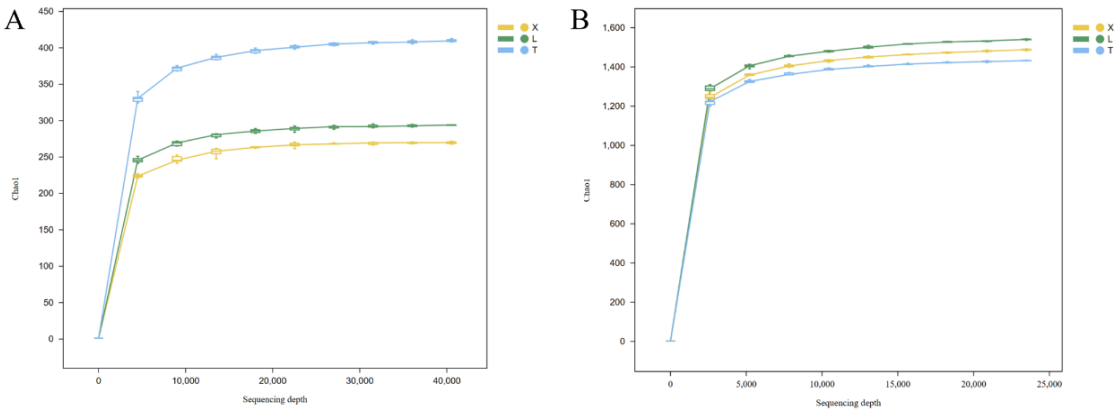
1.1 Site Description

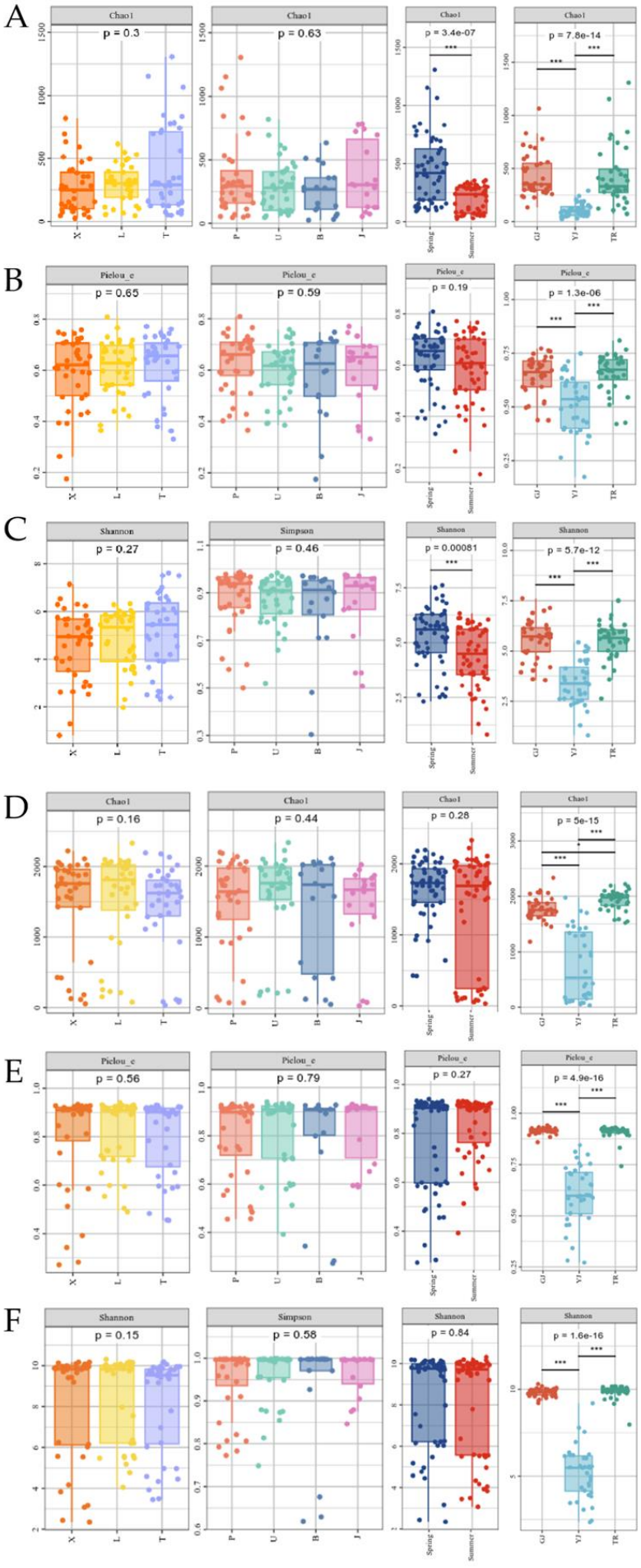
The research area was situated in Qinyuan County, central southern Shanxi Province, at the eastern foot of Taiyue Mountain and northwest of Changzhi City (36°20′20″—37°00′42″N, 111°58′30″—112°32′30″E) [1]. Qinyuan County lies within the Loess Plateau, encompassing the main vein of the Taiyue Mountains in the western uplift area of the Qinshui Basin. The terrain features a northwest rise and a southeast slope, with an average elevation of approximately 1,400 meters. The county is characterized by a complex natural environment and diverse landforms, categorized into three primary geomorphic units: mountains, hills, and river valley terraces. The mountainous terrain is undulating, with forests distributed throughout the mountainous areas. The woodland area covers 1,400 million square meters, and the forest coverage rate reaches 55.3%, the highest in the province [2]. Qinyuan County is situated within a warm temperate continental monsoon climate zone, exhibiting a mild climate and humid atmosphere. Mineral resources are abundant, diverse, and widely distributed, with the primary mined minerals currently including coal, iron, bauxite, and limestone [3]. Qinyuan County has the highest number of mines in Changzhi City, resulting in extensive land degradation due to mining activities [4].

1.2. Sample Naming

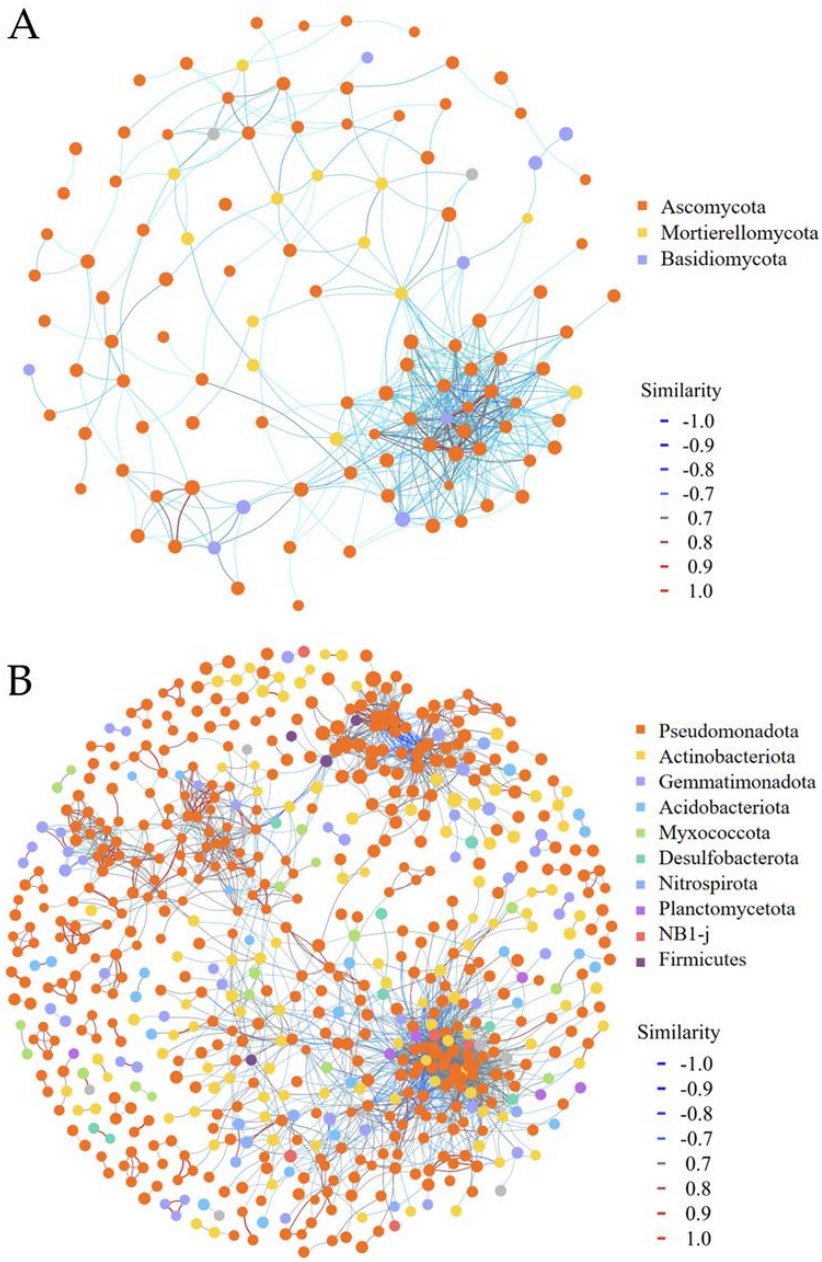
In the sample naming convention, the first letter X indicates that the sampling location is Xuanmeichang, the letter L indicates Liushenyu, and the letter T indicates the Taiyueshan Forest Farm. The second letter B represents *Betula platyphylla*, U represents *Ulmus pumila*, P represents *Populus davidiana*, and J represents *Juglans mandshurica*. The third letter G indicates that the sample was collected from the rhizosphere, Y indicates collection from the phyllosphere, and T indicates collection from the soil. The final letter A represents samples collected in spring (April), while J represents those collected in summer (July). For example, XPGA refers to rhizosphere samples of *Populus davidiana* collected at Xuanmeichang in spring.



Supplementary Figure 1. Rarefaction curves of microbial species at different sampling plots fungal samples (A) and bacterial samples (B).


A
Chao1
p = 0.3
Chao1
p = 0.63
Chao1
p = 3.4e-07
Chao1
p = 7.8e-14
B
Pielou_e
p = 0.65
Pielou_e
p = 0.59
Pielou_e
p = 0.19
Pielou_e
p = 1.3e-06
C
Shannon
p = 0.27
Simpson
p = 0.46
Shannon
p = 0.00081
Shannon
p = 5.7e-12
D
Chao1
p = 0.16
Chao1
p = 0.44
Chao1
p = 0.28
Chao1
p = 5e-15
E
Pielou_e
p = 0.56
Pielou_e
p = 0.79
Pielou_e
p = 0.27
Pielou_e
p = 4.9e-16
F
Shannon
p = 0.15
Simpson
p = 0.58
Shannon
p = 0.84
Shannon
p = 1.6e-16
X
L
T
P
U
B
J
Spring
Summer
GJ
YJ
TR

Supplementary Figure 2. Alpha– diversity index of fungi (A–C) and bacteria (D–F) for different groups. Chao l (A,D), Pielou's evenness (B,E), Shannon indices (C,F). The numbers in the box plot represent the *p*–values of the Kruskal–Wallis test, and *** indicates significant differences between groups (Kruskal–Wallis, $p < 0.05$)



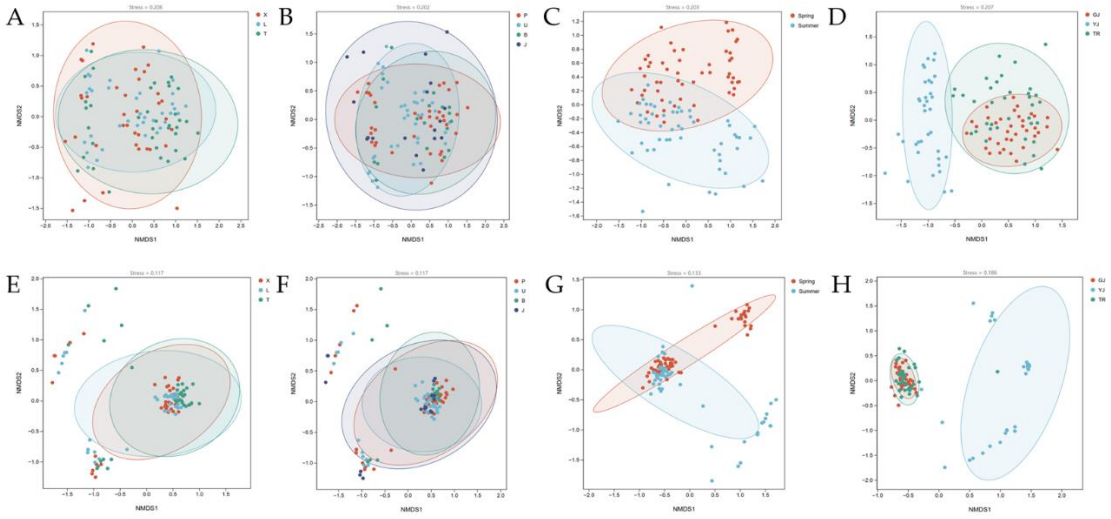
Supplementary Figure 3. Horizontal correlation network analysis of fungi (A) and bacteria (B).

Supplementary Table 1. Percentage of fungal phyla in different groups

ID	X	L	T	P	U	B	J	Spring	Summer	GJ	YJ	TR
Ascomycota	67.99%	69.75%	68.69%	70.91%	68.84%	70.33%	63.02%	68.25%	69.37%	69.34%	71.31%	65.78%
Basidiomycota	20.97%	18.09%	17.71%	21.43%	14.39%	24.04%	17.84%	14.84%	23.00%	21.88%	11.38%	23.50%
Mortierellomycota	1.19%	3.94%	1.56%	1.27%	3.79%	1.30%	1.95%	0.97%	3.49%	3.68%	0.01%	3.00%
Rozellomycota	0.04%	0.20%	0.67%	0.12%	0.14%	0.06%	1.25%	0.08%	0.53%	0.29%	0.00%	0.63%
Chytridiomycota	0.12%	0.21%	0.06%	0.22%	0.06%	0.16%	0.06%	0.25%	0.01%	0.08%	0.00%	0.31%
Glomeromycota	0.03%	0.06%	0.01%	0.02%	0.05%	0.03%	0.02%	0.06%	0.00%	0.03%	0.00%	0.07%
Aphelidiomycota	0.02%	0.00%	0.05%	0.03%	0.02%	0.00%	0.05%	0.03%	0.02%	0.03%	0.00%	0.04%
Zoopagomycota	0.00%	0.00%	0.02%	0.02%	0.00%	0.01%	0.00%	0.02%	0.00%	0.01%	0.00%	0.01%
Calcarisporiellomycota	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.03%
Blastocladiomycota	0.00%	0.00%	0.01%	0.01%	0.00%	0.00%	0.01%	0.01%	0.00%	0.01%	0.00%	0.01%
Others	9.62%	7.72%	11.23%	5.93%	12.70%	4.07%	15.81%	15.47%	3.58%	4.66%	17.29%	6.62%

Supplementary Table 2. Percentage of bacterial phyla in different groups

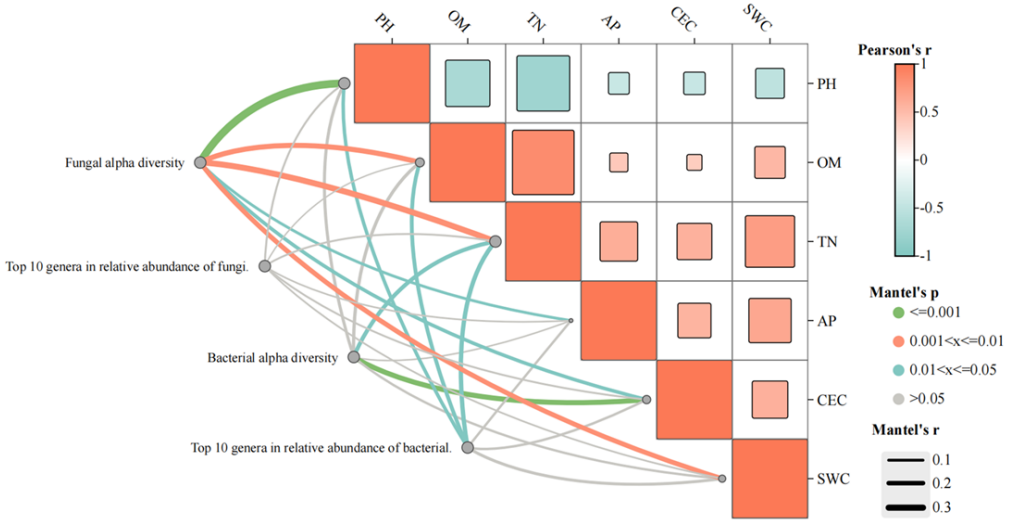
ID	X	L	T	P	U	B	J	Spring	Summer	GJ	YJ	TR
Pseudomonadota	68.46%	67.33%	66.21%	67.54%	67.24%	65.15%	69.31%	68.08%	66.59%	54.53%	91.58%	55.89%
Actinobacteriota	14.49%	17.47%	15.45%	15.47%	16.12%	16.82%	14.82%	16.53%	15.08%	23.47%	3.31%	20.62%
Gemmatimonadota	6.25%	4.79%	3.71%	4.94%	5.31%	3.01%	6.01%	3.36%	6.48%	6.95%	0.62%	7.19%
Acidobacteriota	4.01%	3.70%	4.82%	4.48%	4.25%	4.22%	3.39%	4.13%	4.23%	5.95%	0.52%	6.06%
Myxococcota	2.10%	2.73%	2.21%	2.71%	2.38%	2.24%	1.65%	2.74%	1.95%	2.80%	1.04%	3.20%
Firmicutes	1.41%	1.13%	1.98%	1.59%	1.53%	1.39%	1.42%	1.53%	1.49%	0.88%	2.59%	1.05%
Nitrospirota	0.96%	0.52%	0.92%	0.46%	0.91%	1.25%	0.81%	0.75%	0.85%	1.14%	0.05%	1.22%
Desulfobacterota	0.50%	0.51%	1.33%	0.68%	0.52%	1.75%	0.81%	0.52%	1.05%	0.96%	0.05%	1.33%
NB1-j	0.36%	0.45%	1.40%	0.59%	0.43%	1.96%	0.40%	0.66%	0.80%	1.06%	0.02%	1.12%
Planctomycetota	0.40%	0.36%	0.62%	0.50%	0.30%	0.66%	0.49%	0.48%	0.44%	0.66%	0.03%	0.69%
Others	1.06%	1.01%	1.35%	1.05%	0.99%	1.55%	1.18%	1.23%	1.05%	1.59%	0.20%	1.63%



Supplementary Figure 4. Microbial community NMDS analysis based on Bray–Curtis distance matrix of fungi (A–D) and bacteria (E–H) in different groups. Different sampling plots (A, E), different tree species (B, F), different seasons (C, G) and different sampling locations (D, H).

Supplementary Table 3. Correlation analysis of soil physicochemical indicators

R value	PH	TN	OM	AP	CEC	SWC
PH	1	–0.68	–0.77	–0.43	–0.44	–0.52
TN	–0.68	1	0.86	0.41	0.38	0.53
OM	–0.77	0.86	1	0.61	0.58	0.73
AP	–0.43	0.41	0.61	1	0.56	0.66
CEC	–0.44	0.38	0.58	0.56	1	0.59
SWC	–0.52	0.53	0.73	0.66	0.59	1



Supplementary Figure 5. Correlation analysis of soil physicochemical indicators and mantle analysis of the top 10 genera in terms of Alpha–diversity index and abundance of fungal and bacterial communities.

The size of the squares in the image represents the magnitude of the correlation between the physicochemical factors; and the Microbial Community Composition at the Genus Level

1.3. Microbial Community Composition at Genus Level

On the whole, the dominant fungal genera (genera with a relative abundance greater than 2%) included *Nothophoma* (6.74%), *Fusarium* (3.26%), *Solicoccozyma* (3.05%), *Humicola* (2.46%), *Cladosporium* (2.37%), and *Arxiella* (2.03%). The dominant bacterial genera comprised *Sphingomonas* (8.60%), *Ralstonia* (7.59%), *MB–A2–108* (MB–A2–108, 6.28%), *Bradyrhizobium* (6.07%), *Pseudomonas* (5.73%), *Ellin6067* (Nitrosomonadaceae, 3.09%), and *Massilia* (2.43%).

The dominant fungal genera in plot X were *Nothophoma*, *Fusarium*, *Solicoccozyma*, *Taphrina*, *Cladosporium*, *Cryptocline*, *Inocybe*, and *Vishniacozyma*; in plot L, the dominant genera were *Nothophoma*, *Solicoccozyma*, *Xenodidymella*, *Fusarium*, *Humicola*, *Arxiella*, *Cladosporium*, *Aspergillus*; and in plot T, the dominant genera were *Nothophoma*, *Humicola*, *Fusarium*, *Subulicystidium*. *Nothophoma* and *Fusarium* were the dominant genera shared among the three plots, with *Nothophoma* exhibiting the highest relative abundance across all three (Figure S6A). The dominant bacterial genera in plot X included *Sphingomonas*, *Ralstonia*, *Bradyrhizobium*, *Pseudomonas*, *MB–A2–108*, *Ellin6067*, *Massilia*; in plot L, they were *Sphingomonas*, *Ralstonia*, *MB–A2–108*, *Bradyrhizobium*, *Massilia*, *Pseudomonas*, *Methylobacterium–Methylorubrum*, *Ellin6067*; and in plot T, they were *MB–A2–108*, *Ralstonia*, *Pseudomonas*, *Bradyrhizobium*, *Ellin6067*, *Sphingomonas*, *Methylobacterium–Methylorubrum*, *Craurococcus–Caldovatus*. The dominant genera shared among the three plots included *Sphingomonas*, *Ralstonia*, *Bradyrhizobium*, *Pseudomonas*, *MB–A2–108*, *Ellin6067* (Figure S6E). The UPGMA clustering dendrogram results indicated that the fungal compositions with higher relative abundance in the T and L plots were more similar, while the bacterial compositions with higher relative abundance in the X and L plots exhibited greater similarity (Figure S7A, E).

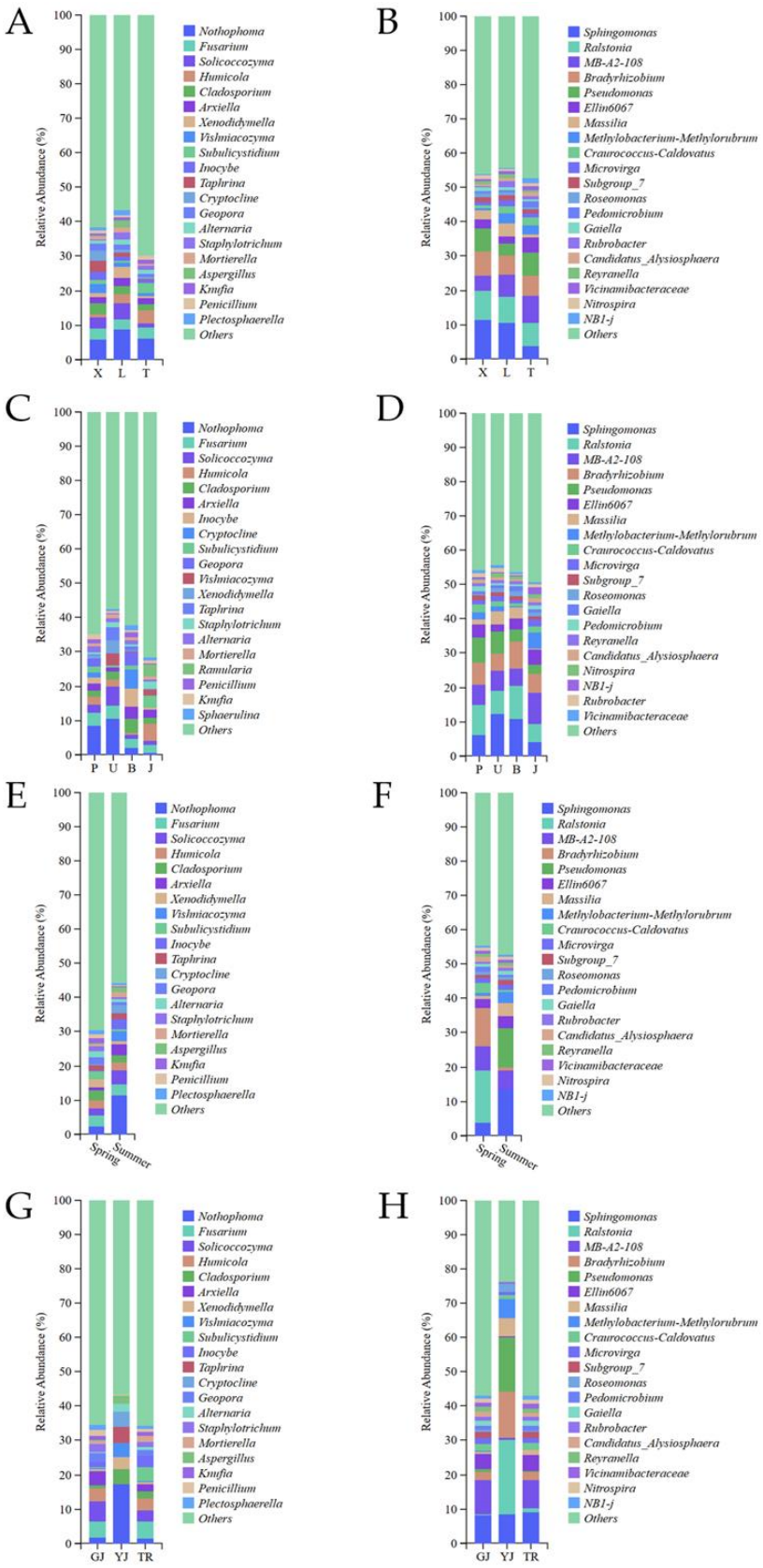
The dominant fungal genera in plot X were *Nothophoma*, *Fusarium*, *Solicoccozyma*, *Taphrina*, *Cladosporium*, *Cryptocline*, *Inocybe*, and *Vishniacozyma*; in plot L, the dominant genera were *Nothophoma*, *Solicoccozyma*, *Xenodidymella*, *Fusarium*, *Humicola*, *Arxiella*, *Cladosporium*, *Aspergillus*; and in plot T, the dominant genera were *Nothophoma*, *Humicola*, *Fusarium*, *Subulicystidium*. *Nothophoma* and *Fusarium* were the dominant genera shared among the three plots, with *Nothophoma* exhibiting the highest relative abundance across all three (Figure S6A). The dominant bacterial genera in plot X included *Sphingomonas*, *Ralstonia*, *Bradyrhizobium*, *Pseudomonas*, *MB–A2–108*, *Ellin6067*, *Massilia*; in plot L, they were *Sphingomonas*, *Ralstonia*, *MB–A2–108*, *Bradyrhizobium*, *Massilia*, *Pseudomonas*, *Methylobacterium–Methylorubrum*, *Ellin6067*; and in plot T, they were *MB–A2–108*, *Ralstonia*, *Pseudomonas*, *Bradyrhizobium*, *Ellin6067*, *Sphingomonas*, *Methylobacterium–Methylorubrum*, *Craurococcus–Caldovatus*. The dominant genera shared among the three plots included *Sphingomonas*, *Ralstonia*, *Bradyrhizobium*, *Pseudomonas*, *MB–A2–108*, *Ellin6067* (Figure S6E). The UPGMA clustering dendrogram results indicated that the fungal compositions with higher relative abundance in the T and L plots were more similar, while the bacterial compositions with higher relative abundance in the X and L plots exhibited greater similarity (Figure S7A, E).

The dominant fungal genera for *P. davidiana* included *Nothophoma*, *Fusarium*, *Humicola*, *Solicoccozyma*, *Geopora*, *Aspergillus*is; for *U. pumila*, they were *Nothophoma*, *Solicoccozyma*, *Xenodidymella*, *Fusarium*, *Taphrina*, *Vishniacozyma*, *Cladosporium*, *Humicola*; for *B. platyphylla*, the genera included *Humicola*, *Ramularia*, *Subulicystidium*, *Oliveonia*, *Fusarium*, *Arxiella*; and for *J. mandshurica*, the dominant genera were *Cryptocline*, *Inocybe*, *Cladosporium*, *Geopora*, *Arxiella*, *Cortinarius*, *Fusarium*, *Colletotrichum* and *Nothophoma*. Significant differences were observed in

the dominant fungal genera among the four tree species, with only *Fusarium* being a common dominant genus (Figure S6B). Among the bacterial samples, the dominant genera for *P. davidiana* included *Ralstonia*, *Pseudomonas*, *Bradyrhizobium*, *Sphingomonas*, *MB–A2–108*, *Ellin6067*, *Craurococcus–Caldovatus*; for *U. pumila*, they were *Sphingomona*, *Pseudomonas*, *Ralstonia*, *MB–A2–108*, *Bradyrhizobium*, *Massilia*; for *B. platyphylla*, the genera included *MB–A2–108*, *Bradyrhizobium*, *Ralstonia*, *Methylobacterium–Methylorubrum*, *Ellin6067*, *Sphingomonas*, *Pseudomonas*, *Craurococcus–Caldovatus*; and for *J. mandshurica*, the dominant genera were *Sphingomonas*, *Ralstonia*, *Bradyrhizobium*, *MB–A2–108*, *Pseudomonas*, *Massilia*, *Ellin6067*. The genera shared among the four tree species included *Ralstonia*, *Pseudomonas*, *Bradyrhizobium*, *Sphingomonas*, *MB–A2–108*, and *Ellin6067* (Figure S6F). The UPGMA clustering dendrogram indicated that the genera with higher relative abundances in the fungal samples of *P. davidiana* and *J. mandshurica* were more similar, while the bacterial samples of *P. davidiana* and *U. pumila* exhibited greater similarity (Figure S7B, F).

The dominant fungal genera in spring were *Fusarium*, *Cladosporium*, *Humicola*, *Subulicystidium*, *Xenodidymella*, *Nothophoma*, whereas in summer, they included *Nothophoma*, *Solicoccozyma*, *Fusarium*, *Arxiella*, *Inocybe*, *Vishniacozyma*, *Cryptocline* and *Humicola* (Figure S6C). Among the bacterial samples, the dominant genera in spring were *Ralstonia*, *Bradyrhizobium*, *MB–A2–108*, *Sphingomonas*, *Craurococcus–Caldovatus*, *Ellin6067*, while in summer, they were *Sphingomonas*, *Pseudomonas*, *MB–A2–108*, *Massilia*, *Ellin6067*, *Methylobacterium–Methylorubrum*. The common dominant genera in both seasons were *MB–A2–108*, *Sphingomonas*, and *Ellin6067* (Figure S6G). The UPGMA clustering results indicated a significant difference in the composition of genera with higher relative abundances in fungal and bacterial samples between the two seasons (Figure S7C, G).

The dominant fungal genera in the rhizosphere samples were *Solicoccozyma*, *Fusarium*, *Arxiella*, *Humicola*, *Geopora* and *Staphylotrichum*. In the phyllosphere, the dominant genera included *Nothophoma*, *Taphrina*, *Cryptocline*, *Cladosporium*, *Vishniacozyma*, *Xenodidymella*, *Alternaria*, *Aspergillus*, while the soil samples were characterized by *Fusarium*, *Subulicystilum*, *Humicola*, *Solicoccozyma*, *Inocybe*, *Arxiella* (Figure S6D). No dominant fungal genera were shared among the three sampling locations. Among the bacterial samples, the dominant genera in the rhizosphere were *MB–A2–108*, *Sphingomonas*, *Ellin6067*, *Bradyrhizobium*, *Craurococcus–Caldovatus*. In the phyllosphere, the dominant genera included *Ralstonia*, *Pseudomonas*, *Bradyrhizobium*, *Sphingomonas*, *Methylobacterium–Methylorubrum*, *Massilia*, *Roseomonas*. The soil samples were dominated by *Sphingomonas*, *MB–A2–108*, *Ellin6067*, *Bradyrhizobium*. The only common dominant bacterial genus across the three sampling locations was *Sphingomonas*, with additional shared genera between the rhizosphere and soil samples (Figure S6H). The UPGMA clustering dendrogram indicated that the compositions of fungal and bacterial samples with higher relative abundances from the rhizosphere and soil were more similar, showing significant differences compared to the phyllosphere samples (Figure S7D, H).



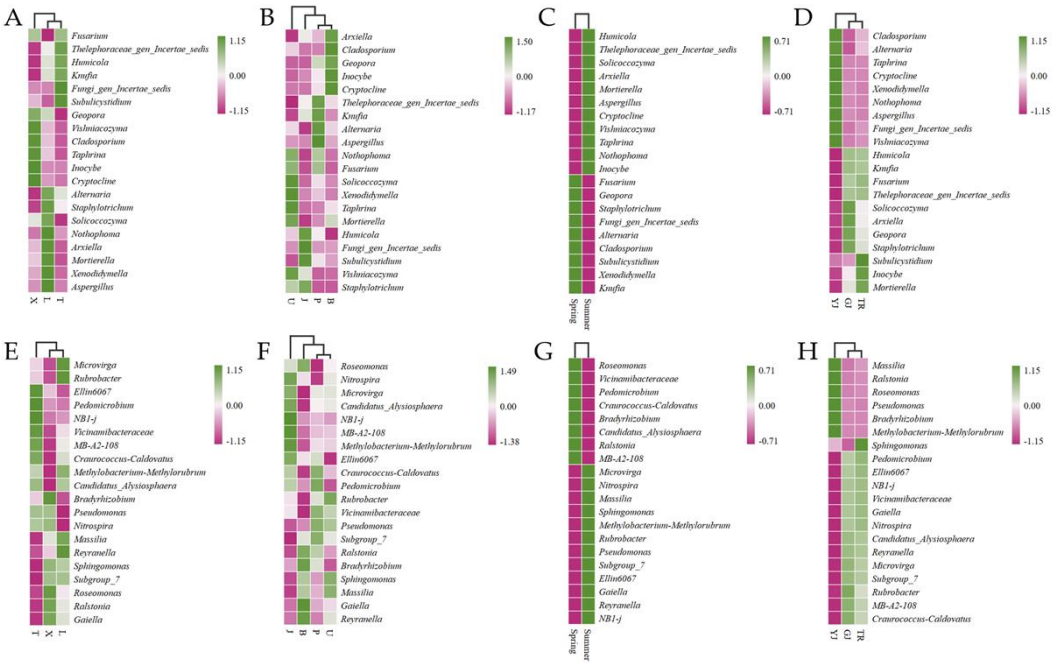
Supplementary Figure 6. Relative abundance of fungi (A, C, E, G) and bacteria (B, D, F, H) in different groups at the genus level. Different sampling plots (A, B), different tree species (C, D), different seasons

Supplementary Table 4. Percentage of fungal genus in different groups

ID	X	L	T	Spring	Summer	GJ	YJ	TR	**ID**	P	U	B	J
Nothophoma	5.67%	8.61%	5.95%	2.22%	11.27%	1.71%	17.12%	1.40%	*Nothophoma*	8.49%	10.43%	0.60%	2.01%
Fusarium	3.37%	3.01%	3.39%	3.29%	3.23%	4.61%	0.09%	5.08%	*Fusarium*	3.61%	3.76%	2.37%	2.44%
Solicoccozyma	3.32%	4.71%	1.12%	1.94%	4.16%	6.01%	0.00%	3.15%	*Solicoccozyma*	2.37%	5.55%	1.04%	1.43%
Humicola	0.77%	2.73%	3.88%	2.43%	2.48%	3.74%	0.00%	3.63%	*Humicola*	2.49%	2.12%	5.09%	0.43%
Cladosporium	3.17%	2.18%	1.76%	2.82%	1.92%	0.93%	4.40%	1.78%	*Cladosporium*	1.83%	2.32%	1.76%	4.16%
Arxiella	1.93%	2.40%	1.76%	0.91%	3.15%	3.97%	0.00%	2.11%	*Arxiella*	1.93%	1.15%	2.36%	3.63%
Xenodidymella	1.13%	3.18%	0.67%	2.31%	1.01%	0.79%	3.54%	0.65%	*Inocybe*	1.73%	0.00%	0.52%	5.15%
Vishniacozyma	2.42%	1.29%	0.89%	0.24%	2.83%	0.12%	4.14%	0.35%	*Cryptocline*	1.60%	0.01%	0.01%	5.71%
Subulicystidium	1.18%	0.63%	2.78%	2.34%	0.72%	0.42%	0.00%	4.17%	*Subulicystidium*	1.62%	0.61%	3.54%	1.17%
Inocybe	2.57%	1.02%	0.98%	0.20%	2.84%	1.46%	0.00%	3.11%	*Geopora*	2.30%	0.01%	0.01%	3.84%
Taphrina	3.22%	1.16%	0.18%	1.35%	1.69%	0.00%	4.53%	0.03%	*Vishniacozyma*	0.10%	3.50%	1.78%	0.22%
Cryptocline	2.86%	0.93%	0.69%	0.42%	2.56%	0.00%	4.47%	0.01%	*Xenodidymella*	0.89%	3.85%	0.28%	0.21%
Geopora	1.93%	1.60%	0.70%	1.89%	0.93%	2.63%	0.00%	1.60%	*Taphrina*	0.24%	3.74%	0.04%	1.13%
Alternaria	0.97%	1.44%	1.27%	1.78%	0.67%	0.33%	2.39%	0.96%	*Staphylotrichum*	0.64%	1.59%	1.98%	0.65%
Staphylotrichum	0.42%	1.97%	1.16%	1.65%	0.71%	2.16%	0.00%	1.39%	*Alternaria*	1.74%	1.07%	0.67%	1.06%
Mortierella	0.86%	1.50%	0.54%	0.65%	1.28%	1.10%	0.00%	1.80%	*Mortierella*	0.79%	1.26%	0.66%	1.04%
Aspergillus	0.28%	2.14%	0.17%	0.23%	1.50%	0.21%	2.24%	0.15%	*Ramularia*	0.00%	0.02%	3.68%	0.00%
Knufia	0.42%	0.93%	1.19%	1.40%	0.29%	1.16%	0.27%	1.11%	*Penicillium*	1.33%	0.30%	0.24%	1.54%
Penicillium	1.01%	0.58%	0.94%	1.24%	0.44%	1.69%	0.04%	0.80%	*Knufia*	1.36%	0.43%	0.91%	0.60%
Plectosphaerella	0.99%	1.22%	0.25%	0.98%	0.66%	1.63%	0.00%	0.83%	*Sphaerulina*	0.17%	0.81%	0.91%	1.27%
Others	61.51%	56.77%	69.73%	69.68%	55.66%	65.34%	56.77%	65.90%	*Others*	64.75%	57.46%	71.55%	62.31%

Supplementary Table 5. Percentage of bacterial genus in different groups

ID	X	L	T	Spring	Summer	GJ	YJ	TR	**ID**	P	U	B	J
Sphingomonas	11.50%	10.46%	3.86%	3.78%	13.43%	8.21%	8.45%	9.15%	*Sphingomonas*	6.12%	12.31%	3.96%	10.80%
Ralstonia	8.34%	7.69%	6.74%	15.14%	0.05%	0.09%	21.65%	1.04%	*Ralstonia*	8.66%	6.53%	5.45%	9.72%
MB-A2-108	4.57%	6.43%	7.84%	7.05%	5.51%	10.10%	0.57%	8.17%	*MB-A2-108*	5.91%	5.98%	8.87%	5.02%
Bradyrhizobium	6.82%	5.46%	5.93%	11.14%	0.99%	2.35%	13.48%	2.37%	*Bradyrhizobium*	6.57%	4.88%	5.56%	7.94%
Pseudomonas	6.74%	3.71%	6.73%	0.17%	11.29%	0.86%	15.93%	0.39%	*Pseudomonas*	7.42%	6.65%	2.71%	3.51%
Ellin6067	2.79%	2.04%	4.44%	2.66%	3.52%	4.31%	0.24%	4.73%	*Ellin6067*	3.58%	1.94%	4.36%	3.14%
Massilia	2.67%	3.79%	0.83%	0.86%	4.00%	0.80%	5.26%	1.23%	*Massilia*	1.68%	3.74%	0.53%	3.20%
Methylobacterium-Methylorubrum	0.57%	2.92%	2.45%	0.71%	3.25%	0.11%	5.71%	0.12%	*Methylobacterium-Methylorubrum*	1.85%	1.71%	4.44%	0.31%
Craurococcus-Caldovatus	0.89%	1.93%	2.43%	2.95%	0.55%	2.23%	1.06%	1.97%	*Craurococcus-Caldovatus*	2.29%	1.48%	2.03%	0.94%
Microvirga	0.91%	1.99%	1.32%	1.39%	1.42%	1.67%	0.97%	1.57%	*Microvirga*	1.44%	1.48%	1.86%	0.73%
Subgroup_7	1.23%	1.23%	1.08%	0.94%	1.42%	1.83%	0.07%	1.64%	*Subgroup_7*	1.33%	1.17%	0.90%	1.18%
Roseomonas	1.26%	0.96%	0.71%	1.03%	0.92%	0.37%	2.12%	0.44%	*Roseomonas*	0.40%	1.09%	1.25%	1.63%
Pedomicrobium	0.66%	0.56%	1.61%	1.34%	0.55%	1.31%	0.02%	1.51%	*Gaiella*	0.87%	0.93%	0.79%	1.27%
Gaiella	1.13%	0.98%	0.71%	0.82%	1.06%	1.33%	0.07%	1.42%	*Pedomicrobium*	1.38%	0.53%	1.15%	0.69%
Rubrobacter	0.34%	1.64%	0.79%	0.79%	1.06%	1.47%	0.23%	1.08%	*Reyranella*	0.85%	0.92%	0.84%	1.00%
Candidatus_Alysiosphaera	0.55%	1.06%	1.11%	1.37%	0.44%	1.34%	0.13%	1.25%	*Candidatus_Alysiosphaera*	0.90%	0.95%	1.33%	0.42%
Reyranella	0.86%	1.09%	0.73%	0.82%	0.97%	1.35%	0.06%	1.27%	*Nitrospira*	0.46%	0.91%	1.25%	0.81%
Vicinamibacteraceae	0.70%	0.83%	1.02%	0.95%	0.75%	1.20%	0.08%	1.27%	*NB1-j*	0.59%	0.43%	1.96%	0.40%
Nitrospira	0.96%	0.52%	0.92%	0.75%	0.85%	1.13%	0.05%	1.21%	*Rubrobacter*	0.93%	1.29%	0.80%	0.33%
NB1-j	0.36%	0.45%	1.40%	0.66%	0.80%	1.06%	0.02%	1.12%	*Vicinamibacteraceae*	1.02%	0.91%	0.78%	0.47%
Others	46.17%	44.26%	47.34	44.66	47.18%	56.88	23.83%	57.06%	*Others*	45.75%	44.18	49.20%	46.48%



Supplementary Figure 7. Heat map of top 20 genera in relative abundance of fungi (A–D) and bacteria (E–H) in different groups. Different sampling plots (A, E), different tree species (B, F), different seasons (C, G) and different sampling locations (D, H).

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