Article
Promotion of Soil Microbial Community Restoration in the Mu Us Desert (China) by Aerial Seeding

Yina Ma 1, Lei Zu 1, Fayu Long 1, Xiaofan Yang 2, Shixiong Wang 1,*, Qing Zhang 3,4, Yuejun He 1, Danmei Chen 1, Mingzhen Sui 1, Guangqi Zhang 1, Leping Zang 1 and Qingfu Liu 1,3,6

1 Research Center of Forest Ecology, Forestry College, Guizhou University, Guiyang 550025, China
2 Chang’an Dublin International College of Transportation, Chang’an University, Xi’an 710018, China
3 Ministry of Education Key Laboratory of Ecology and Resource Use of the Mongolian Plateau, School of Ecology and Environment, Inner Mongolia University, Hohhot 010021, China
4 Collaborative Innovation Center for Grassland Ecological Security (Jointly Supported by the Ministry of Education of China and Inner Mongolia Autonomous Region), Hohhot 010021, China
* Correspondence: sxwang3@gzu.edu.cn

Abstract: Soil microbial communities link soil and plants and play a key role in connecting above-ground and below-ground communities in terrestrial ecosystems. Currently, how artificial revegetation promotes the restoration of soil microbial community diversity in degraded ecosystems attracts extensive attention. In this study, soil samples were collected from long-term artificially restored mobile sandy lands (aerial seeding sample plots) from 1983 to 2015 in the Mu Us Desert. The second-generation high-throughput sequencing technology was adopted to identify soil microorganisms and analyze the changes in their community structure and diversity. The relationships between changes in microbial diversity and soil nutrients were explored by Pearson correlation analysis and canonical correspondence analysis. In addition, the restoration of subsurface soil microbial communities in this area was evaluated. The results are as follows: (1) The alpha diversity of the soil microorganisms increased significantly with the restoration period, and the composition and diversity of the soil microbial communities in the sample plots in different restoration years varied significantly. (2) Soil nutrient indexes, such as total carbon, total nitrogen and nitrate nitrogen, significantly increased with the restoration period and were significantly positively correlated with soil fungal and bacterial diversity. (3) Key soil fungal and bacterial phyla contributed to nutrient cycling in degraded ecosystems. It can be concluded that afforestation by aerial seeding facilitates the change in community structure and increases the diversity of soil microorganisms in the Mu Us Desert. This paper provides a basis for future measures and policies for restoring degraded lands and ecosystems.

Keywords: soil microorganism; soil nutrient; aerial seeding; restoration

1. Introduction
Soil microbial communities link soil and plants and play an important role in the formation and development of soil [1,2]. They can decompose organic matters and minerals in the soil, release nutrients that can be taken up by plants, form humus and eventually improve soil quality. Soil microbial communities contribute to key ecological processes, such as organic matter decomposition and nutrient cycling. They connect the above-ground and below-ground communities in terrestrial ecosystems [3,4]. Therefore, more and more scholars are focusing on soil microbial communities, especially those in degraded lands (e.g., mobile sandy lands after aerial seeding), during long-term artificial restoration. The dynamics of soil microbial communities in such lands are still unclear. Soil fertility has been restored through artificial revegetation [5,6]. Revegetation is the key to ecosystem restoration and stability, and microorganisms play a significant role during ecosystem reconstruction [7]. The impact of artificial restoration on soil microorganisms in degraded ecosystems has been hotly studied by soil scientists and ecologists.
To tackle ecological degradation, including desertification, a series of major ecological restoration policies, including the Three-North Shelter Forest Program, Combating of Desertification Program, Natural Forest Protection Program, and Grain for Green Project, have been implemented in northern China since 1978 [8–10]. The specific implementation measures advocated by these ecological restoration projects are as follows [11]: aerial seeding for trees and grass; afforesting; sand blocking; fencing of grassland; cultivation of high-quality grass seeds; construction of wind-breaks on sand dunes; prohibition of grazing; construction of livestock barns; provision of fodder and machinery to herders; strengthening of forest zoning; prohibition of deforestation and provision of food, livelihood and afforestation subsidies to farmers; return of the property rights of forests (grassland) to farmers. In the past decades, the effectiveness of related ecological restoration measures has become an important research topic. The ecological restoration of soil microbial communities needs further evaluation.

The structure, distribution and diversity of fungal communities are influenced by natural factors such as climate, precipitation and soil, and vary with external environmental conditions. A study revealed that simultaneously increasing atmospheric CO$_2$ concentration and raising temperature could significantly reduce the diversity of fungi in the soil cultivated with wheat [12]. By simulating rainfall on the typical grassland of the Loess Plateau, scholars found that both increasing and decreasing rainfall could increase soil microbial diversity and that the relative abundance of dominant species decreased with rainfall [13]. Soil microbial communities also change with the physico-chemical properties of soil. Soil particle composition and water content affect the aeration conditions of soil, thereby influencing the distribution and diversity of soil microbial communities. Soil nutrient conditions also affect the structural composition of soil fungal communities [14]. In addition, anthropogenic disturbances, such as fertilization, reclamation, grazing and burning, greatly impact the structure and diversity of soil microbial communities. Soil microorganisms are most sensitive to fertilizer application, which can significantly increase their diversity in the *Leymus chinensis* meadow [15]. Reclaiming rice fields or mining sand in wetlands along rivers can significantly decrease the alpha diversity of soil microorganisms [16]. Oliver, et al. [17] concluded that frequent prescribed burning could maintain fire-selected soil fungal communities that may support plant communities and dominate the frequently burned areas.

Afforestation by aerial seeding refers to using aircraft to sow the seeds of trees or grass on suitable lands. The seeds may root, germinate and grow into forests with natural rainfall at a suitable temperature, thus increasing vegetation coverage and controlling desertification. Aerial seeding is an effective way for revegetation on sandy lands and is a fast sand-control measure [7]. Scholars have mainly focused on the effect of revegetation by aerial seeding on sandy lands and soil properties, enzyme activity changes and ecosystem services during vegetation restoration [18]. However, research on the changes in the structure of subsurface soil microbial communities in different aerial seeding years is scarce.

Located in northern China, the Mu Us Desert is one of the four sandy lands in China, with a total area of 3.2 km$^2$, spanning Shaanxi Province, Inner Mongolia Autonomous Region and Ningxia Hui Autonomous Region, China. This area is threatened by severe desertification, with single tree species, sparse biological populations and relatively low biological stability. It is a typical ecologically fragile area and one of the key areas for wind and sand control in China. Since the 1970s, several ecological restoration projects have been implemented in this area to curb desertification and afforestation by aerial seeding is one of the ecological restoration measures adopted there [19]. Soil microorganisms are critical to the growth of sand-fixing plants, soil formation from quicksand, the improvement of soil fertility, and nutrient uptake by plants [20]. In this study, the soil microorganisms in the Mu Us Desert in 30 different aerial seeding years were explored using high-throughput sequencing technology to investigate the composition and changes in the diversity of soil microbial communities. The results revealed that aerial seeding changed the structure
and diversity of soil microbial communities in the Mu Us Desert. This paper provides a theoretical basis for afforestation by aerial seeding in this desert.

2. Materials and Methods

2.1. Study Area

The study site is located in the hinterland of the Mu Us Desert, which is characterized by a temperate continental monsoon climate with an average annual temperature of 6.8 °C. Precipitation in this region is concentrated from July to September, with an annual precipitation of 350–400 mm and an annual evaporation of 2200–2800 mm. Soil types mainly include zonal soils (chestnut and brown soils) and azonal soils (aeolian sandy, meadow and saline soils). Aeolian sandy soil is characterized by a loose structure and poor adhesion [21]. *Thymus serpyllum* L. and *Stipa bungeana* Trin. are important plants in this area, and sandy vegetation is dominated by *Artemisia ordosica* Antoine, *Salix psammophila* C. Wang & Chang Y. Yang, and *Sabina vulgaris* Antoine.

Aerial seeding means using aviation technology to sow grass seeds that can adapt to the climate on barren hills, wastelands and sand. The seeds will be protected and managed effectively (e.g., by prohibiting grazing) until vegetation is restored. *Hedysarum laeve* Maxim. and *Hedysarum scoparium* Pall. var. mongolicum (Turcz.) Turcz. ex B. Fedtsch are the main planting species. Before aerial seeding, the degraded land formed an active sand dune.

2.2. Sites and Sampling

Field sampling was conducted on 32 sites, including 30 sites where aerial seeding had been performed from 1983 to 2015 (excluding 1986, 1988, and 2003), one top community site that has been undisturbed for >30 years and one mobile dune site where aerial seeding had not been conducted (Figure 1). To eliminate the influence of topographic features, sample plots were set in flat areas between sand dunes. Three 1 m × 1 m quadrats were set in each plot. For each sample, 0–60 cm of soil was extracted using a soil auger, mixed and divided into two groups. One group was stored at room temperature for soil nutrient content determination, and the other was stored at −20 °C for soil microorganism DNA extraction.

Figure 1. The 32 sampling sites at the Mu Us Desert.
2.3. Determination of Soil Nutrient Indexes

Six soil nutrient indexes, total carbon (TC), total nitrogen (TN), total phosphorus (TP), ammonium nitrogen (NH$_4^+$), nitrate nitrogen (NO$_3^-$), and available phosphorus (AP), were evaluated. TC was measured using the potassium dichromate ($K_2Cr_2O_7$) heating oxidation method. TN was measured using the selenium-cupric sulfate (CuSO$_4$)-potassium sulfate (K$_2$SO$_4$) heating digestion method [7]. TP was measured using the alkali fusion-Mo-Sb colorimetric method. NH$_4^+$ and NO$_3^-$ were measured using the Kjeldahl nitrogen determination method [22], and AP was measured using the sodium bicarbonate (NaHCO$_3$) leaching-Mo-Sb colorimetric method [23]. Soil nutrient content was directly measured by experiments without other calculations.

2.4. Soil Microbial Sequencing

Fungal and bacterial DNAs were extracted from different samples using the E.Z.N.A. Soil DNA Kit (D4015, Omega, Inc., Norwalk, UT, USA) according to the instruction of the manufacturer. The ITS2 region of the fungal small-subunit rRNA gene was amplified with slightly modified versions of primers fITS7 (5′-GTGARTCATCGAATCTTTG-3′) and ITS4 (5′-TCCCTCCGCTTATTGATATGC-3′). The V3–V4 region of the bacterial small-subunit (16S) rRNA gene was amplified with slightly modified versions of primers 338F (5′-ACTCCTACGGGAGGCAGCAG-3′) and 806R (5′-GGACTACHVGGGTWTCTAAT-3′) [24]. These amplified polymerase chain reaction products were sequenced on the Illumina HiSeq 2500 platform (Illumina Inc., San Diego, CA, USA) using 250-bp paired-end reads. Quality filtering on the raw tags was performed under specific filtering conditions to obtain high-quality clean tags according to the FastQC (V 0.10.1, Bioinformatics Group, Cambridge, UK). Vsearch (v2.3.4) [25] was used to filter chimeric sequences. Sequences with a similarity of ≥97% were assigned to the same operational taxonomic units (OTUs) using Vsearch (v2.3.4). Representative sequences were selected for each OTU [26], and taxonomic data were then assigned to each representative sequence using the ribosomal database project (RDP) classifier [27].

2.5. Data Analyses

The histograms of species abundances at the phylum level were plotted based on the relative abundances of soil microorganisms using the “vegan” package in R. The alpha diversity indexes of Shannon, Simpson, Chao1 and Observed species of bacteria and fungi were calculated at the species level. Principal coordinate analysis (PCoA) was then performed based on the Bray–Curtis distance matrix between samples, with the two axes of PCoA representing species differences between sites, i.e., beta diversity.

To determine the changes in soil microbial diversity and soil nutrient indexes with restoration year, Pearson correlation analysis was performed.

The correlation between the alpha diversity of the soil microorganisms and soil nutrient indexes was evaluated by the Pearson correlation analysis and canonical correspondence analysis (CCA). All data analyses were based on R 4.2.1 (http://www.r-project.org/, accessed on 1 September 2022) unless otherwise noted.

3. Results

3.1. Changes in Soil Microbial Diversity with Restoration Period

Rarefaction curves were plotted to reflect the reasonableness of the amount of extracted sequencing data and the species richness in the samples. Figure 2 shows that the curves tend to be flat as the amount of sequencing data increases, indicating that the number of sequences measured in different aerial seeding years can well reflect the number of soil microbial community species, and the amount of sequencing data is reasonable.
A total of 7 phyla, 20 classes, 57 orders, 115 families, 174 genera, and 284 species of fungi and 17 phyla, 47 classes, 79 orders, 147 families, 273 genera 313 species of bacteria were observed in the soil samples corresponding to different aerial seeding years. The histograms of the abundance of species at the phylum level show that the structures of soil fungal and bacterial communities vary in different aerial seeding years (Figure 3). The alpha diversity of fungi and bacteria shows significant increasing trends with the restoration period (Figure 4). In addition, the PCoA reveals a clear chronocline in the restoration time series of soil microorganisms (Figure 5).
Figure 3. Structure of soil fungal (A) and bacterial (B) communities in different aerial seeding years at the phylum level.
Figure 4. Relationship between the alpha diversity of soil microbial communities and restoration period. The alpha diversity include: (A)—bacteria ACE; (B)—fungus ACE; (C)—bacteria Chao1; (D)—fungus Chao1; (E)—bacteria Shannon; (F)—fungus Shannon; (G)—bacteria Simpson; (H)—fungus Simpson; (I)—bacteria observed species; (J)—fungus ACE.
3.2. Changes in Soil Nutrient Indexes with Restoration Period

Pearson correlation analysis suggests that with an increase in restoration year, TC, TN, and NO$_3^-$ significantly increase, while TP, NH$_4^+$, and AP do not change significantly (Figure 6).

Figure 5. PCoA of soil fungi and bacteria.

Figure 6. Relationship between soil nutrient indexes and restoration period. The soil nutrient indexes include: (A)—soil ammonium nitrogen; (B)—soil nitrate nitrogen; (C)—soil available phosphorus; (D)—total soil carbon; (E)—total soil nitrogen; (F)—total soil phosphorus.
3.3. Relationship between Soil Microbial Diversity and Soil Nutrient Indexes

The relationship between soil microbial diversity and soil nutrient indexes shows that the alpha diversity is significantly positively correlated with TC, TN and NO₃⁻ (Figure 7) but significantly negatively correlated with AP (Figure 7B). The CCA indicates that edaphic factors can explain 20.02% and 34.94% of soil fungi and bacteria at the phylum level, respectively (Figure 8). TC, TN and NO₃⁻ have strong correlations. With regard to the fungal community, Ascomycota and Glomeromycota are highly correlated with these soil nutrient indexes (Figure 8A). In terms of the bacterial community, Acidobacteria, Gemmatimonadetes and Nitrospirae are highly correlated with these soil nutrient indexes (Figure 8B).

![Figure 7](image-url) **Figure 7.** Relationship between the alpha diversity of soil fungal (A) and bacterial (B) communities and soil nutrient indexes. * represents p < 0.05, ** represents p < 0.01, *** represents p < 0.001.

![Figure 8](image-url) **Figure 8.** CCA results of the relationship of soil fungi (A) and bacteria (B) with soil nutrient indexes at the phylum level.
4. Discussion

The structure and composition of soil microbial communities are important for the conversion of soil organic matters and nutrient cycling [28]. The structure and diversity of microbial communities are sensitive to soil changes. Therefore, changes in diversity indexes can reflect soil degradation or restoration [29]. This study suggests that the diversity of soil microbial communities gradually increases with the period of revegetation by aerial seeding (Figure 4). The PCoA shows a clear chronocline of soil microorganisms in the restoration time series (Figure 5). This finding is consistent with the study result of Abakumov, et al. [30] that the diversity of the soil microbial community increases with the natural restoration of limestone quarries. The possible reason is that with the revegetation by aerial seeding, the surface vegetation grows, and the plant diversity gradually increases. Moreover, a plant community with a high degree of diversity can provide various litter and then diverse organic matters, leaving microorganisms less constrained by resource availability [31]. Therefore, the community composition of soil microorganisms can be further changed, and their diversity increases [32]. This phenomenon is consistent with the results of the present study (Figures 3–5). Furthermore, plant growth can dramatically alter soil microbial communities by releasing root exudates [33,34]. The functions of soil microbial communities, such as litter decomposition, are enhanced, improving soil functions [35] and then the microenvironment where soil microorganisms grow. Ultimately, plants and microorganisms can coevolve to increase the diversity of soil microbial communities [36]. It can be concluded that aerial seeding can promote the restoration of soil microbial communities and the accumulation of soil nutrients in the Mu Us Desert.

The Pearson correlation analysis demonstrates that the structure and diversity of microbial communities are significantly influenced by TC, TN and NO$_3^-$ (Figure 7), and these soil nutrient indexes increase significantly with the restoration period (Figure 6B,D,E). These results are consistent with the findings of Esmaeilzadeh-Salestani, et al. [37] that the cropping system with high organic carbon content increased the diversity of soil microorganisms. Liu et al. [2] analyzed the dominant microbial communities and soil chemical factors in different soil layers under different nitrogen deposition treatments on Stipa baicalensis and found that TN and NO$_3^-$ mainly influenced the structure of soil microbial communities. This finding also supported the conclusion of the present study. The possible reasons are as follows: First, soil nutrients directly affect the structure of soil microbial communities. For example, soil microorganisms can be divided into different nutritional groups according to nutritional requirements [38]. Gao et al. [39] also found that the content of nutrients, such as NO$_3^-$, could affect soil microbial diversity, when studying the influence of edaphic factors on soil microbial diversity in the vegetation protection area. Second, a mutual-feedback relationship exists between soil nutrients and plants. In addition, in the restoration process, several soil nutrients, such as TC, TN and NO$_3^-$, increase significantly (Figure 6B,D,E), possibly because with the restoration, the above-ground plants are restored. Both the diversity of plants and the biomass increase, providing more litter sources for the soil. As the main source of organic compounds, they can be decomposed by soil microorganisms, promoting the development of soil microbial communities. After microbial decomposition, the organic matters are converted to organic carbon and inorganic nutrients in the soil, in turn increasing soil nutrient content [40]. The correlation analysis in the present study indicates a significant positive correlation between soil nutrients and soil microbial communities. In summary, soil nutrient indexes, such as TC, TN, and NO$_3^-$, may significantly affect the structure and diversity of soil microbial communities through various pathways. Soil microbial communities, in turn, influence soil nutrients.

This study suggests that Ascomycota and Basidiomycota are dominant phyla (Figure 8A) in all aerial seeding years, which is consistent with the results of several studies [41,42]. Ascomycota is mostly saprophytic. It can take up multiple nutrients and plays a key role in degrading complex organic matters [43], which is evidenced by its strong correlation with soil nutrient indexes, such as TC, TN and NO$_3^-$ (Figure 8A). Basidiomycota is more capable of decomposing lignocelluloses from plant residues [44].
It is generally acknowledged that fungi play a vital role in degrading wilted substances. However, research shows that in addition to fungi, bacteria also contribute to litter transformation [45]. The biomass of bacteria gradually increases during decomposition [46,47], and the diversity gradually increases [48]. Moreover, bacteria are involved in a series of processes fundamental to biogeochemical cycles in soil, mediating several key steps in carbon and nitrogen cycling, such as nitrogen fixation [49]. These processes are reflected in the CCA for bacteria and various soil nutrient indexes at the phylum level (Figure 8B). For example, TN is highly correlated with Acidobacteria, which can degrade plant residues to release nitrogen into the soil [50,51]; the bacterial phyla that are highly associated with NO$_3^-$ are Nitrospirae and Gemmatimonadetes, the main functions of which are soil nitrification and nitrogen fixation [52–54]. It can be concluded that key soil fungal and bacterial phyla contribute to nutrient cycling in degraded ecosystems.

5. Conclusions

The analysis of 32 sample plots from 1983 to 2015 shows that aerial seeding contributes to the restoration of both soil microbial diversity and soil nutrients in mobile sandy lands. The alpha diversity of soil microorganisms increases significantly with the restoration period. The composition and diversity of soil microbial communities change over time. Soil nutrient indexes, such as TC, TN and NO$_3^-$, significantly increase with the restoration period and are significantly positively correlated with the diversity of soil fungi and bacteria. The results suggest that key soil fungal and bacterial phyla contribute to nutrient cycling in degraded ecosystems during restoration. In summary, aerial seeding promotes the restoration of soil microbial communities and soil nutrients in the Mu Us Desert. This paper can provide a reference for future measures and policies for the restoration of degraded lands and ecosystems by aerial seeding.

Author Contributions: Q.Z. and Q.L. conducted the field experiment; Y.M., L.Z. (Lei Zu), F.L., S.W., X.Y., Y.H., D.C., M.S., G.Z., L.Z. (Lipeng Zang) and Q.L. analyzed the data; Y.M. and S.W. contributed to drafting the paper; Y.M., S.W. and Q.L. contributed to the concept and design of the paper; S.W. was in charge of the final version of the paper. All authors have read and agreed to the published version of the manuscript.

Funding: This work was supported by the Guizhou Provincial Science and Technology Projects ([2019]1060, ZK [2022] General 079, ZK [2022] General 036, ZK [2022] General 098, ZK [2021] General 094, [2020]1Y124, [2019]2874). The Growth Project of Young Scientific and Technological Talents of Guizhou Provincial Department of Education (KY [2018]098). The Talent Introduction Project of Guizhou University (2017[38]).

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: The original contributions presented in the study are included in the article: further inquiries can be directed to the corresponding author.

Conflicts of Interest: The authors declare no conflict of interest.

References

1. Sokol, N.W.; Slessarev, E.; Marschmann, G.L.; Nicolas, A.; Blazewicz, S.J.; Brodie, E.L.; Firestone, M.K.; Foley, M.M.; Hestrin, R.; Hungate, B.A.; et al. Life and death in the soil microbiome: How ecological processes influence biogeochemistry. Nat. Rev. Microbiol. 2022, 20, 415–430. [CrossRef] [PubMed]

2. Liu, H.; Zhang, A.; Huangfu, C.; Li, J.; Wang, H.; Yang, D. Effects of Increasing Nitrogen Deposition on Soil Microbial Community Structure of Stipa Baicalensis Steppe in Inner Mongolia, China. Ecol. Environ. Sci. 2017, 26, 1100–1106.

3. Van Der Heijden, M.G.; Bardgett, R.D.; Van Straalen, N.M. The unseen majority: Soil microbes as drivers of plant diversity and productivity in terrestrial ecosystems. Ecol. Lett. 2008, 11, 296–310. [CrossRef] [PubMed]

4. Wardle, D.A.; Bardgett, R.D.; Klironomos, J.N.; Setälä, H.; Van Der Putten, W.H.; Wall, D.H. Ecological linkages between aboveground and belowground biota. Science 2004, 304, 1629–1633. [CrossRef]

5. Acosta-Martinez, V.; Dowd, S.; Sun, Y.; Allen, V. Tag-encoded pyrosequencing analysis of bacterial diversity in a single soil type as affected by management and land use. Soil Biol. Biochem. 2008, 40, 2762–2770. [CrossRef]
6. Maron, P.-A.; Lejon, D.P.; Carvalho, E.; Bizet, K.; Lemanceau, P.; Ranjard, L.; Mougel, C. Assessing genetic structure and diversity of airborne bacterial communities by DNA fingerprinting and 16S rDNA clone library. *Atmos. Environ.* **2005**, *39*, 3687–3695. [CrossRef]

7. Liu, Q.; Zhang, Q.; Jarvie, S.; Yan, Y.; Han, P.; Liu, T.; Guo, K.; Ren, L.; Yue, K.; Wu, H.; et al. Ecosystem restoration through aerial seeding: Interacting plant-soil microbiome effects on soil multifunctionality. *Land Degrad. Dev.* **2021**, *32*, 5334–5347. [CrossRef]

8. Li, M.-m.; Liu, A.-t.; Zou, C.-j.; Xu, W.-d.; Shimizu, H.; Wang, K.-y. An overview of the “Three-North” Shelterbelt project in China. *For. Stud. China* 2012, **14**, 70–79.

9. Wu, Z.; Wu, J.; Liu, J.; He, B.; Lei, T.; Wang, Q. Increasing terrestrial vegetation activity of ecological restoration program in the Beijing–Tianjin Sand Source Region of China. *Ecol. Eng.* **2013**, *52*, 37–50. [CrossRef]

10. Jia, X.; Fu, B.; Feng, X.; Hou, G.; Liu, Y.; Wang, X. The tradeoff and synergy between ecosystem services in the Grain-for-Green areas in Northern Shanxi, China. *Ecol. Indic.* 2014, **43**, 103–113. [CrossRef]

11. Gao, X.; Wang, Y.; Wang, J.; Van, C.; Li, Z. Analysis on desertification dynamics based on remote sensing and GIS in zones along the Great Wall in northern Shanxi province. *J. Desert Res.* **2005**, *25*, 63–67.

12. Liu, Y.; Zhang, H.; Xiong, M.; Li, F.; Zhang, X.; Pan, G.; Wang, G. Effect of climate change on soil microbial diversity and function. *China Environ. Sci.* **2016**, *36*, 3793–3799.

13. Wang, Y.; Li, J.; Jiang, L.; Zhang, Y.; Zhang, J. Effects of different precipitation treatments on soil fungal community and microbial diversity in the Loess Plateau. *Acta Ecol. Sin.* **2020**, *40*, 1517–1531.

14. Kuramae, E.; Gampfer, H.; van Veen, J.; Kowalchuk, G. Soil and plant factors driving the community of soil-borne microorganisms across chronosequences of secondary succession of chalk grasslands with a neutral pH. *FEMS Microbiol. Ecol.* **2011**, *77*, 285–294. [CrossRef]

15. Dai, J.; Yan, R.; Wei, Z.; Bai, Y.; Zhang, S.; Wang, T.; Sun, S. Effects of short-term fertilization on soil microorganisms in the riparian wetland along the downstream of the songhua river. *Environ. Sci.* **2021**, *42*, 2531–2540.

16. Oliver, A.K.; Callaham, M.A., Jr.; Jumpponen, A. Soil fungal communities respond compositionally to recurring frequent prescribed burning in a managed southeastern US forest ecosystem. *For. Ecol. Manag.* **2015**, *345*, 1–9. [CrossRef]

17. Zhang, L.; Hong, G.; Li, Z.; Gao, X.; Wu, Y.; Wang, X.; Wang, P.; Yang, J. Assessment of the ecosystem service function of Sandy Lands at different times following aerial seeding of an endemic species. *Sustainability* **2018**, *10*, 902. [CrossRef]

18. Liu, Q.; Zhang, Q.; Yan, Y.; Zhang, X.; Niu, J.; Svenning, J.-C. Ecological restoration is the dominant driver of the recent reversal of desertification in the Mu Us Desert (China). *J. Clean. Prod.* **2020**, *268*, 122241. [CrossRef]

19. Liu, X.; Huang, Z.; Havrilla, C.A.; Liu, Y.; Wu, G.L. Plant litter crust role in nutrients cycling potentials by bacterial communities in a sandy land ecosystem. *Land Degrad. Dev.* **2021**, *32*, 3194–3203. [CrossRef]

20. Wang, G.; Su, Z.; Mao, L.; Zhang, Q.; Ma, Y. Characteristics of Soil Surface Grain Size in Ordos Plateau along the Agro-pastoral Ecotone of North China. *J. Desert Res.* **2019**, *39*, 183.

21. Xue, F.; Zhang, T.; Huai, B.-D.; Sui, W.-Z.; Yang, X. Effects of land use changes on soil fungal community structure and function in the riparian wetland along the downstream of the songhua river. *Environ. Sci.* **2021**, *42*, 2531–2540.

22. Corre, M.D.; Beese, F.O.; Brumme, R. Soil nitrogen cycle in high nitrogen deposition forest: Changes under nitrogen saturation and liming. *Ecol. Appl.* **2003**, *13*, 287–298. [CrossRef]

23. Zhang, Q.; Buyantuev, A.; Li, F.Y.; Jiang, L.; Niu, J.; Ding, Y.; Kang, S.; Ma, W. Functional dominance rather than taxonomic diversity and functional diversity mainly affects community aboveground biomass in the Inner Mongolia grassland. *Ecol. Evol.* 2017, *7*, 1605–1615. [CrossRef] [PubMed]

24. Fadrosh, D.W.; Ma, B.; Gajer, P.; Sengamalay, N.; Ott, S.; Brotman, R.M.; Ravel, J. An improved dual-indexing approach for multiplexed 16S RNA gene sequencing on the Illumina MiSeq platform. *Microbiome* **2014**, *2*, 6. [CrossRef]

25. Rognes, T.; Flouri, T.; Nichols, B.; Quince, C.; Mahé, F. VSEARCH: A versatile open source tool for metagenomics. *PeerJ* **2016**, *4*, e2584. [CrossRef]

26. Blaxter, M.; Mann, J.; Chapman, T.; Thomas, F.; Whitton, C.; Floyd, R.; Abebe, E. Defining operational taxonomic units using DNA barcode data. *Philos. Trans. R. Soc. B Biol. Sci.* **2005**, *360*, 1935–1943. [CrossRef]

27. Caporaso, J.G.; Lauber, C.L.; Walters, W.A.; Berg-Lyons, D.; Lozupone, C.A.; Turnbaugh, P.J.; Fierer, N.; Knight, R. Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. *Proc. Natl. Acad. Sci. USA* **2011**, *108*, 4516–4522. [CrossRef]

28. Bell, T.; Newman, J.A.; Silverman, B.W.; Turner, S.L.; Lilley, A.K. The contribution of species richness and composition to bacterial services. *Nature* **2005**, *436*, 1157–1160. [CrossRef]

29. Cao, C.; Yao, J.; Han, X.; Zhang, Y. Soil microbes functional diversity in sand-fixing Caragana microphylla communities in Horqin Sandy Land. *Chin. J. Appl. Ecol.* **2011**, *22*, 2309–2315.

30. Abakumov, E.; Zverev, A.; Kichko, A.; Kimelkis, A.; Andronov, E. Soil microbiome of different-aged stages of self-restoration of ecosystems on the mining territories of the Leningrad region (Elizavetino). *Open Agric.* 2021, *6*, 57–66. [CrossRef]

31. Zak, D.R.; Holmes, W.E.; White, D.C.; Peacock, A.D.; Tilman, D. Plant diversity, soil microbial communities, and ecosystem function: Are there any links? *Ecology* **2003**, *84*, 2042–2050. [CrossRef]

32. Hooper, D.U.; Bignell, D.E.; Brown, V.K.; Brussard, L.; Dangerfield, J.M.; Wall, D.H.; Wardle, D.A.; Coleman, D.C.; Giller, K.E.; Lavalle, P. Interactions between aboveground and belowground biodiversity in terrestrial ecosystems: Patterns, mechanisms, and feedbacks. *Bioscience* **2000**, *50*, 1049–1061. [CrossRef]

33. Badri, D.V.; Vivanco, J.M. Regulation and function of root exudates. *Plant Cell Environ.* **2009**, *32*, 666–681. [CrossRef] [PubMed]
34. Shi, S.; Nuccio, E.E.; Shi, Z.J.; He, Z.; Zhou, J.; Firestone, M.K. The interconnected rhizosphere: High network complexity dominates rhizosphere assemblages. *Ecol. Lett.* 2016, 19, 926–936. [CrossRef]

35. Cai, Q.; Ding, G. A discussion on evaluation indexes of forestry soil eco-environment quality. *J. Mt. Agric. Biol. 2006*, 25, 256–261.

36. Delgado-Baquerizo, M.; Maestre, F.T.; Reich, P.B.; Jeffries, T.C.; Gaitan, J.J.; Encinar, D.; Berdugo, M.; Campbell, C.D.; Singh, B.K. Microbial diversity drives multifunctionality in terrestrial ecosystems. *Nat. Commun.* 2016, 7, 10541. [CrossRef]

37. Esmailzadeh-Salestani, K.; Bahrami Moheb Seraj, R.; Gohar, D.; Tohidfar, M.; Eremeet, V.; Talgre, L.; Khaleghdoust, B.; Mirmajlesi, S.M.; Luik, A.; et al. Cropping systems with higher organic carbon promote soil microbial diversity. *Agric. Ecosystems. Environ.* 2021, 319, 107521. [CrossRef]

38. Zhang, Q.; Zhao, W.; Zhou, Z.; Huang, G.; Wang, X.; Han, Q.; Liu, G. The Application of Mixed Organic and Inorganic Fertilizers Drives Soil Nutrient and Bacterial Community Changes in Teak Plantations. *Microorganisms* 2022, 10, 958. [CrossRef]

39. Gao, Y.; He, Z. Study on Soils Effect Factors to Fungi Diversity in Hebei Province. *Chin. Agric. Sci. Bull.* 2010, 26, 177–181.

40. Su, N.; Jarvie, S.; Yan, Y.; Gong, X.; Li, F.; Han, P.; Zhang, Q. Landscape context determines soil fungal diversity in a fragmented habitat. *CATENA* 2022, 213, 106163. [CrossRef]

41. Jiang, X.; Ma, D.; Zang, S.; Zhang, D.; Sun, H. Characteristics of soil bacterial and fungal community of typical forest in the Greater Khingan Mountains based on high-throughput sequencing. *Microbiol. China* 2021, 48, 1093–1105.

42. Chen, X.; Zhu, D.; Zhao, C.; Zhang, L.; Chen, L.; Duan, W. Community Composition and Diversity of Fungi in Soils under Different Types of Pinus koraiensis Forests. *Acta Pedol. Sin.* 2019, 56, 1221–1234.

43. Beimforde, C.; Feldberg, K.; Nylander, S.; Rikkinen, J.; Tuovila, H.; Dörfelt, H.; Gube, M.; Jackson, D.J.; Reitner, J.; Seyfullah, L.J. Estimating the Phanerozoic history of the Ascomycota lineages: Combining fossil and molecular data. *Mol. Phylogenetics Evol.* 2014, 78, 386–398. [CrossRef][PubMed]

44. Frey, S.D.; Knorr, M.; Parrent, J.L.; Simpson, R.T. Chronic nitrogen enrichment affects the structure and function of the soil microbial community in temperate hardwood and pine forests. *For. Ecol. Manag.* 2004, 196, 159–171. [CrossRef]

45. Štursová, M.; Žižák, L.; Leith, M.B.; Burgess, R.; Baldrian, P. Cellulose utilization in forest litter and soil: Identification of bacterial and fungal decomposers. *FEMS Microbiol. Ecol.* 2012, 80, 735–746. [CrossRef]

46. Urbanová, M.; Šnajdr, J.; Brabcová, V.; Merhautová, V.; Dobiášová, P.; Cai, Z.; Vaněk, D.; Frouz, J.; Šantářková, H.; Baldrian, P. Litter decomposition along a primary post-mining chronosequence. *Biol. Fertil. Soils* 2014, 50, 827–837. [CrossRef]

47. Voříšková, J.; Baldrian, P. Fungal community on decomposing leaf litter undergoes rapid successional changes. *ISME J.* 2013, 7, 477–486. [CrossRef][PubMed]

48. Purahong, W.; Schlote, M.; Peczyňa, M.J.; Kapturska, D.; Däumlich, V.; Mital, S.; Buscot, F.; Hofrichter, M.; Gutknecht, J.L.; Krüger, D. Uncoupling of microbial community structure and function in decomposing litter across beech forest ecosystems in Central Europe. *Sci. Rep.* 2014, 4, 7014. [CrossRef]

49. Lladó, S.; López-Mondejar, R.; Baldrian, P. Forest soil bacteria: Diversity, involvement in ecosystem processes, and response to global change. *Microbiol. Mol. Biol. Rev.* 2017, 81, e00063-16. [CrossRef]

50. Eichorst, S.A.; Kuske, C.R.; Schmidt, T.M. Influence of plant polymers on the distribution and cultivation of bacteria in the phylum Acidobacteria. *Appl. Environ. Microbiol.* 2011, 77, 586–596. [CrossRef]

51. Pankratov, T.A.; Ivanova, A.O.; Dedys, S.N.; Liesack, W. Bacterial populations and environmental factors controlling cellulose degradation in an acidic Sphagnum peat. *Environ. Microbiol.* 2011, 13, 1800–1814. [CrossRef][PubMed]

52. Attard, E.; Poly, F.; Commeaux, C.; Laurent, F.; Terada, A.; Smets, B.F.; Recous, S.; Roux, X.L. Shifts between Nitrospira-and Nitrobacter-like nitrite oxidizers underlie the response of soil potential nitrite oxidation to changes in tillage practices. *Environ. Microbiol.* 2010, 12, 315–326. [CrossRef][PubMed]

53. Xia, W.; Zhang, C.; Zeng, X.; Feng, Y.; Weng, J.; Lin, X.; Zhu, J.; Xiong, Z.; Xu, J.; Cai, Z. Autotrophic growth of nitrifying community in an agricultural soil. *ISME J.* 2011, 5, 1226–1236. [CrossRef][PubMed]

54. Canbolat, M.Y.; Bilen, S.; Cakmak, R.; Sahin, F.; Aydin, A. Effect of plant growth-promoting bacteria and soil compaction on barley seedling growth, nutrient uptake, soil properties and rhizosphere microflora. *Biol. Fertil. Soils* 2006, 42, 350–357. [CrossRef]