222*, 213–222. [CrossRef]
67. Che, R.; Wang, Y.; Li, K.; Xu, Z.; Hu, J.; Wang, F.; Rui, Y.; Li, L.; Pang, Z.; Cui, X. Degraded patch formation significantly changed microbial community composition in alpine meadow soils. *Soil Tillage Res.* **2019**, *195*, 104426. [CrossRef]
68. Urbanová, M.; Šnajdr, J.; Baldrian, P. Composition of fungal and bacterial communities in forest litter and soil is largely determined by dominant trees. *Soil Biol. Biochem.* **2015**, *84*, 53–64. [CrossRef]