**Artificial reseeding promotes biodiversity restoration in alpine sandy meadow of the eastern Qinghai-Tibet Plateau**

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**Abstract**

Alpine grasslands have undergone severe desertification due to climate warming and overgrazing. Artificial reseeding has been widely employed for the restoration of these alpine sandy grasslands. However, its effectiveness in enhancing biodiversity, as well as the consistency of responses in aboveground plant diversity and belowground microbial diversity, remains unclear. To investigate the impacts of artificial reseeding on plant and microbial diversity of sandy meadows, we conducted field investigations in alpine grasslands of the eastern Tibetan Plateau that had undergone artificial reseeding, natural restoration, or remained as sandy meadows. The findings revealed that artificial reseeding yields inconsistent restoration outcomes for aboveground plant diversity and belowground soil microbial diversity in alpine sandy meadows, thereby altering the relationship between above- and belowground biodiversity. Artificial reseeding significantly promoted plant diversity in alpine sandy meadows, while its impact on restoring soil microbial diversity was less pronounced. Introducing new plant species through reseeding improved vegetation cover, plant diversity, and fungal richness. In addition, artificial reseeding altered soil properties, such as pH and nutrient content, which in turn influenced the composition and structure of plant and microbial communities. These results have essential implications for regional ecological security and the sustainable development of alpine meadows.

**Keywords:** Desertification; Alpine sandy meadow; Reseeding restoration; Biodiversity; Soil microbial communities; Tibetan Plateau

**1 Introduction**

Over the past decades, the humid alpine grasslands of the Qinghai-Tibet Plateau (QTP) have experienced severe desertification primarily driven by climate warming and overgrazing (Harris, 2010; Liu et al., 2019; Wu et al., 2021). Restoring desertified grasslands presents considerable challenges due to the Plateau’s unique geographical location and the profound impact of climate change ( Liu et al., 2019; Wang et al., 2008). Desertification is widely recognized as a global ecological and environmental issue, with extensive research conducted in arid and semi-arid regions (Gang et al., 2014; James et al., 2007). The high-altitude alpine grasslands of the Tibetan Plateau, located above 3,000 meters, are undergoing serious desertification, and their fragile ecosystems struggle to recover from degradation ( Liu et al., 2022). The desertification issue in the eastern QTP has also garnered considerable attention, as changes in plant communities, soil microbes, and soil properties caused by desertification can lead to loss of biodiversity (Allan et al., 2015; Reynolds et al., 2011; Zhao et al., 2016). Typically, desertification alters the plant community, some plant species with high requirements for water and soil conditions gradually decline or even disappear, the composition and structure of the plant community change, and plant diversity decreases (Zhao et al., 2016). Changes in the types and quantities of plants lead to alterations in the food sources and living environments of soil microorganisms (Zhang et al., 2023). The changes in the plant community and soil microorganisms, have effect on soil properties, such as, reduced plant coverage makes the soil more vulnerable to erosion by wind and water (Wang et al., 2019; Fay et al., 2016). Then, these changes, in turn, affect biodiversity and ecosystem functions (Allan et al., 2015; Reynolds et al., 2011).

Previous studies have proven that biodiversity underpins fundamental ecological processes (Shangguan et al., 2024), both plant diversity and soil microbial diversity are closely related to functions of the ecosystem (Dainese et al., 2019). Among them microorganisms are the primary driving force behind the vast majority of processes that regulate the energy and material fluxes in ecosystems (Yin et al., 2021). And soil microorganisms play a crucial role in regulating biogeochemical processes such as organic matter decomposition, nitrogen fixation, soil structure formation, plant-soil nutrient transformation, and pollutant degradation, which ultimately will influence plant productivity, soil fertility, and overall ecosystem functions in alpine meadows (Chen et al., 2017; Sun et al., 2024; Xie et al., 2024). The interactions between plants and soil microorganisms can enhance nutrient acquisition, thus promoting plant growth after disturbances (Brady et al., 2024; Hopkins et al., 2023). When an ecosystem changes due to disturbances, plants, bacteria, and fungi will all make certain adjustments to cope with the relevant environmental changes (Dong et al., 2025). Additionally, in the process of ecological restoration, soil microorganisms play a crucial role and are the core driving force for soil health and the resilience of the ecosystem (Liu et al., 2025; Breidenbach et al., 2025). Soil microorganisms are more sensitive to environmental changes than plants and soil animals, usually responding more rapidly to shifts in grassland degradation (Shen et al., 2015), changes in soil microbial diversity can have certain impacts on the sustainable use of soil (Yin et al., 2024). Soil microbial activity and diversity typically decrease with increasing grassland degradation, which in turn diminishes ecosystem services and functions (Pereira et al., 2022). This underscores the importance of understanding biodiversity dynamics in degraded grassland ecosystems. Hence, it is essential to examine how ecological restoration practices, such as artificial reseeding, impact biodiversity.

Ecological restoration measures have been implemented to counter the adverse effects of grassland desertification on biodiversity in high-mountain areas (Dong et al., 2022; Huang, et al., 2019). Previous studies have examined the impacts of various restoration measures on plants, microorganisms, and soil physicochemical properties in different degraded grasslands (Guo et al., 2021; Lu et al., 2018). Artificial reseeding has become a widely adopted strategy for restoring high-altitude sandy grasslands (Jian et al., 2022; Liu et al., 2019; Tian et al., 2023; Wu et al., 2011). Reseeding has received considerable attention for its positive impacts on biodiversity, soil nutrient accumulation, and soil microbial activity in grassland ecosystems (Gou et al., 2019; Hu et al., 2022; Hu et al., 2016; Liu et al., 2019; Liu et al., 2022; Polley et al., 2005; Wang et al., 2006; Wu et al., 2011; Zhang et al., 2019). In alpine sandy grasslands, recent studies have shown that artificial reseeding can significantly impact plant and microbial diversity, productivity, and soil physicochemical properties in degraded alpine meadows, ultimately reshaping the relationship between aboveground and belowground biodiversity (Gou et al., 2019; Li et al., 2021; Liu et al., 2019). However, the influence of desertification and artificial reseeding on aboveground plant diversity, belowground microbial diversity, and soil properties remains unclear. Additionally, few studies have explored how artificial reseeding affects the relationship between aboveground plant diversity and belowground microbial diversity ( Li et al., 2023; Su et al., 2023). These knowledge gaps hinder our ability to identify potential relationships between aboveground plant diversity and belowground microbial diversity during grassland restoration processes.

Although artificial reseeding has demonstrated benefits for enhancing biodiversity and soil fertility, its impacts on the biodiversity in sandy meadows still remain unclear and need further investigation. We hypothesize that artificial reseeding will modify the structure and composition of both aboveground and belowground communities, including plants, soil bacteria, and soil fungi, while simultaneously enhancing productivity and improving soil nutrient conditions. To address these gaps, we conducted an observational study across sandy meadows, restored meadows, and native meadows in the eastern Tibetan Plateau. We examined how artificial reseeding affects the changes in plant and soil microbial community, as well as soil physicochemical properties in alpine sandy meadows. Specifically, we aimed to answer the following key questions: (1) How did artificial reseeding affect the composition and structure of plants and microbial communities in alpine sandy meadows? (2) Which factors primarily govern the impact of artificial reseeding on biodiversity in alpine sandy meadows? (3) Did artificial reseeding modify the relationships between aboveground and belowground biodiversity? The findings of this study can provide important theoretical guidance for the restoration of alpine sandy grasslands.

**2 Materials and methods**

**2.1. Study site description**

The study area was located in Hongyuan County (102°37′34″E, 33°10′43″N, 3418 m a.s.l), which was located on the eastern of the Tibetan Plateau (Fig. 1). The average elevation of this region is over 3400 m. The mean annual precipitation in this region is 736.1mm, with approximately 60-75% occurring from May to September. The mean annual temperature is 2.1℃ ( Liu et al., 2019), and the mean temperatures are -10.3℃ and 10.9℃ in the coldest and the hottest months, respectively. In the alpine meadow, *Kobresia setchwanensis* predominates. The other species that coexist mainly include *Kobresia pygmaea*, *Carex praeclara*, *Thalictrum alpinum*, *Artemisia roxburghiana*, and *Potentilla anserina*. The soil here belongs to the typical aeolian sand type. It is loose in texture and contains low levels of organic matter, making it especially vulnerable to wind erosion (Gou et al., 2019).

**2.2 Experiment design**

In April 2019, we selected *Avena sativa, Poa litwinowiana*, and *E. nutans* for planting in the alpine sandy meadow. The planting process involved using a mixed ratio of 10:3:3 and a density of 130 kg ha-1. The inclusion of *A. sativa* was primarily aimed at creating a protective barrier against quicksand and establishing a suitable environment for the growth of herbaceous species. To prevent herbivore grazing, fences were installed after the planting was completed. By mid-August 2021, three sites were identified: the sandy meadow (SM), restored meadow (RM), and native meadow (NM) (Fig 1). Each site had a plot measuring 30 m × 30 m established. Within each plot, eight quadrats measuring 50 cm × 50 cm were randomly selected. In total, we sampled 24 quadrats (3 sites × 8 quadrats).

**2.3 Vegetation and soil sampling**

We recorded the height and percentage cover of individual species as well as the grassland community within each sampled quadrat. To determine the aboveground biomass (AGB), we harvested the aboveground plant tissues at ground level in each quadrat. For the estimation of belowground biomass (BGB), we collected five soil cores from each quadrat and carefully washed them to separate the roots from the soil. Both the AGB and BGB were then oven-dried at 65℃ for 48 hours to obtain their dry weights. Soil samples (0-10 cm) were collected from the four corners and center of each quadrat. Each soil sample was divided into two parts. One part was air-dried, while the other part was retained at 4℃ for measuring soil physical and chemical properties. The bulk density (BD) and soil water content (SW) were determined by weighing the oven-dried soils (100 cm3) at 100℃ for 48 hours. The soil organic carbon (SOC) and soil total nitrogen (TN) contents were analyzed using an elementary analyzer (vario MICRO cube, Elementar, Germany). Soil inorganic nitrogen (NH4+-N and NO3--N) levels were measured using an auto-analyzer (Auto Analyzer 3, Bran Luebbe, Germany). The soil total phosphorus (TP) content was measured using the molybdate/ascorbic acid method, while the soil available phosphorus (AP) content was determined using the Olsen method with NaHCO3 as an extractant.

**2.4. DNA extraction, amplification and HiSeq sequencing**

Soil microbial genome PCR amplification and determination: Total DNA was extracted from different soil samples using the CTAB method, and the extracted genomic DNA was determined by 2% agarose gel electrophoresis. The V3~V4 hypervariable region of the bacterial 16S rRNA gene was amplified using primers 338F (5'-ACTCCTACGGGAGGCAGCA-3') and 806R (5'-GGACTACHVGGGTWTCTAAT-3'). The fungal diversity was sequenced using the ITS1 region of the 18S rDNA, with primers ITS1F (5'-CTTGGTCATTTAGAGGAAGTAA-3') and ITS2R (5'-GCTGCGTTCTTCATCGATGC-3') (Caporaso et al., 2011). The amplification conditions were as follows: 98℃ pre-denaturation for 1 min, 98℃ denaturation for 10 s, 50℃ annealing for 30 s, 72℃ extension for 60 s, 30 cycles, and 72℃ extension for 5 min. Sequencing was performed using the Illumina HiSeq platform.

**2.5 Statistical analysis**

We used the plant richness and plant Shannon-Wiener index as metric for biodiversity, and these indices can be calculated as follows ( Wu et al., 2009):

where *S* is the total number of plant species, and *Pi* represents importance value for the *i*th plant species by calculating the mean value of relative coverage and relative height. The differences of vegetation characteristics, microbial diversity and soil proprieties across SM, RM, and NM were analyzed by one-way analysis of variance (ANOVA) and the Tukey-HSD test. Pearson correlations were applied to assess the relationships among microbial diversity and plant diversity. Statistical analyses were carried out using SPSS 26.0 software (SPSS Inc., Chicago, IL, USA) and R (v.4.0.5), graphics were drawn by the Origin 2023 software (Originlab Corporation, Northampton, MA, USA).

OTU analysis: RDP Classifier Bayesian algorithm was used to classify and analyze the OTU sequences with 97% similarity (USEARCH, 10.0). The threshold for filtering OTUs was set to 0.005% of the total number of sequences, and the community composition of each sample was calculated at the phylum level. Bacterial and fungi alpha diversity was calculated using the Shannon-Wiener index by the ‘diversity’ function in the R (v.4.0.5) Vegan package. The relative abundances of the microbes were determined as percentages. The significance of the effects of soil physicochemical properties on the aggregate distribution was tested via redundancy analysis (RDA) and the Monte Carlo permutation test, using the vegan package of R (Crist et al., 2003).

1. **Results**
   1. **Plant community composition and structure during desertification remediation**

*K. setschwanensis*, *K. pygmaea*, and *C. praeclara* dominate the native meadow, with important values of 0.17, 0.14, and 0.13, respectively. The sandy meadow is characterized by the dominance of *K. setschwanensis* (0.26) and *C. praeclara* (0.20), followed by *E. dahuricus* (0.15) and *C. carvi* (0.13). In contrast, the restored meadow is primarily dominated by the grasses *E. dahuricus* (0.20) and *P. sparsipilosum* (0.15). The relative importance value of the grasses functional group is higher in the restored meadow (0.12) compared to both the sandy meadow and native meadow, whereas the relative important values of the sedges and forbs functional groups tend to be lower (Fig. 2).

Artificial reseeding significantly increases vegetation cover, species richness, and plant diversity. These community variables are significantly higher in the restored meadow compared to the sandy meadow (Fig. 3a, e, and f). However, vegetation cover in the restored meadow remains significantly lower than in the native meadow, while species richness and plant diversity show no significant differences between the restored and native meadows (Fig. 3a, e, and f). Overall, the findings indicate that reseeding promotes vegetation cover, plant diversity, and productivity (Fig. 3).

**3.2 Soil microbial community diversity during desertification remediation**

Analysis of soil microbial alpha diversity identified variations among the three types of soil sites in the desertification remediation plots (Fig. 4). Soil bacterial species was highest in sandy meadow, followed by restored meadow, and lowest in the native meadow. Conversely, soil fungal species was highest in native meadow, followed by restored meadow, with the sandy meadow having the lowest fungal diversity. The soil bacterial species richness in native meadow is similar to that in sandy meadow, while it is significantly higher in restored meadow. For bacterial diversity indices (Shannon, Pielou, and Chao1 indices), there is no significant difference between sandy meadow and restored meadow, and the values in restored meadow are higher than those in the other two types of meadows. Regarding soil fungal species richness, the species richness in restored meadow was significantly higher than that in sandy meadow.

**3.3 Soil microbial communities composition and structure during desertification remediation**

To investigate the composition of soil microbial communities, soil bacteria and fungal OTUs were annotated with Greengene and Unite gene Bank respectively. A phylum-level comparison showed soil bacteria had significantly higher species richness than fungal (Fig. 5). In the native meadow, dominant bacteria at the phylum level included Proteobacteria, Actinobacteria, Firmicutes, Acidobacteria, and Bacteroidetes, with a relative abundance of more than 1%. The relative abundance of these bacterial phyla differed among different soil plots (Fig. 5a). At the soil fungal phylum level, dominant fungal phyla consisted of Ascomycota, Basidiomycota, Mucoromycota, and Chytridiomycota. Among them, Ascomycota had the highest relative abundance in all three plots. The distribution of fungal phyla differed among different soil plots (Fig. 5b).To evaluate soil-microbial-community diversity differences, we performed PCoA with a weighted UniFrac distance matrix and NMDS based on the Bray-Curtis distance for soil bacteria and fungi in three sampling sites, and the results, showed distinct and significant differences in bacterial and fungal communities among the three meadow types (NM, SM, and RM) (Fig. 6 and 7).

**3.4 Correlation between soil microorganisms and environmental factors**

The Redundancy Analysis (RDA) analysis revealed a strong correlation between microbial community variation and the measured environmental variables. The combined environmental variables accounted for 35.76% of the variation in bacterial composition and 23.17% of the variation in fungal composition. The RDA biplot visually represents the arrangement of microbial communities in relation to environmental variables (Fig. 8). Notably, soil pH, plant diversity, vegetation cover, soil water content，and dissolved organic carbon showed the most significant correlations with microbial community composition.

**3.5 Correlation between plant and soil microbial diversity**

The analysis of the richness and diversity of aboveground plant species as well as belowground bacteria and fungi reveals that there are significant correlations between plant richness and fungal richness, and between bacterial richness and fungal diversity (Fig. 9). In native meadow, fungi richness showed a significant positive correlation with plant richness and diversity. However, this correlation diminishes under desertification. After artificial reseeding, there is no reestablishment of the correlation between fungi richness and plant species diversity Instead, a significant negative correlation emerged between plant species richness and diversity and bacterial diversity (Fig. 10), indicating potential shifts in plant-microbe interactions following artificial reseeding restoration.

1. **Discussion**

Artificial reseeding is an effective strategy for restoring high-altitude sandy grasslands. In the short to medium term, artificial reseeding improves soil the water-holding capacity and overall quality by increasing vegetation cover and covering exposed, vulnerable surfaces in degraded grassland (Carter & Blair, 2012). Multiple studies consistently demonstrate that restoration efforts usually result in intermediate levels of biodiversity, intermediate between degraded and reference sites. This observation is in line with earlier research, suggesting that restoration frequently only partially reverts the degraded state and seldom achieves complete restoration to the reference state (Atkinson et al., 2022; Benayas et al., 2009; Jones et al., 2018; Meli et al., 2017). Previous studies also have shown that alterations in vegetation cover affect the composition of soil microbial community (Calderón et al., 2001; Eisenhauer et al., 2010; Zak et al., 2003). In our study, we observed that artificial reseeding promoted vegetation cover, plant diversity, productivity, and soil microbial diversity (Fig. 3 and Fig. 4), highlighting the crucial role of reseeding in combating desertification and vegetation recovery in alpine sandy meadows. Despite the positive impacts of artificial reseeding on vegetation cover and plant biomass in alpine sandy meadow, a noticeable disparity persists compared to native meadow, generally situating the restored meadow in an intermediate state between the restored and native meadows (Fig. 3 and Fig. 4). Additionally, artificial reseeding promotes microbial diversity, but the microbial community structure remains still differs from that of the natural meadows. Thus, our study suggests that short-term reseeding interventions enhance vegetation cover, productivity, and biodiversity in sandy meadows but seldom achieve complete restoration to the natural ecosystem, indicating that complete ecological recovery may require longer-term processes or additional restoration strategies.

In this study, we observed that desertification changes the abundance, community diversity, and dominant phyla of soil bacteria and fungi, which was in agreement with previous study (Araújo et al., 2013). In case of severe desertification, the decrease in actinomycete abundance can be largely attributed to reduced soil substrates, as actinomycetes are oligotrophic microorganisms (Li et al., 2016). Vegetation is crucial in supplying organic nutrients and rhizospheric microhabitats for soil bacteria and fungi, which results in alterations to the soil microbial community (Li et al., 2016; Wardle et al., 2004). Our results show that Actinobacteria and Acidobacteria are more abundant in native meadows than in sandy meadows and restored meadows (Fig. 5). Soil nutrients play a crucial role in governing soil microbial diversity, and their response is strongly connected to alterations in plant diversity, productivity, and carbon availability (Liu et al., 2019). In our research, alongside vegetation cover and plant diversity, we have identified soil total nitrogen content, soil soluble organic carbon, soil organic carbon, soil moisture content, and pH as the primary determinants of soil bacterial diversity (Fig. 8). These results emphasize the considerable impact of environmental factors on the structure and composition of soil microbial communities in desertification remediation sites, underscoring the pivotal role of these factors in shaping the dynamics of microbial communities during ecosystem restoration.

Plant diversity regulates soil microbial diversity by providing different plant litter and root exudates, supporting diverse microbial groups, enhancing resource availability, and altering microhabitats and environmental conditions (Wardle et al., 2004; Liu et al., 2025). Our research demonstrates that grassland desertification affects plant diversity and soil microbial diversity differently, as indicated by changes in the Shannon diversity index of plants, bacteria, and fungi (Fig. 9). This study highlights the distinct responses of plant and soil microbial diversity to both desertification and reseeding. The soil microbiome, with its diverse genetics, ecology, functions, and taxonomy, serves as a crucial source of microbial traits important for plant growth and health (Bardgett & Shine, 1999). Therefore, changes in plant and microbial diversity are consistent. Ecological restoration can modify the soil environment, which includes soil texture, nutrient content, and microbial communities, thereby influencing plant-soil interactions and the rate and extent of subsurface biodiversity recovery. The recovery rate of aboveground and belowground biodiversity may temporally differ in restored grasslands (Wardle et al., 2004). Plants tend to re-establish vegetation cover more rapidly, while microorganisms and other soil-dwelling organisms may take longer to fully recover. These temporal differences may contribute to the disparities in aboveground and belowground diversity during the initial stage of ecological restoration.

In summary, artificial reseeding is an effective ecological restoration strategy for enhancing biodiversity in alpine sandy meadows on the eastern Tibetan Plateau. Artificial reseeding induces changes in microbial community structure that positively impact soil health and ecosystem functioning by promoting nutrient cycling and plant growth. However, in addition to plants and soil microorganisms, soil animals also play a crucial role in biodiversity. Furthermore, factors such as soil animals, soil characteristics, vegetation types, and environmental conditions should be taken into account when evaluating the impact of artificial reseeding on biodiversity (Bardgett et al., 2021). Further research is needed to comprehensively assess the long-term effects of artificial reseeding on biodiversity across various environmental conditions and to evaluate its impact on the overall health and functioning of degraded alpine grassland ecosystems.

1. **Conclusion**

This study revealed that artificial reseeding in sandy meadows significantly promotes plant diversity and fungal richness while having comparatively lesser impact on microbial diversity restoration. In addition, artificial reseeding alters soil properties, such as pH and nutrient content, thereby influencing the composition and structure of both plant and microbial communities. Artificial reseeding in alpine sandy grasslands restores both aboveground plant diversity and belowground microbial diversity and alters the relationship between aboveground and belowground biodiversity. However, it is important to note that ecological restoration involves not only plants and soil microorganisms but also soil animals, productivity, and soil characteristics. Further research is needed to comprehensively assess the long-term effects of artificial reseeding on biodiversity across different environmental conditions and evaluate the overall ecosystem health and functioning of degraded alpine grassland ecosystems, providing crucial theoretical guidance for the restoration of alpine sandy meadows.

**Acknowledgements**

This work was funded by the National Natural Science Foundation of China (42071058 and 91837312, 32230068), the Second Tibetan Plateau Scientific Expedition and Research Program (2019QZKK0106) ，the grant from Grassland Science Institute of TAAAS (CYS-TC-2021-001) and the Fundamental Research Funds for the Central Universities (lzujbky-2022-33).

**Declaration of Competing Interest**

The authors declare no competing financial interests.

**Data Availability Statement**

## All data used for this manuscript are available when manuscript be accepted for publication.

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**Figure captions**

**Figure 1.** Location of study area in Hongyuan county on the east Tibetan Plateau (a and b). The photos beside the map represent (c) native meadow (NM), (d) sandy meadow (SM), (e) restored meadow (RM).

**Figure 2.** Differences in the importance values of the four functional groups, namely grasses, sedges, forbs, and legumes, among the native meadow (NM), sandy meadow (SM), and restored meadow (RM). Different letters indicate significant differences among treatments.

**Figure 3** Differences in (a) vegetation cover (Cover), (b) plant height (Height), (c) aboveground biomass (AGB), (d) belowground biomass (BGB), (e) plant richness (Richness), and (f) plant Shannon-Wiener diversity index (Shannon index) among native meadow (NM), sandy meadow (SM), and restored meadow (RM). Different letters indicate significant differences among treatments.

**Figure 4.** The alpha diversity of soil microorganisms among native meadow (NM), sandy meadow (SM), and restored meadow (RM). (a) bacteria richness, (b) bacteria Shannon Index, (c) bacteria Pielou Index, (d) bacteria Chao1 Index, (e) fungi richness, (f) fungi Shannon Index, (g) fungi Pielou Index, (h) fungi Chao1 Index. Different letters indicate significant differences among treatments.

**Figure 5.** The community composition of soil microbes among native meadow (NM), sandy meadow (SM), and restored meadow (RM). (a) Bacteria phylum level, (b) Fungi phylum level.

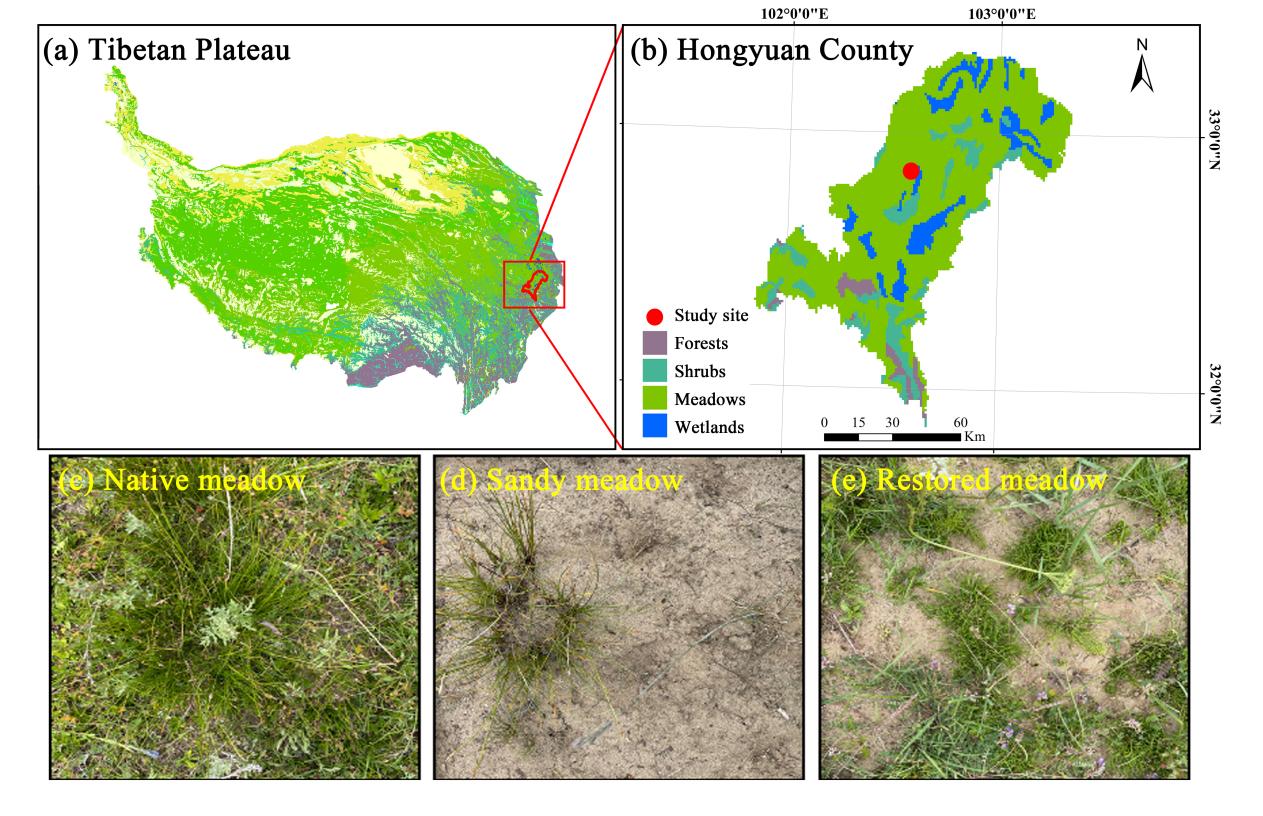
**Figure 6.** Principal Coordinate Analysis (PCoA) of the bacteria (a) and fungi (b) community structures among native meadow (NM), sandy meadow (SM), and restored meadow (RM).

**Figure 7.** Non-metric multidimensional scaling (NMDS) of the bacteria (a) and fungi (b) community structures among native meadow (NM), sandy meadow (SM), and restored meadow (RM).

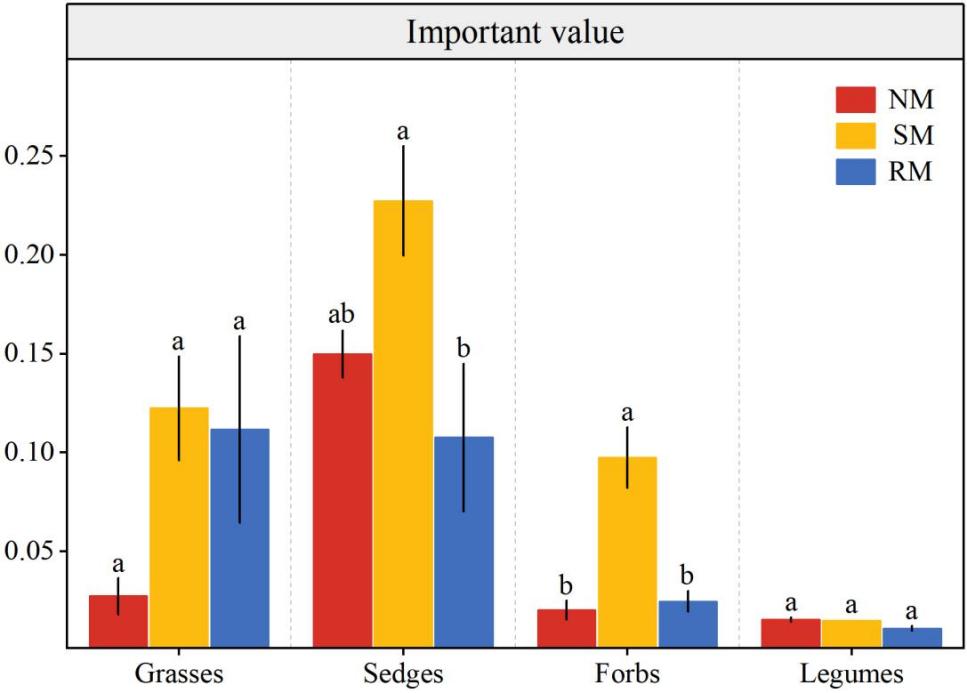
**Figure 8.** Redundancy analysis of the bacteria (a) and fungi (b) community structures among native meadow (NM), sandy meadow (SM), and restored meadow (RM) and their driving factors. Cover, vegetation cover (%); Height, plant height (cm); Richness, plant richness; Shannon index, plant Shannon-Wiener diversity index; AGB, aboveground plant biomass (g m-2 ); BGB, belowground plant biomass (g m-2 ); pH, soil pH; SW, soil water content; BD, soil bulk density; SOC, soil organic carbon; DOC, dissolved organic carbon; TP, soil total phosphorus; AP, soil available phosphorus; TN, soil total nitrogen; NH4+–N, soil ammonia nitrogen; NO3––N, soil nitrate nitrogen.

**Figure 9.** Scatter matrix plot represents the correlation analysis between pairwise relationships of plant richness, plant diversity, bacterial richness, bacterial diversity, fungal richness and fungal diversity in native meadow (NM), sandy meadow (SM), and restored meadow (RM). Asterisk was considered to be significant. \*, *p* < 0.05; \*\*, *p* < 0.01; \*\*\*, *p* < 0.001.

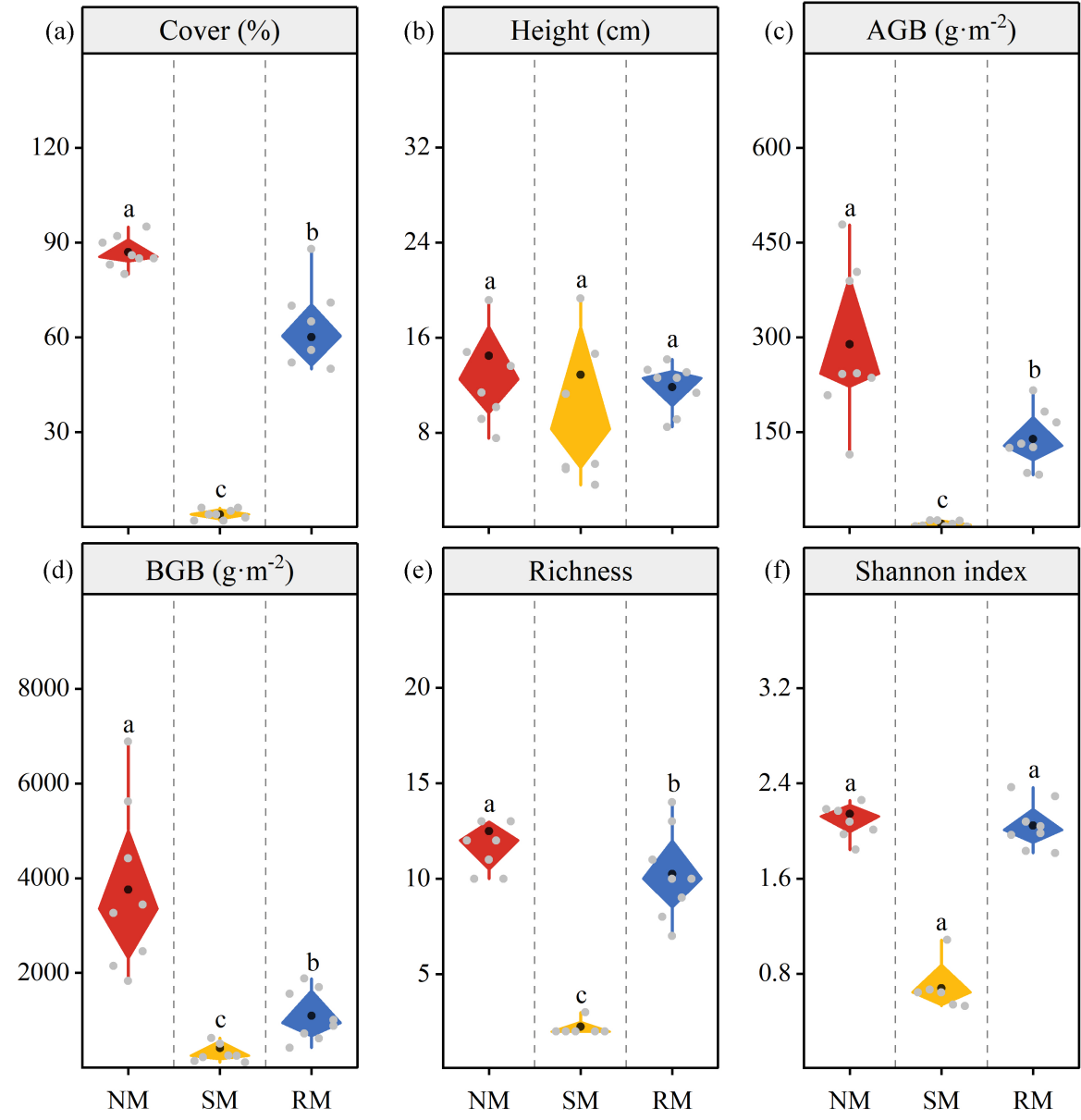
**Figure 10.** The diagram depicts the correlation between the diversity and abundance of plants, bacteria, and fungi in three vegetation types during the process of desertification restoration. Solid lines indicate significant correlations (*p* < 0.05), while dashed lines indicate no correlation (*p* > 0.05). Red arrows represent positive correlations, and blue arrows represent negative correlations



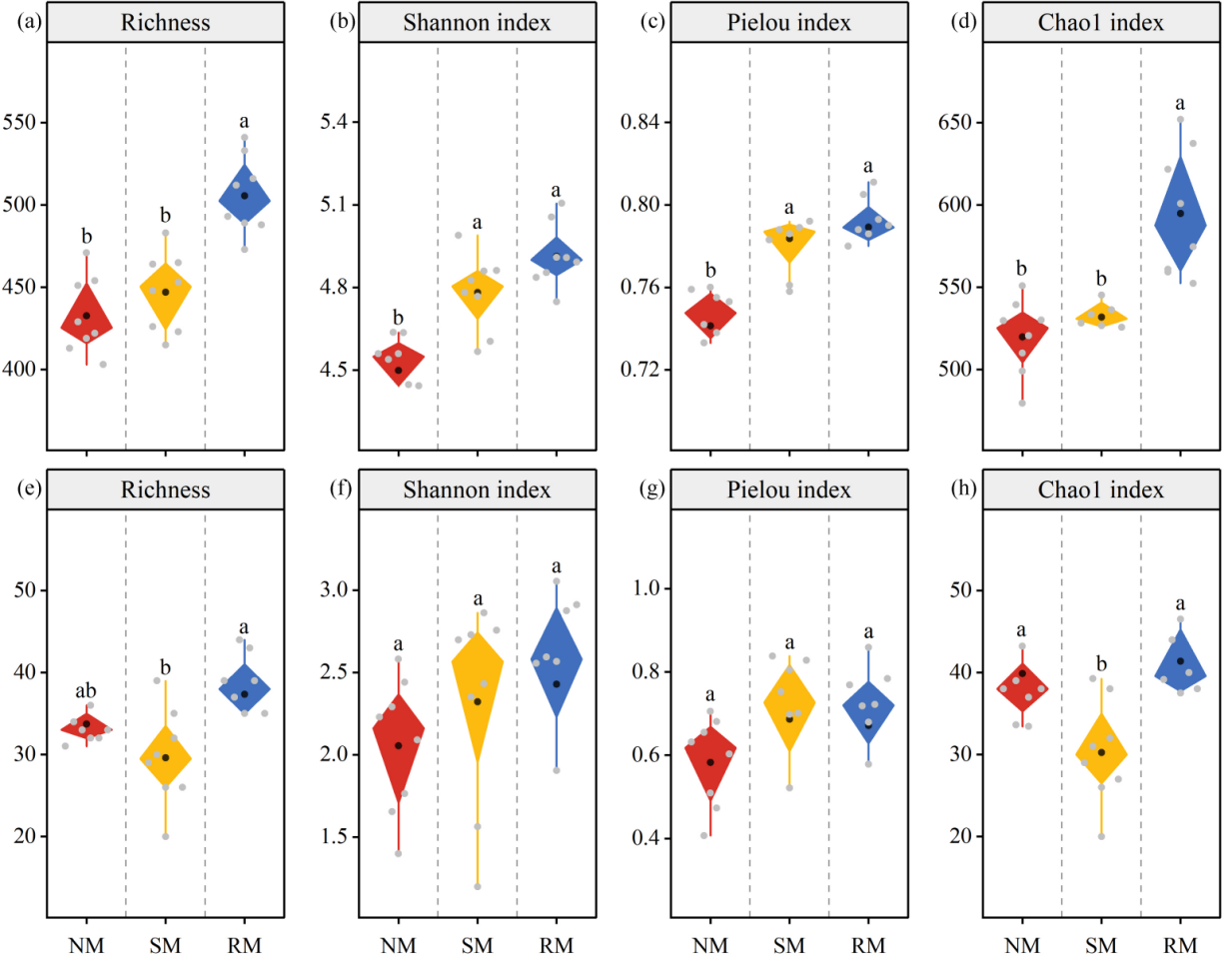
**Figure 1**



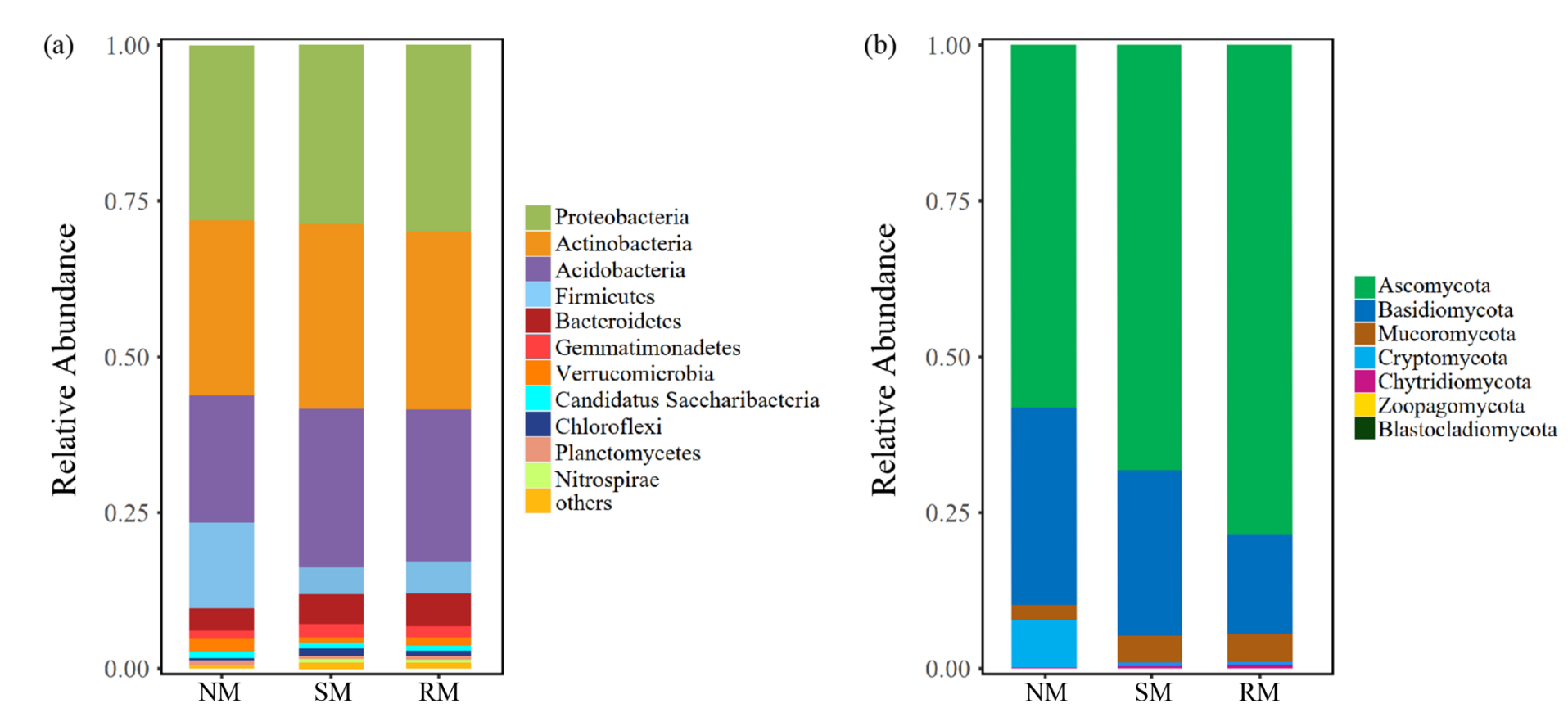
**Figure 2**



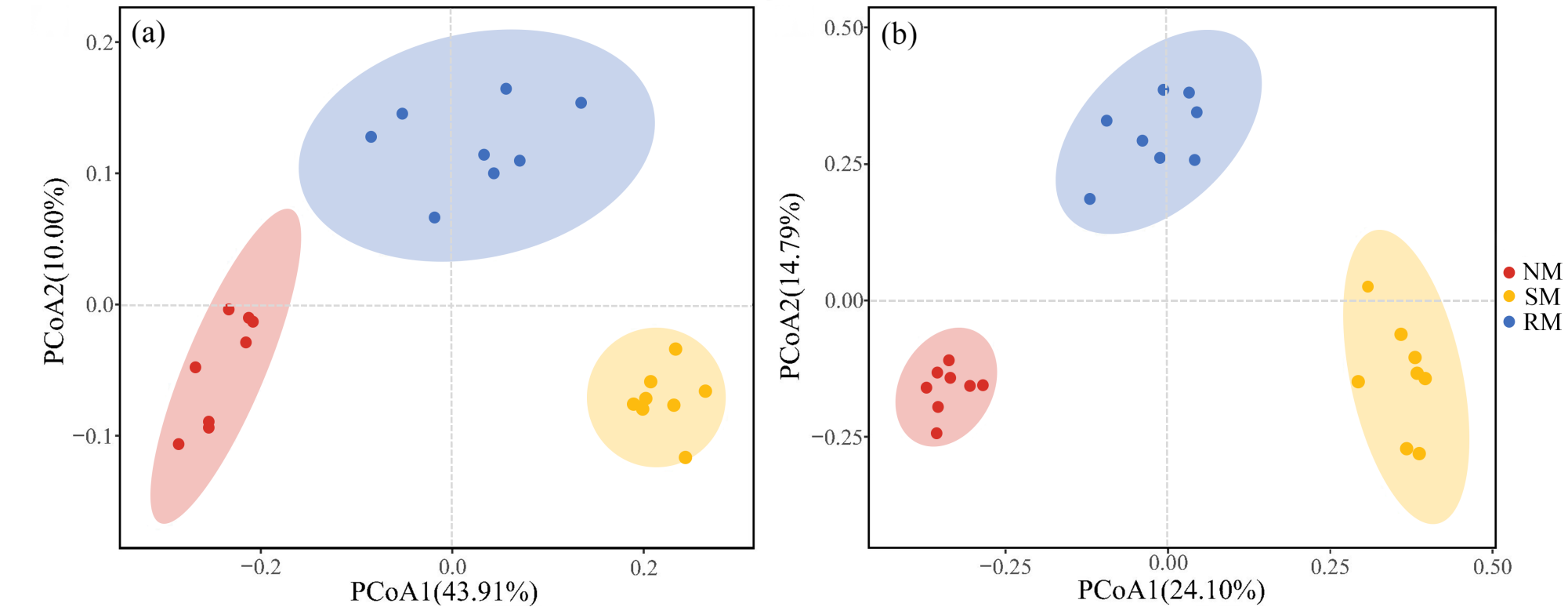
**Figure 3**



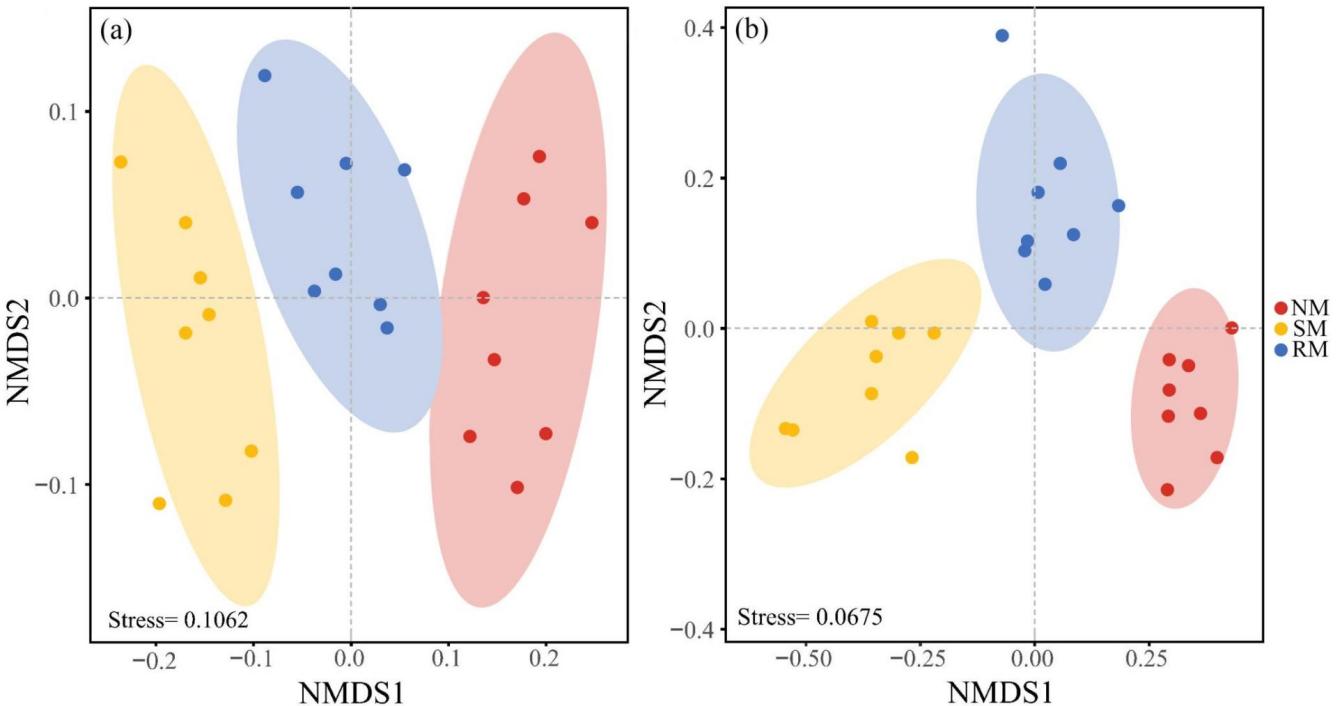
**Figure 4**



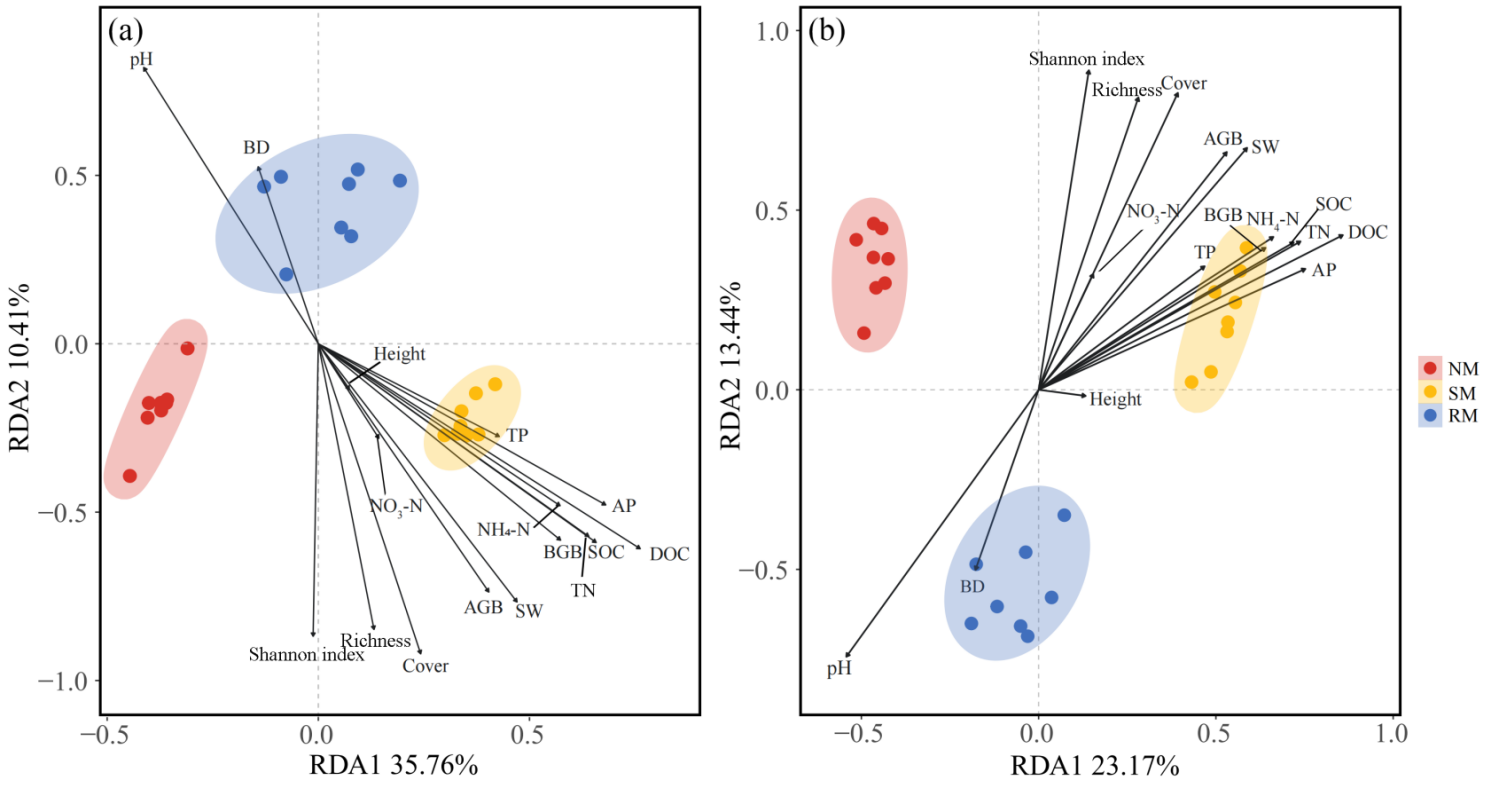
**Figure 5**



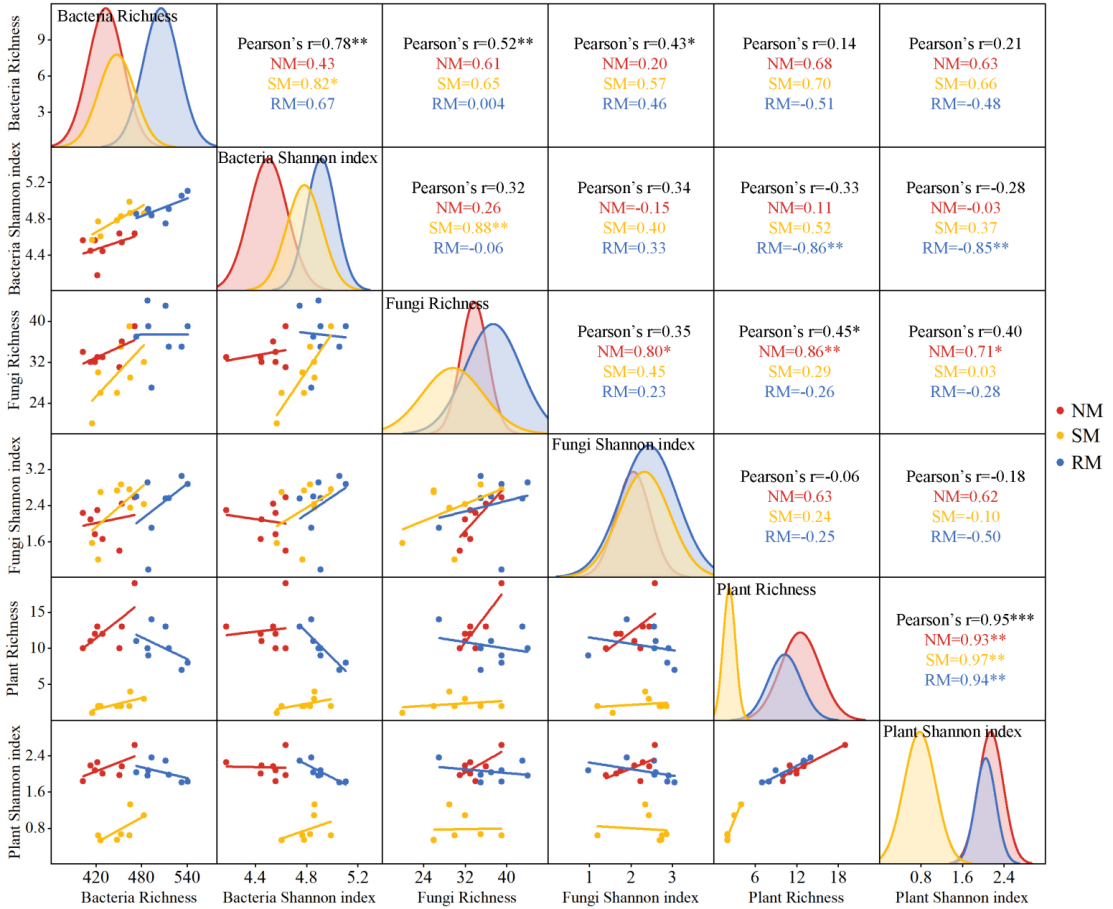
**Figure 6**



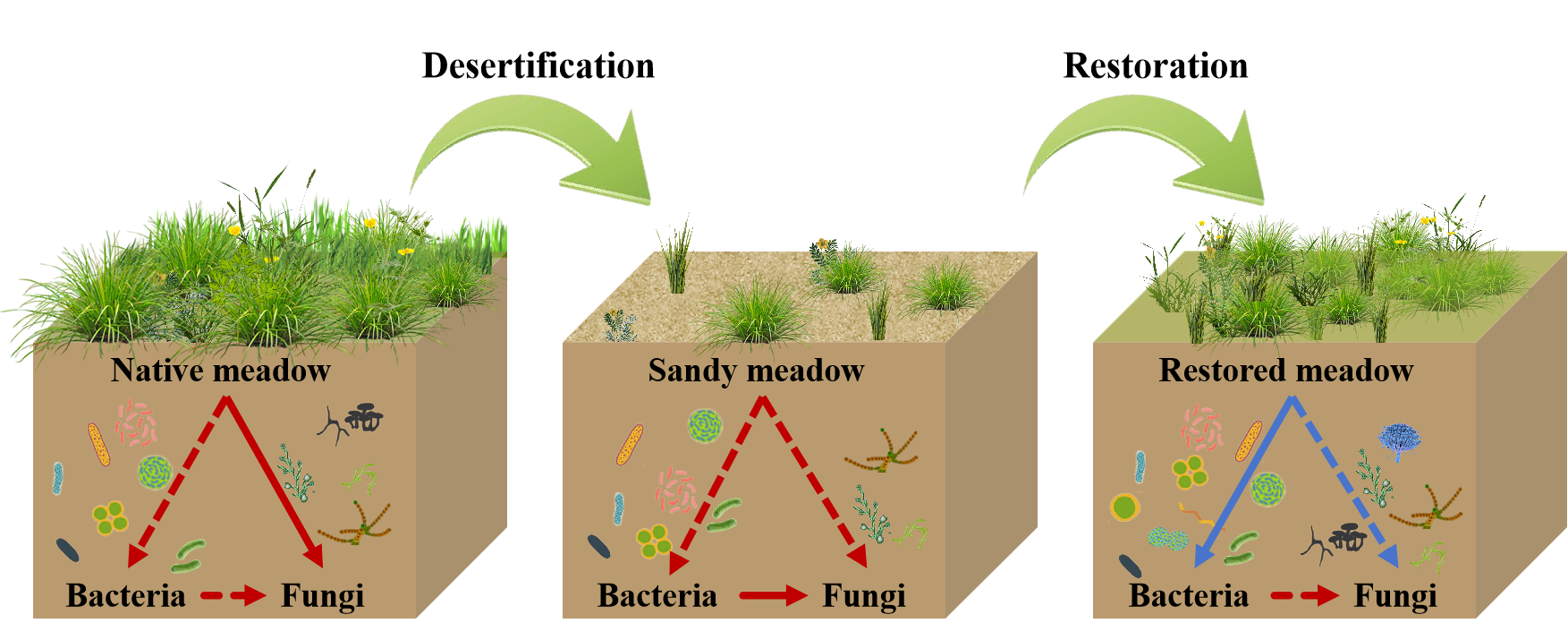
**Figure 7**



**Figure 8**



**Figure 9**

 **Figure 10**

|  |  |  |  |
| --- | --- | --- | --- |
| **Species** | **NM** | **SM** | **RM** |
| *Kobresia setschwanensis* | 0.17 | 0.26 | - |
| *Carex parvula* | 0.14 | - | 0.07 |
| *Carex praeclara* | 0.13 | 0.20 | 0.15 |
| *Thalictrum alpinum* | 0.07 | - | - |
| *Potentilla saundersiana* | 0.06 | - | 0.07 |
| *Elymus dahuricus* | 0.06 | 0.15 | 0.20 |
| *Artemisia roxburghiana* | 0.05 | - | - |
| *Potentilla anserina* | 0.04 | 0.09 | - |
| *Festuca rubra* | 0.03 | - | - |
| *Lancea tibetica* | 0.03 | - | - |
| *Poa annua* | 0.02 | - | 0.09 |
| *Carum carvi* | 0.02 | 0.13 | 0.04 |
| *Koeleria litvinowii* | 0.01 | 0.10 | - |
| *Artemisia scoparia* | 0.01 | 0.08 | 0.03 |

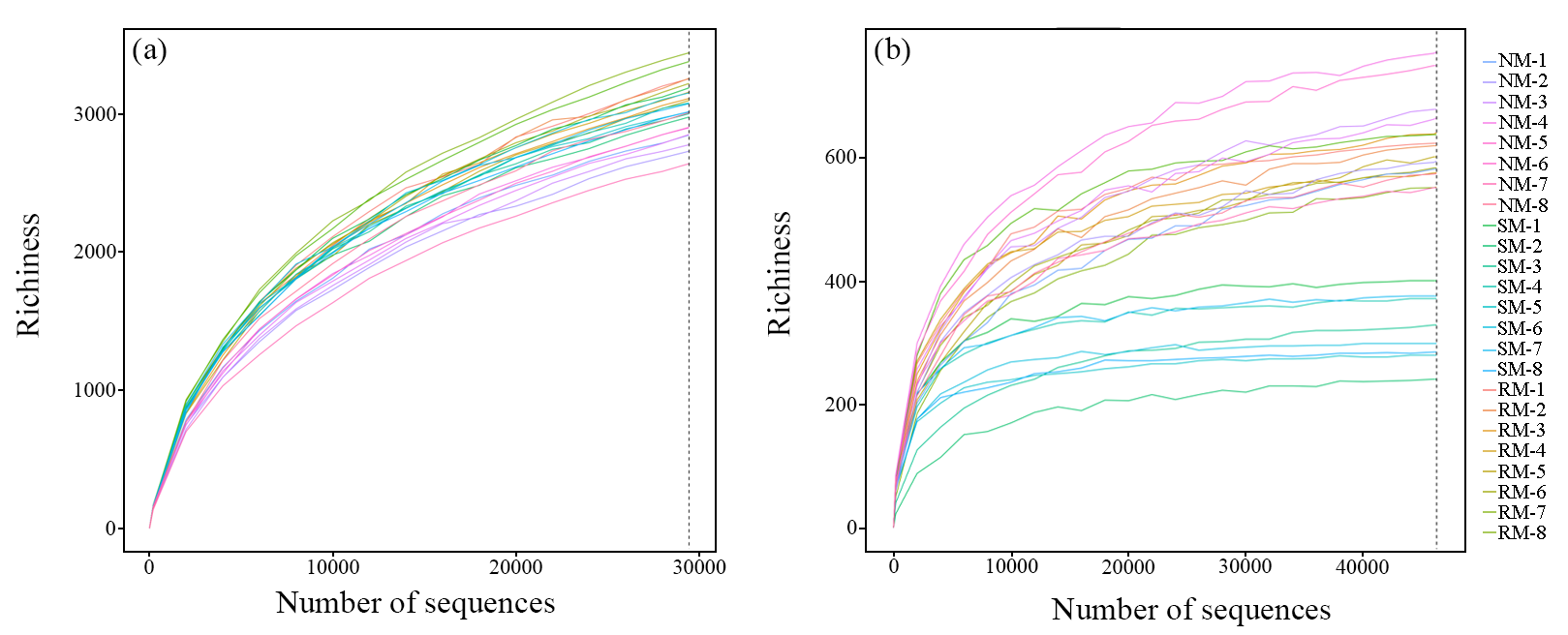
**Table 1.** Dominant species composition and their respective importance values in native meadow (NM), sandy meadow (SM), and restored meadow (RM).

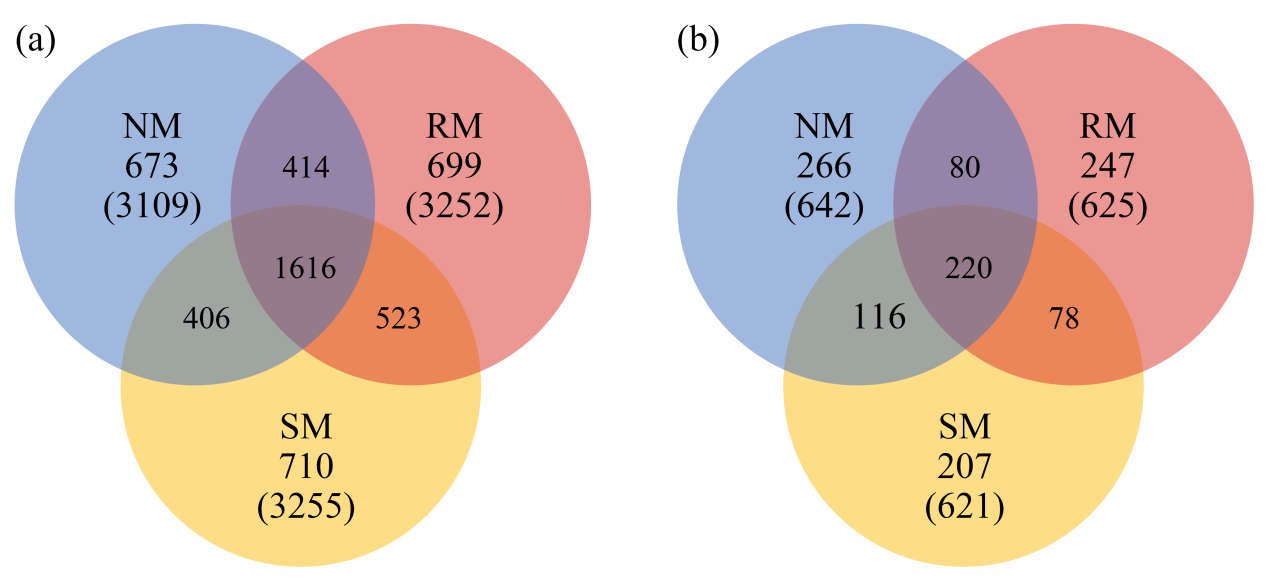
**Table S1** Comparison of soil pH, soil water content (SW), soil bulk density (BD), soil organic carbon (SOC), dissolved organic carbon (DOC), soil total phosphorus (TP), soil available phosphorus (AP), soil total nitrogen (TN), soil ammonia nitrogen (NH4+–N), soil nitrate nitrogen (NO3––N) among native meadow (NM), sandy meadow (SM), and restored meadow (RM). Different letters indicate significant differences among treatments.

|  |  |  |  |
| --- | --- | --- | --- |
|  | **NM** | **SM** | **RM** |
| **pH** | 5.14±2.24c | 6.69±0.07a | 6.34±0.15b |
| **SW** | 6.26±2.37a | 0.69±0.23c | 3.42±1.80b |
| **BD** | 1.18±0.12a | 1.36±0.27a | 0.99±0.41b |
| **SOC** | 12.17±1.52a | 1.96±0.26b | 3.83±0.47b |
| **DOC** | 117.89±3.26a | 28.24±1.77c | 37.31±1.83b |
| **TP** | 0.37±0.01a | 0.34±0.01a | 0.33±0.01a |
| **AP** | 7.39±0.34a | 4.86±0.30b | 4.81±0.37b |
| **TN** | 1.02±0.11a | 0.16±0.02b | 0.31±0.04b |
| **NH4+-N** | 10.97±0.67a | 6.87±0.50b | 7.34±0.65b |
| **NO3--N** | 8.36±0.70a | 6.52±0.47a | 7.60±0.77a |

**Figure S1** Soil samples OTU dilution curve of microorganism. Different colors represent different samples (a) soil bacteria, (b) soil fungi.

**Figure S2** Different colors represent different samples categorized among native meadow (NM), sandy meadow (SM), and restored meadow (RM). (a) Soil bacteria, (b) Soil fungi.

**Figure S1**



**Figure S2**