

Rhizosphere Soil Fungal Diversity and Soil Physicochemical Properties of Different Vegetations in Tundra of Changbai Mountain

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Abstract

By studying the diversity and community structure of rhizosphere soil fungi of different plants in the tundra on the northern slope of Changbai Mountain, it provides theoretical support for the restoration of environmental degradation and in-depth study of fungal diversity in the tundra of Changbai Mountain. High-throughput sequencing technology was used to determine the ITS1 region of fungal amplicons, so as to analyze the diversity of fungal communities in the rhizosphere soil of six plants in the tundra of Changbai Mountain, and to analyze the correlation between the environment and the diversity and richness of fungal communities in combination with relevant soil physical and chemical factors. The diversity and richness of fungal community in the rhizosphere soil of six plants in Changbai Mountain tundra were different. The Simpson and Shannon indexes of *Saxifraga stolonifera* Curt were the highest, and the richness of fungal community in *Dryas octopetala* was the highest. The analysis of fungal community composition showed that the fungal colonies in plant rhizosphere soil samples mainly belonged to Ascomycota and Basidiomycota, which were the main dominant phyla. *Mortierella*, *Fusarium* and Sordariomycetes are common fungal genera in the rhizosphere soil of six plants, but their abundances are different among different plants. Water content was negatively correlated with fungal diversity, and TP was positively correlated with fungal community diversity. There were some differences in the composition and diversity of rhizosphere soil fungal communities of six plants in Changbai Mountain tundra. Ascomycota and Basidiomycota were the main soil fungal phyla in the rhizosphere of six plants in Changbai Mountain tundra. The results could provide theoretical guidance for ecological protection of Changbai Mountain tundra.

Keywords

Changbai Mountain, Rhizosphere Soil, Fungal Diversity, Soil Environmental Factors

1. Introduction

Changbai Mountain is the highest mountain system in the eastern margin of Eurasia. The main peak Baiyun Peak is also the first peak in Northeast China. The only alpine tundra in Northeast China is of great significance for maintaining regional animal and plant habitats, biodiversity and regional ecological balance (Wu et al., 2002). However, the degradation of the tundra caused by climate problems is a serious problem facing the tundra at present. The ecosystem of the tundra is changing due to global warming, and forests have appeared in some places. This change may further aggravate global warming, which will change the physical and chemical properties and biodiversity of the tundra zone to some extent (Bjorkman et al., 2018). The tundra zone of Changbai Mountain is also facing the phenomenon of forest invasion of tundra zone, but there are still abundant tundra plants, which are the dominant plants in the tundra zone of the northern slope of Changbai Mountain and play an important role in maintaining the ecological balance of the tundra zone of Changbai Mountain (Alexander et al., 2016). Rhizosphere soil fungi are important components of soil-plant ecosystem (Philippot et al., 2013), composition and diversity of fungal community structure affect plant growth and development (Coats & Rumpho, 2014). Although soil nutrients (Zhou et al., 2017; Leewis et al., 2022) and water content (Lin et al., 2021) have a certain effect on soil microbial community structure. However, the characteristics of the soil itself and the root exudates of the vegetation have a greater impact on the fungal community structure and diversity (Gao et al., 2021; Hu et al., 2019). Fungal diversity is of great significance in maintaining ecological balance, fungal diversity is closely related to climate, vegetation types and soil nutrients (Huang et al., 2023). By studying the diversity of different plant rhizosphere soil fungi, we can further understand the fungal community structure, but also conducive to understanding changes in the environment for the ecological restoration of Changbai Mountain tundra to provide theoretical support.

In recent years, high-throughput sequencing technology has been widely used in the study of fungal diversity and community structure with the advantages of high sequencing throughput and high accuracy (Dong et al., 2017). Chen et al. (2021) used high-throughput sequencing technology to explore the differences in fungal community composition in the rhizosphere soil of medicinal Yinxing from different producing areas. Wu et al. (2021) studied the rhizosphere and non-rhizosphere soils of *Artemisia argyi*, and found that there were some differences in the composition and diversity of fungal communities between rhi-

zosphere and non-rhizosphere soils. Zhang et al. (2021) analyzed the fungal community diversity in rhizosphere soil of 6 halophytes in Ebinur Lake wetland and found that soil physical and chemical factors had significant effects on the fungal diversity in rhizosphere soil. At present, the study of forest soil fungal community in Changbai Mountain is more common in Yao et al. (2007) and Yang et al. (2009). However, there are few studies on soil fungal community diversity in Changbai Mountain tundra zone, and most of them focus on the effects of tourism (Wang, 2022) and human disturbance (Zhang et al., 2022) on soil fungal community. The use of high-throughput sequencing technology to analyze the same period in Changbai Mountain tundra different plant rhizosphere soil fungal community diversity and richness of research is rarely reported.

In this paper, the rhizosphere soils of six dominant plants, *Orosta. chys fimbriata* (Turcz.) Berg, *Saxifraga stolonifera* Curt, *Dryas octopetala*, *Rhondodendron aureum*, *Vaccinium uliginosum*, *Rhondodendron confertissimum* collected from the tundra zone of Changbai Mountain were studied. The diversity and community structure of fungi in rhizosphere soil of different plants were studied, and the correlation between environmental factors and them was analyzed. The potential influence mechanism of fungal community in rhizosphere soil of different vegetation on plant growth in tundra of Changbai Mountain was explored, which provided theoretical guidance for ecological environment protection in Changbai Mountain.

2. Research Area and Research Methods

2.1. Overview of the Study Area

Changbai Mountain tundra is located at an altitude of more than 2000 m, belonging to the upper part of the volcanic vertebral body, cold and windy. It is covered with snow for at least six months of the year (Wang et al., 2014). According to the vegetation condition, the tundra belt is divided into two sub-belts. The upper tundra subzone is located at an altitude of more than 2300 m. The main features are cold and foggy, precipitation and wind. The average temperature was lower than -20°C in January, 8°C - 10°C in July, and the frost-free period was less than 60 days. The soil is alpine desert soil. The lower tundra subzone is located at 2000 - 2300 m, cold and windy. The active accumulated temperature of $\geq 10^{\circ}\text{C}$ is 300°C - 500°C , and the annual precipitation is 1100 - 1300 mm, soil is alpine tundra soil and Mossy lichens mainly. The main plants are *Orosta. chys fimbriata* (Turcz.) Berg, *Saxifraga stolonifera* Curt, *Dryas octopetala*, *Rhondodendron aureum*, *Vaccinium uliginosum*, *Rhondodendron confertissimum* et al. (Chen et al., 1983).

2.2. Sampling

In this study, three-point sampling method was used to sample the rhizosphere soil of six dominant plants in the tundra of Changbai Mountain in September 2022. The rhizosphere soil of six dominant plants, namely, *Orosta. chys fimbria-*

ta (Turcz.) Berg, *Saxifraga stolonifera* Curt, *Dryas octopetala*, *Rhondodendron aureum*, *Vaccinium uliginosum*, *Rhondodendron confertissimum*, was sampled at a fixed point. Specific sampling information is shown in **Table 1**. Three plant community areas were randomly selected for each plant, and the rhizosphere soil of three plants was selected for each community area. A total of 9 soil samples were collected for each plant. The 9 soil samples were mixed well as the rhizosphere soil samples of a plant, label after filling in sterile ziplock bag. Fungal Taxonomy Laboratory, College of Environment and Resources, Dalian Minzu University, Divide the soil sample into two parts: A natural air drying, grinding, 4 mm nylon sieve screening, determination of soil physical and chemical properties; the other is stored in a -80°C refrigerator for high-throughput sequencing.

2.3. Extraction of Soil Total DNA

Using the TGuide S96 Magnetic Soil/Stool DNA Kit (Tiangen Biotech (Beijing) Co. Ltd.) total DNA of soil samples was extracted with three replicates for each sample and diluted total DNA was used as template, Using standard specific primers for ITS1: ITS1F (CTTGGTCATTTAGAGGAAGTAA) R (GCTGCGTTCTTCATCGATGC) Amplification. PCR reaction mixture (25 μL): $2 \times \text{PCRmix}$ 10 μL , Upstream and downstream primers 1 μL each, template 3 μL , Replenishment ddH₂O to 25 μL . PCR reaction condition: 95°C 5 min; 95°C 30 s, 50°C 30 s, 72°C 40 s, 25 cycles; 72°C 7 min. After detected by 1.8% agarose gel electrophoresis. Five PCR products belonging to the same sample were mixed

Table 1. Sampling information of tundra zone in Changbai Mountain.

Sample names	Vegetation species	Longitude	Latitude	Season	Soi Type	ASL
A1	<i>Orosta. chys fimbriata</i> (Turcz.) Berg	128.0772	42.0684	Summer	Tundra soils	2203 \pm 5
B1	<i>Saxifraga stolonifera</i> Curt	128.0772	42.0685	Summer	Tundra soils	2117 \pm 5
C1	<i>Rhondodendron confertissimum</i>	128.0771	42.0683	Summer	Tundra soils	2176 \pm 5
D1	<i>Vaccinium uliginosum</i>	128.0774	42.0683	Summer	Tundra soils	2235 \pm 5
E1	<i>Dryas octopetala</i>	128.0772	42.0684	Summer	Tundra soils	2206 \pm 5
F1	<i>Rhondodendron aureum</i>	128.0774	42.0683	Summer	Tundra soils	2223 \pm 5

The different capital letter abbreviations represent different vegetation species. A1: *Orosta. chys fimbriata* (Turcz.) Berg; B1: *Saxifraga stolonifera* Curt; C1: *Rhondodendron confertissimum*; D1: *Vaccinium uliginosum*; E1: *Dryas octopetala*; F1: *Rhondodendron aureum*. The same as below.

evenly into one sample and sent to Qingdao Biomarker Technologies Technology Co., Ltd. for high-throughput sequencing.

2.4. Soil Physical and Chemical Properties

The soil moisture content (SM), total nitrogen (TN), total phosphorus (TP), nitrate nitrogen (NO_3), available phosphorus (AP) and ammonium nitrogen (NH_4^+) were measured by conventional soil analysis methods (Chen, 2005; Bao, 2018; Li, 2008).

2.5. Bioinformatics Analysis

Data preprocessing after removing barcodes and primers, FLASH, QIIME, MOTHUR and other software were used to obtain valid data. OTUs were divided with a similarity of 0.97 and representative sequences were selected. Species annotation and statistics were performed on the representative sequences of OTUs. SPSS26.0 was used for data analysis and C Programming Language was used for drawing.

3. Results and Analysis

3.1. Sequencing Results of Soil Fungal Samples

After Illumina Novaseq high-throughput sequencing and optimization, a total of 453,217 effective sequences were obtained from fungi in rhizosphere soil samples of 6 plants. On the basis of an average of 75,536 Clean Reads generated by each sample, the samples were clustered and annotated to obtain 2981 ASVs (amplicon sequence variants).

According to the dilution curve (Figure 1), it can be seen that the curve tends to be gentle with the increase of the number of sequencing, that is, the number of new OTUs will not increase with the increase of sequencing depth, indicating that the test has obtained the vast majority of sample information, which can reflect the microbial community composition of soil samples, and the sequencing data is reasonable.

3.2. Statistical Analysis of Fungal Community Richness Diversity

It can be seen from Table 1 that the coverage rate of sequencing depth index of each sample was above 0.997, indicating that the sequencing amount was sufficient to cover the colony composition of the sample. After merging according to 97% similarity, the number of fungal OTUs in 6 groups of samples were 289, 524, 637, 913, 936 and 472, respectively, The Sequence of OUT Number in 6 Rhizosphere Soils in Changbai Mountain Tundra: XNM > ZSYJ > MZDJ > HEC > NPDJ > WS. Alpha diversity was used to analyze the richness and diversity of fungal communities in the soil, and the richness index (Ace) of different plant rhizosphere fungal communities was ranked as follows: XNM > ZSYJ > MZDJ > HEC > NPDJ > WS. Shannon's diversity index and Simpson's diversity index showed the following order: HEC > WS > XNM > ZSYJ > MZDJ > NPDJ.

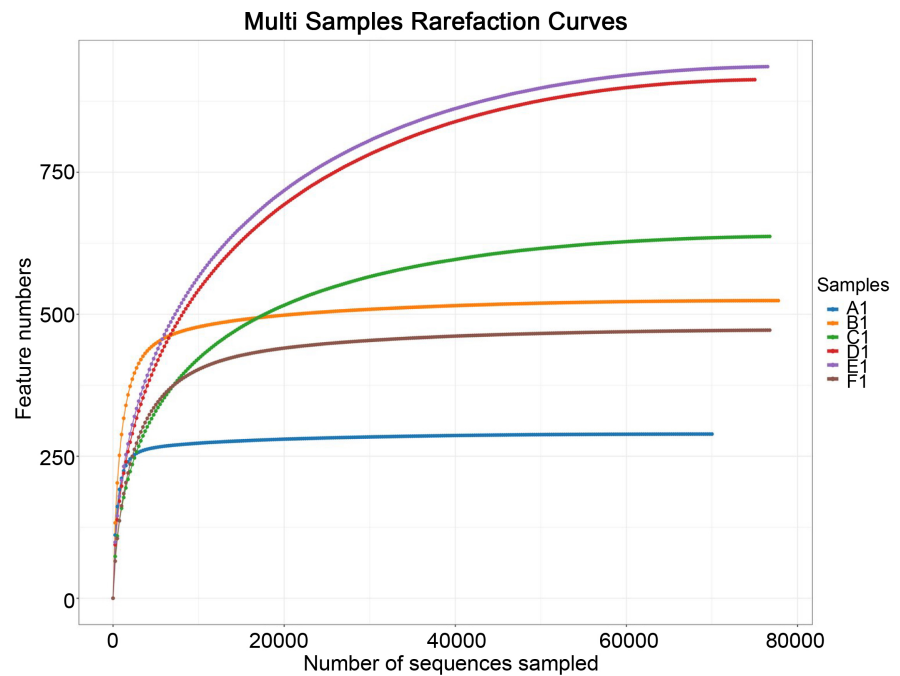


Figure 1. Dilution curves of rhizosphere soil samples of six species in tundra of Changbai Mountain.

The results showed that the fungal diversity in the rhizosphere soil of *Saxifraga stolonifera* Curt was more abundant than that of *Rhododendron aureum* at the same altitude, which may be due to the selectivity of *Rhododendron aureum* roots to rhizosphere soil fungi (Li, 2017). *Rhododendron aureum* rhizosphere growth reduced the diversity of soil fungi, so that the types of soil fungal communities tend to be single, and the number of species decreased.

3.3. Analysis of Soil Fungal Community Structure

Species composition analysis can reflect the community structure of samples at taxonomic level. As shown in Table 2, the fungi in the rhizosphere soil of the six Changbai Mountain tundra zones belong to 14 phyla, 51 classes, 113 orders, 239 families and 475 genera. (Table 3) As shown in Figure 2, Ascomycota and Basidiomycota were the main groups of rhizosphere soil of different plants in the six tundra zones of Changbai Mountain. The order of relative abundance was MZDJ (63.68%) > HEC (54.68%) > WS (50.62%) > ZSYJ (44.21%) > XNM (40.79%) > NPDJ (14.46%) and NPDJ (67.96%) > XNM (47.46%) > ZSYJ (46.84%) > MZDJ (31.13%) > HEC (28.53%) > WS (27.09%). Mortierellomycota comes second with a relative abundance of 1.5% to 10%. In addition, Fungi _ unclassified and other groups with relative abundance of about 3% - 8% were not clearly classified in GenBank. As shown in Figure 2, Agaricomycetes, Tremellomycetes, Eurotiomycetes, Sordariomycetes, Archaeorhizomycetes, Dothideomycetes and Mortierellomycetes are the dominant fungal groups in the soil community, The order of total relative abundance was MZDJ (87.62%) > NPDJ (85.41%) > XNM (74.53%) > ZSYJ (63.47%) > WS (59.36%) > HEC (56.82%). In addition, Fungi _

Table 2. Rhizosphere soil fungal community richness and diversity index of six species in tundra of Changbai Mountain.

<i>Plant</i>	OUT	ACE	Chao1	Simpson	Shannon	PD_whole_tree	Coverage
WS	289	289.0000	289.0000	0.9782	6.8355	70.1160	1.0000
HEC	524	524.4172	524.0000	0.9869	7.5808	111.0295	1.0000
MZDJ	637	643.2204	638.4468	0.9296	5.5522	99.7943	0.9998
ZSYJ	913	920.8701	913.8520	0.9754	6.6351	144.6320	0.9997
XNM	936	943.6074	937.0145	0.9776	6.7682	157.6711	0.9997
NPDJ	472	472.5118	472.9130	0.8090	4.5424	122.6454	0.9999

Table 3. Statistical table of species of rhizosphere soil fungal community of six species.

<i>Plant</i>	Kindom	Phylum	Class	Order	Family	Genus	Species
WS	1	9	30	55	90	111	124
HEC	1	9	32	64	115	164	202
MZDJ	1	8	28	65	134	224	300
ZSYJ	1	11	36	80	155	265	373
XNM	1	10	40	85	173	295	406
NPDJ	1	11	36	66	127	172	203
Total	1	14	51	113	239	475	744

unclassified and other groups were not clearly classified in GenBank, and their relative abundance was ranked as WS (8.27%) > HEC (7.46%) > ZSYJ (3.25%) > XNM (2.81%) > MZDJ (2.26%) > NPDJ (2.24%).

3.4. Taxonomic Analysis of Fungal Flora in Rhizosphere Soil of Different Plants

R software was used to cluster the samples according to their abundance information in each soil treatment, and the classification units and samples were sorted according to the clustering results to draw a heat map. Through clustering, it is possible to distinguish between high abundance and low abundance taxa. Red and blue represent the abundance of the genus. The more biased red indicates the higher abundance, and the more biased blue indicates the lower abundance. The relative abundances of Monoblepharomycota, Aphelidiomycota, Blastocladiomycota, Zoopagomycota, Basidiomycota, Kickxellomycota, Chytridiomycota, Glomeromycota, Rozellomycota, Ascomycota, Mucoromycota and Unclassified unclassified fungi of soil fungi in 6 samples were displayed according to different colors by Heatmap. According to the relative abundance characteristics of fungi in 6 samples, the fungi were clustered according to the similarity of fungi. The highest similarity of fungi in *Dryas octopetala* and *Rhondodendron confertissimum* rhizosphere soil was clustered into the first category, and then clustered with *Vaccinium uliginosum* into the second category; the similarity between *Orosta. chys fimbriata* (Turcz.) Berg and *Saxifraga stolonifera* Curt

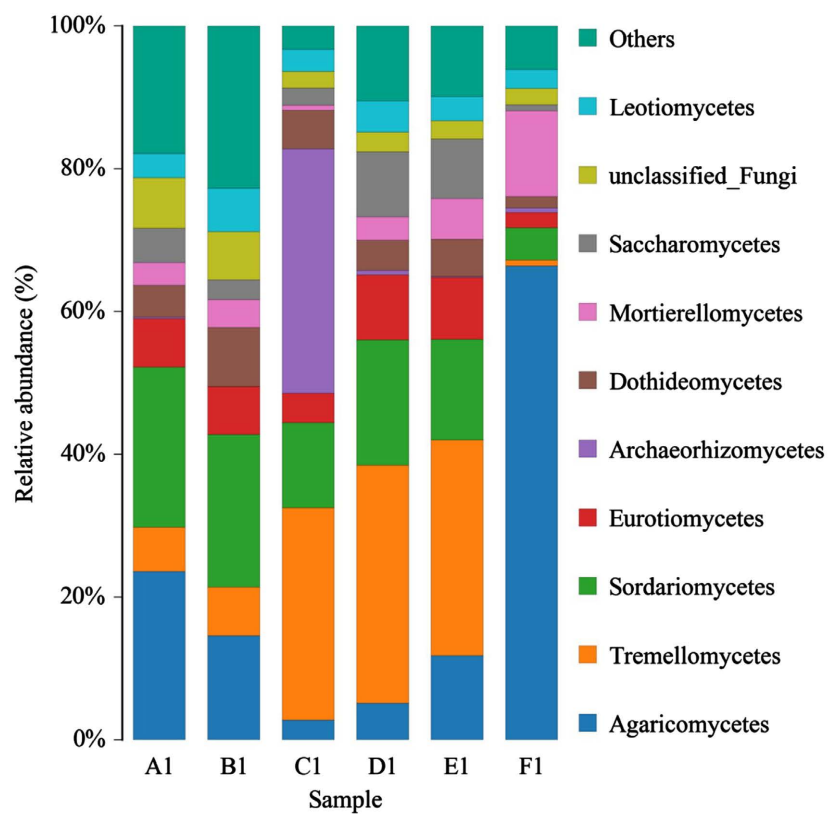
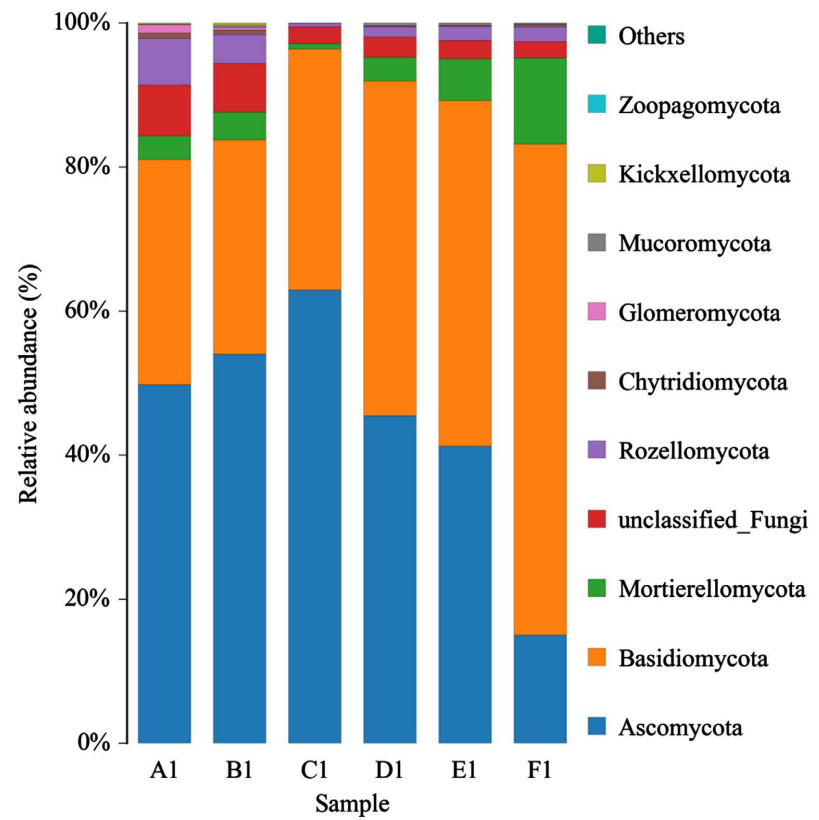


Figure 2. Community structure of six plant rhizosphere soil fungi at phylum, Class level.

rhizosphere soil fungi was the closest to the third category. *Rhondodendron aureum* is a separate category.

According to **Figure 3**, the relative abundance of Glomeromycota in *Orosta chys fimbriata* (Turcz.) Berg samples was the highest; the relative abundance of comb gate was the highest in *Saxifraga stolonifera* Curt samples. The relative abundance of Ascomycota was the highest in *Rhondodendron confertissimum* samples. Basidiomycete and Monoblepharomycota had the highest relative abundance in *Vaccinium uliginosum* samples. The relative abundance of Aphelidiomycota was the highest in *Dryas octopetala* samples. The relative abundance of Zoopagomycota and Blastocladiadia in *Rhondodendron aureum* was the highest. Therefore, the relative abundance and distribution of soil fungi varied greatly among different plants in the same natural zone (Weber et al., 2015).

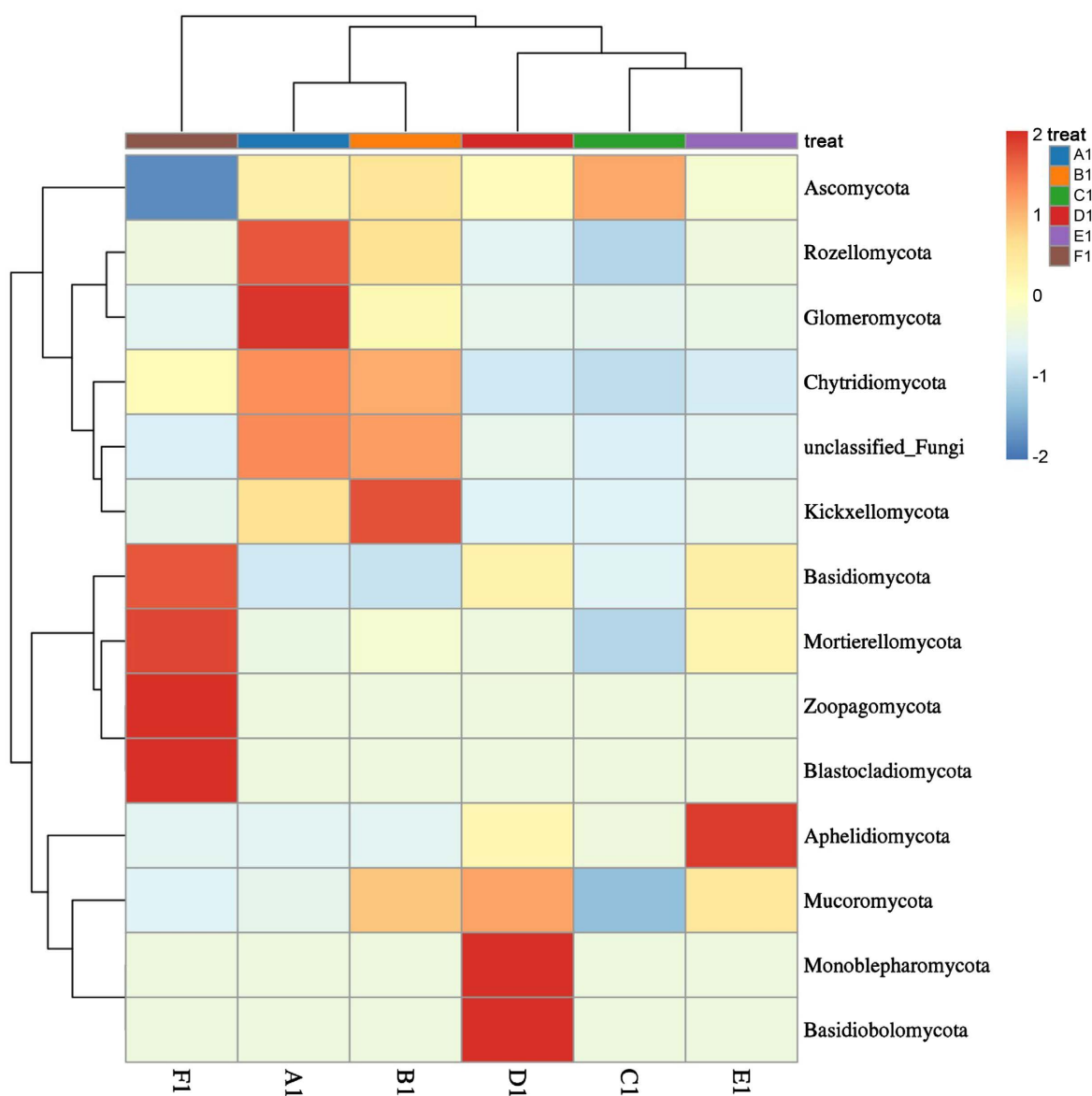


Figure 3. Heat map of genus-level community composition in rhizosphere soils of six species.

3.5. Correlation Analysis between Fungal Diversity and Environmental Factors

RDA (Redundancy analysis) is a ranking method based on the development of correspondence analysis. RDA is mainly used to reflect the relationship between flora or samples and environmental factors. Redundancy analysis showed that *Cutaneotrichosporon* and *Trichosporon* were negatively correlated with NH_4^+ , *Fusarium* was positively correlated with moisture content and negatively correlated with TN and TP. *Entoloma* and *Mortierella* were negatively correlated with NO_3 and positively correlated with NH_4^+ . The rhizosphere soil moisture content of *Saxifraga stolonifera* Curt was the highest, and the fungal diversity index was also the highest, indicating that the moisture content could enrich the growth of fungi to a certain extent. *Orosta. chys fimbriata* (Turcz.) Berg and *Rhondodendron aureum* were significantly positively correlated with NH_4^+ . *Dryas octopetala* and *Vaccinium uliginosum* were positively correlated with NO_3 . However, *Rhondodendron confertissimum* is positively correlated with TN and TP (Figure 4). Through correlation analysis, the relationship between fungal community diversity and environmental factors in rhizosphere soil of six plants was obtained. The results are shown in the table. The correlation between most environmental factors and diversity index of rhizosphere soil of six plants in tundra of Changbai Mountain was not significant. AP was positively correlated with Shannon index and negatively correlated with Simpson index. TP was positively correlated with Shannon, Simpson, Chao1 index, ACE index and OTU number. WC was negatively correlated with Shannon, Simpson, Chao1 index, ACE index and OTU number (Table 4).

4. Discussion and Results

4.1. Diversity and Richness of Fungal Community in Rhizosphere Soil of 6 Plants in Tundra of Changbai Mountain

High throughput sequencing technology can analyze soil fungal colony information accurately, systematically and comprehensively (Lou et al., 2018). The diversity of fungal community in rhizosphere soil of 6 plant species in tundra of Changbai Mountain was analyzed by high-throughput sequencing technology. A total of 2981 OTUs were obtained, including 14 phyla, 51 classes, 113 orders, 239 families, 475 genera and 744 species. Trichosporonaceae, Entolomataceae, Archaerhizomycetaceae, Mortierellaceae, Nectriaceae, debaryomycetaceae, etc. are dominant. Rhizosphere soil fungi of six different plants in Changbai Mountain tundra were analyzed. The results showed that the community structure and diversity of rhizosphere soil fungi of six different plants were different. The overall trend of community richness and diversity was XNM > ZSYJ > MZDJ > HEC > NPDJ > WS. In community composition, the dominant phyla of fungi in rhizosphere soil of 6 plants were Basidiomycota and Ascomycota. The fungal communities in the rhizosphere soils of *Orosta. chys fimbriata* (Turcz.) Berg and *Saxifraga stolonifera* Curt were close to each other. The fungal communities in

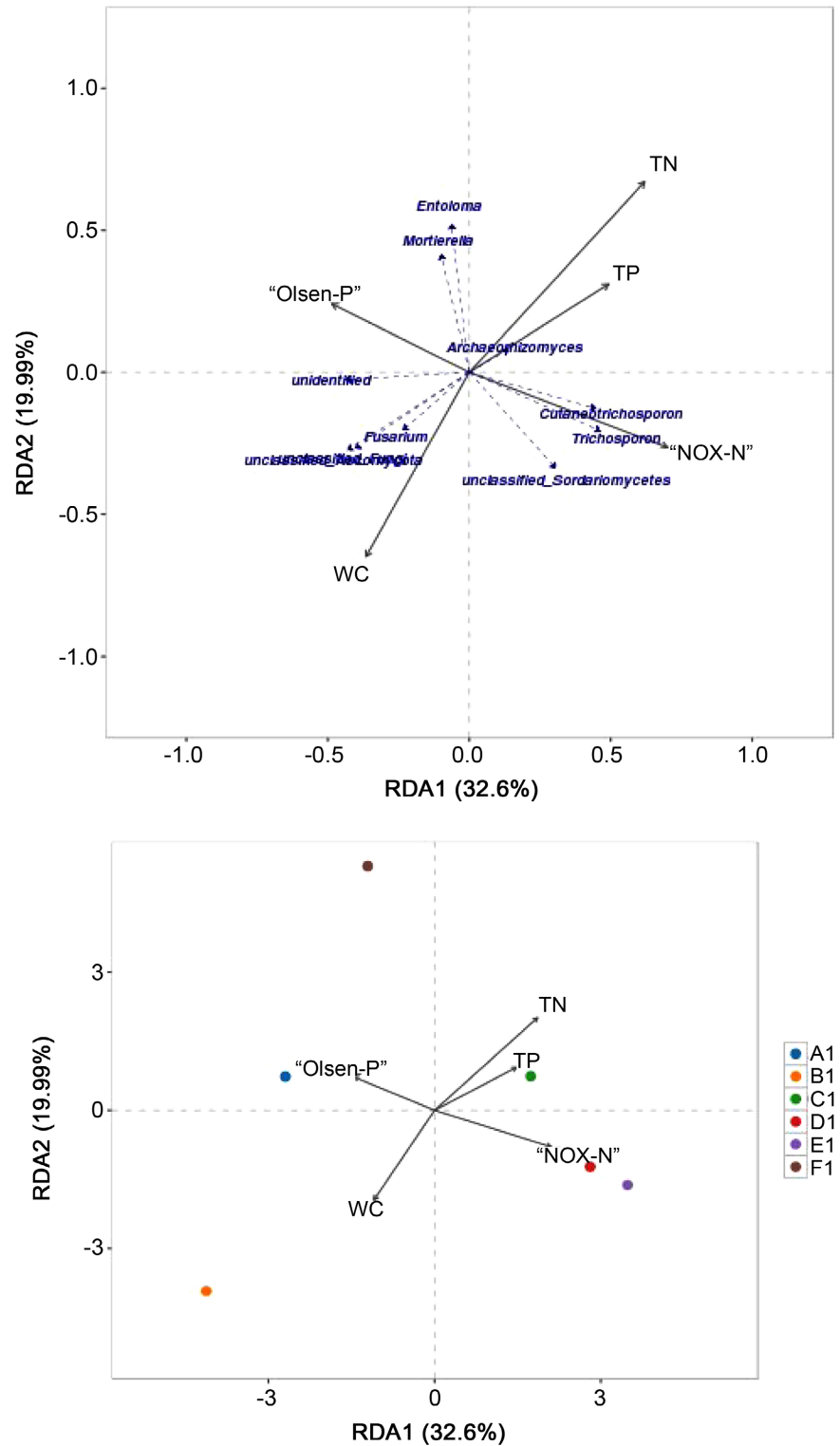


Figure 4. RDA analysis of rhizosphere soil community composition of six species.

the rhizosphere soils of *Vaccinium uliginosum* and *Dryas octopetala* were close to each other. However, the fungal community diversity in the rhizosphere soils of *Rhododendron aureum* and *Rhododendron confertifissimum* was quite

Table 4. Correlation analysis between fungal diversity index and physicochemical properties species.

Indexes	Shannon	Simpson	Chao1	ACE	OTUs
WC	-0.343	-0.229	-0.246	-0.325	-0.196
NO ₃ N	-0.418	0.150	0.171	-0.054	0.246
AP	0.507	-0.400	-0.371	0.179	-0.164
TN	-0.332	0.343	0.300	-0.404	0.104
TP	0.382	0.232	0.179	0.032	0.125
NH ₄ N	0.057	-0.357	-0.361	0.079	-0.09

different. Selectivity of plant roots to rhizosphere fungi will lead to significant differences in community composition and structure of rhizosphere fungi (Hartmann et al., 2009). Plant roots have certain selectivity to rhizosphere soil fungi (Jocrgensen & Wichern, 2008). The fungal diversity in the rhizosphere soil of *Dryas octopetala* was more abundant than that of *Orosta. chys fimbriata* (Turcz.) Berg, and different plants in the same natural zone still had selectivity to the fungal groups colonized in the rhizosphere (Tang et al., 2018).

Soil NH_4^+ is an important environmental factor affecting fungal community structure, and has a significant effect on fungal growth and reproduction (Zhang et al., 2021). In this study, Cutaneotrichosporon and *Trichosporon* were negatively correlated with NH_4^+ . *Fusarium* was positively correlated with moisture content and negatively correlated with TN and TP. *Entoloma* and *Mortierella* were negatively correlated with NO_3 and positively correlated with NH_4^+ . The rhizosphere soil moisture content of *Saxifraga stolonifera* Curt was the highest, and the fungal diversity index was also the highest, indicating that the moisture content could enrich the growth of fungi to a certain extent. *Orosta. chys fimbriata* (Turcz.) Berg and *Rhondodendron aureum* were highly correlated with NH_4^+ , showing a significant positive correlation. *Dryas octopetala* and *Vaccinium uliginosum* were positively correlated with NO_3 . *Rhondodendron confertissimum* was positively correlated with TN and TP. In this study, *Mortierella* was distributed in the rhizosphere soil of 6 plant species and the relative abundance was relatively high, which indicated that *Mortierella* had strong survival ability in alpine environment (Telagathoti et al., 2021).

4.2. Relationship between Fungal Community Diversity and Environmental Factors in Rhizosphere Soil of Different Plants in Tundra of Changbai Mountain

The response of fungi to seasonal changes, soil physical and chemical properties and vegetation types is different, and soil environmental factors are the main factors affecting soil fungal diversity (de Vries et al., 2006). By analyzing the relationship between fungal diversity and soil environmental factors, it can indirectly reflect whether the soil is healthy, and has important guiding significance

in the dynamic succession of soil fungal community and restoration of ecological environment (Bridge & Newsham, 2009). It can also provide a solid theoretical basis for the ecological protection of Changbai Mountain tundra. The results of this study showed that water content was negatively correlated with fungal community diversity, which was consistent with the findings of Wang (Wei et al., 2021) that soil water content beyond the limit would limit the survival of fungi. This study found that TP was positively correlated with fungal community richness, which is similar to the existing results (Yang et al., 2017). This study found that soil NO₃ had a great influence on the dominant genera of fungi, which was similar to the results of Ding Jianli et al. (Ding et al., 2017) who found that soil NO₃ had an important effect on the composition of fungal community in black soil. Dominant bacteria are important factors in determining the balance of fungal community in plant rhizosphere soil and can affect the composition and structure of fungal community (Luo et al., 2018). Ascomycota are mostly saprophytic bacteria (Yelle et al., 2008). It can decompose hard-to-degrade substances such as lignin and keratin (Grinhut et al., 2007). Thus promoting soil nutrient cycling, improve soil quality, and alpine environment is very easy to grow (Egidi et al., 2019). At the phylum level, the fungi in the rhizosphere soil of the six plants were mainly Ascomycota, followed by Basidiomycota, indicating that the dominant flora was significantly affected by environmental factors, which was consistent with the results of Sun Qian et al. (Feng et al., 2016) and Gao Zhiyuan et al. (Soka & Ritchie, 2016).

4.3. Results

This study showed that NO₃ was negatively correlated with *Mortierella*, and positively correlated with *Trichosporon*, *Candida humicola* and *Sordaria*. TN and TP were positively correlated with Archaeorhizomyces. The water content was positively correlated with *Fusarium*, which indicated that the adaptability of fungi to the environment was different, and they were sensitive to the change of environmental factors, which led to the change of fungal community structure. Fungi play the role of decomposers, participate in the degradation of organic matter, soil nutrient transformation and circulation process, can increase soil fertility (Soka & Ritchie, 2016). In this study, the ITS1 region of fungi in the rhizosphere soil of six tundra plants was sequenced, and it was proved that the dominant phylum of fungi in the root zone was Ascomycota, which could be used for the subsequent study of secondary metabolites of cold-resistant fungi to improve the survival threshold of alpine plants. This provides a new idea for maintaining ecological stability in the tundra of Changbai Mountain.

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Authors' Contributions

Hao Ran was responsible for the sample collection and pretreatment of the experiment. Yang Li prepared the soil physical and chemical factors and assisted Wang Yihui in the determination of soil physical and chemical factors.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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