

Table S1. Sequences of the primers for bacteria, fungi, and arbuscular mycorrhizal fungi.

	N	S
1	Ligustrum lucidum	Ligustrum lucidum
2	Forsythia viridissima	Forsythia viridissima
3	Oxalis corniculata	Oxalis corniculata
4	Veronica persica	Veronica persica
5	Bischofia polycarpa	Eriobotrya japonica
6	Ginkgo biloba	Pinus massoniana
7	Cercis chinensis	Lonicera maackii
8	Punica granatum L	Euonymus japonicus
9	Solanum nigrum	Ophiogon japonicus.

Table S2. Sequences of the primers for bacteria, fungi, and arbuscular mycorrhizal fungi.

Soil microbes	Primer code	Primer sequence
Bacteria	338F	5'-ACTCCTACGGGAGGCAGCA-3'
	806R	5'-GGACTACHVGGGTWTCTAAT-3'
Fungi	ITS3F	5'-GCATCGATGAAGAACGCAGC-3'
	ITS4R	5'-TCCTCCGCTTATTGATATGC-3'

Table S3. GenBank number for plastome sequences used in the present study.

Species	GenBank number
<i>Oxalis corniculata</i>	NC051971
<i>Bischofia polycarpa</i>	MZ826267
<i>Euonymus japonicus</i>	MZ567073
<i>Cercis chinensis</i>	MZ128523
<i>Eriobotrya japonica</i>	NC034639
<i>Punica granatum</i>	MT600023
<i>Forsythia viridissima</i>	MW856917
<i>Ligustrum lucidum</i>	MH394207
<i>Veronica persica</i>	NC031344
<i>Solanum nigrum</i>	KM489055
<i>Lonicera maackii</i>	MN256451
<i>Ophiopogon japonicus</i>	MK952744
<i>Ginkgo biloba</i>	MN443423
<i>Pinus massoniana</i>	MF564195

Table S4. Significance of the relative abundance of dominant bacteria phyla in all soils. Values in the same row with different alphabetic superscripts (a, b, c) are significantly different between the four groups.

	Type			
	Herbage	Shrub	Arbor	Soil
Proteobacteria	0.30 ^a	0.27 ^a	0.30 ^a	0.26 ^a
Actinobacteria	0.19 ^a	0.16 ^{ab}	0.14 ^b	0.22 ^a
Cyanobacteria	0.07 ^b	0.18 ^{ab}	0.18 ^a	0.02 ^c
Bacteroidetes	0.15 ^a	0.13 ^{ab}	0.12 ^b	0.07 ^c
Chloroflexi	0.11 ^b	0.08 ^c	0.09 ^{bc}	0.15 ^a
Acidobacteria	0.06 ^b	0.06 ^{ab}	0.05 ^b	0.08 ^a
Patescibacteria	0.04 ^a	0.03 ^a	0.03 ^a	0.02 ^a
Gemmatimonadetes	0.02 ^b	0.02 ^b	0.02 ^b	0.07 ^a
Planctomycetes	0.01 ^b	0.01 ^b	0.01 ^b	0.02 ^a
Others	0.04 ^a	0.03 ^b	0.03 ^b	0.05 ^a
Bacteria_ Others	0.02 ^c	0.02 ^{bc}	0.03 ^b	0.05 ^a

Table S5. Relative abundances of dominant fungal class in all soils. Values in the same row with different alphabetic superscripts (a, b, c) are significantly different between the four groups.

	Type			
	Herbage	Shrub	Arbor	Soil
Sordariomycetes	0.21 ^{ab}	0.22 ^{ab}	0.17 ^b	0.28 ^a
Dothideomycetes	0.26 ^a	0.1 ^b	0.09 ^b	0.07 ^b
Fungi_others1	0.11 ^b	0.15 ^a	0.14 ^{ab}	0.11 ^{ab}
Agaricomycetes	0.13 ^a	0.15 ^a	0.08 ^a	0.07 ^a
Leotiomycetes	0.08 ^a	0.04 ^{ab}	0.11 ^a	0.02 ^b
Fungi_others2	0.03 ^b	0.09 ^a	0.08 ^a	0.09 ^a
Pezizomycetes	0.02 ^b	0.02 ^{ab}	0.11 ^a	0.15 ^a
Eurotiomycetes	0.04 ^a	0.06 ^a	0.05 ^a	0.06 ^a
Ascomycota_others	0.05 ^a	0.05 ^{ab}	0.02 ^b	0.03 ^{ab}
Mortierellomycetes	0.01 ^c	0.03 ^{ab}	0.03 ^b	0.09 ^a
Others	0.05 ^b	0.08 ^{ab}	0.12 ^a	0.04 ^b

Table S6. Correlation between genetic distance or plant vegetation type and bacterial or fungal community structure determined based on the Mantel test ($P < 0.05$, permutation = 999). Significant values are in bold.

	Bacteria		Fungi	
	r	p	r	p
Genetic distance	0.317	0.001	0.116	0.052
Plant vegetation type	0.091	0.002	0.151	0.001

Table S7. The Variance Partitioning Analysis (VPA) of the bacterial and fungal community among the samples.

	Location	Plant Type
Bacteria	0.005	0.011
Fungi	0.017	0.034

Table S8. Multivariate Welch ANOVA ($P < 0.05$, permutation = 99999) among bacteria between all groups.

	N.Herbage	N.Shrub	N.Arbor	N. Bulk soil	S.Herbage	S.Shrub	S.Arbor
N.Herbage							
N.Shrub	0.001						
N.Arbor	0.001	0.001					
N.Bulk soil	0.007	0.062	0.036				
S.Herbage	0.112	0.001	0.001	0.013			
S.Shrub	0.001	0.003	0.001	0.006	0.003		
S.Arbor	0.001	0.001	0.007	0.010	0.001	0.071	
S.Bulk soil	0.004	0.160	0.113	0.088	0.010	0.027	0.067

Table S9. Multivariate Welch ANOVA ($P < 0.05$, permutation = 99999) among fungi between all groups.

	N.Herbage	N.Shrub	N.Arbor	N. Bulk soil	S.Herbage	S.Shrub	S.Arbor
N.Herbage							
N.Shrub	0.001						
N.Arbor	0.001	0.001					
N. Bulk soil	0.018	0.035	0.030				
S.Herbage	0.037	0.001	0.001	0.021			
S.Shrub	0.001	0.004	0.001	0.011	0.014		
S.Arbor	0.001	0.001	0.001	0.017	0.006	0.254	
S. Bulk soil	0.022	0.031	0.030	0.109	0.030	0.063	0.125

FIGURE S1. The schematic diagram of sample collection location(a) (Sampling map was download from <https://www.henu.edu.cn/zjhd/xqsyt.htm> and was modified accordingly) and the phylogenetic tree of 14 species collected in the experiment(b).

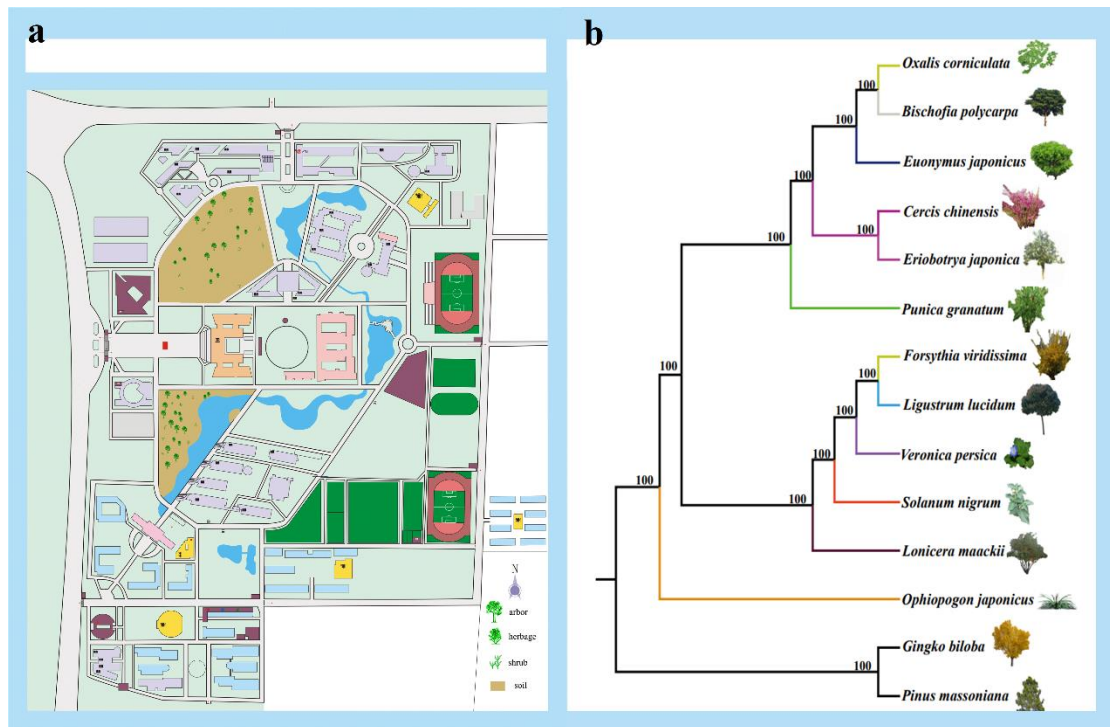


FIGURE S2. α -Diversities of soil bacteria in the four plant types. Shannon(a), Simpson(b), Observed(c) and Chao 1(d) indices of the fungus of rhizosphere soil.

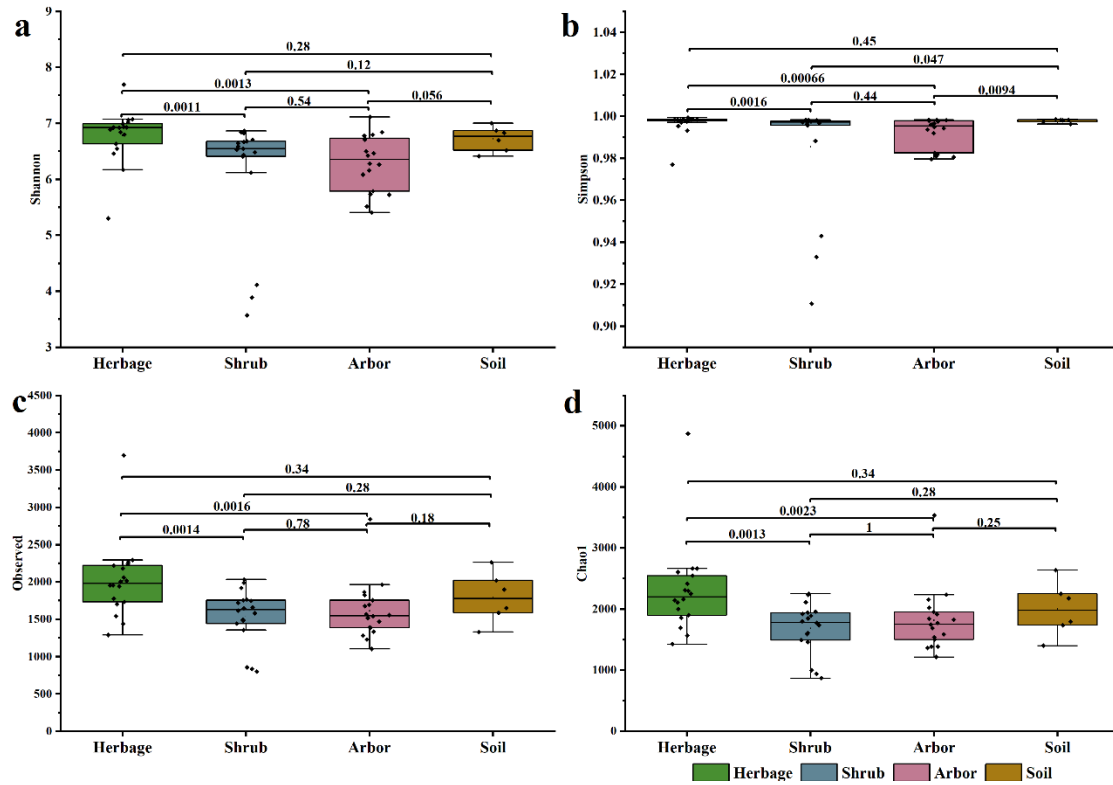


FIGURE S3. α -Diversities of soil fungus in the four plant types. Shannon(a), Simpson(b), Observed(c) and Chao 1(d) indices of the bacteria of rhizosphere soil.

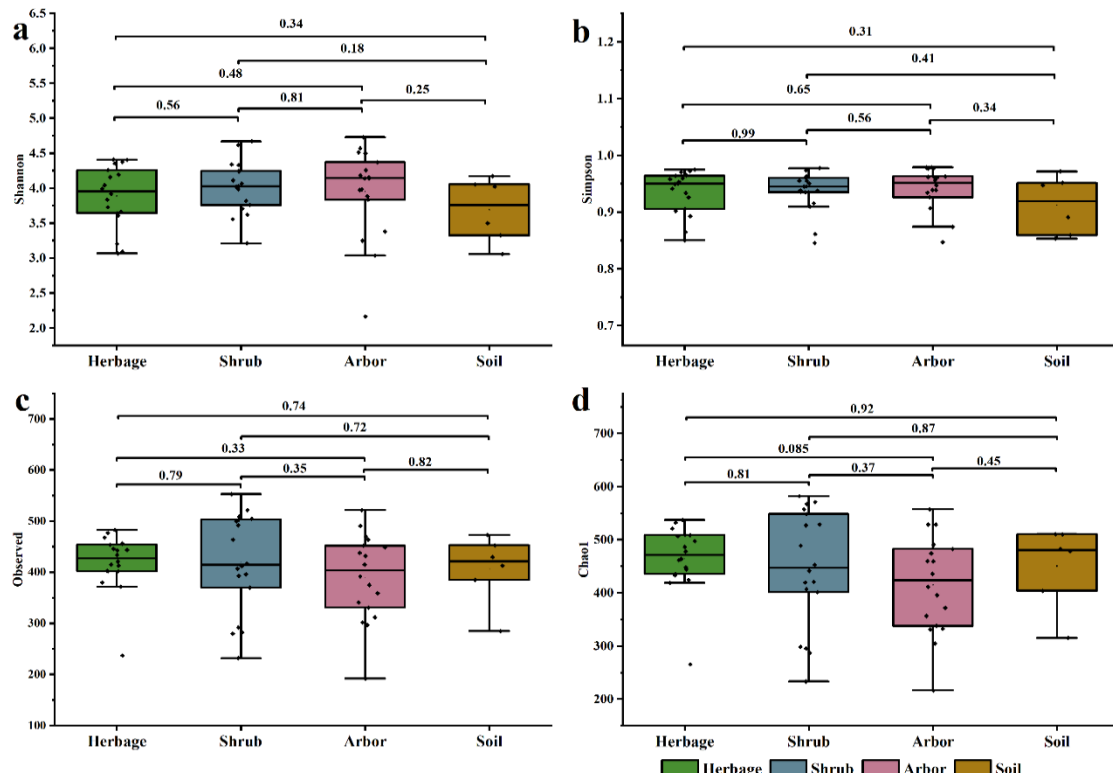


FIGURE S4. Principal coordinate analysis (PCoA) of the bacterial (a) and fungal (b) community among the samples based on Bray-Curtis distances.

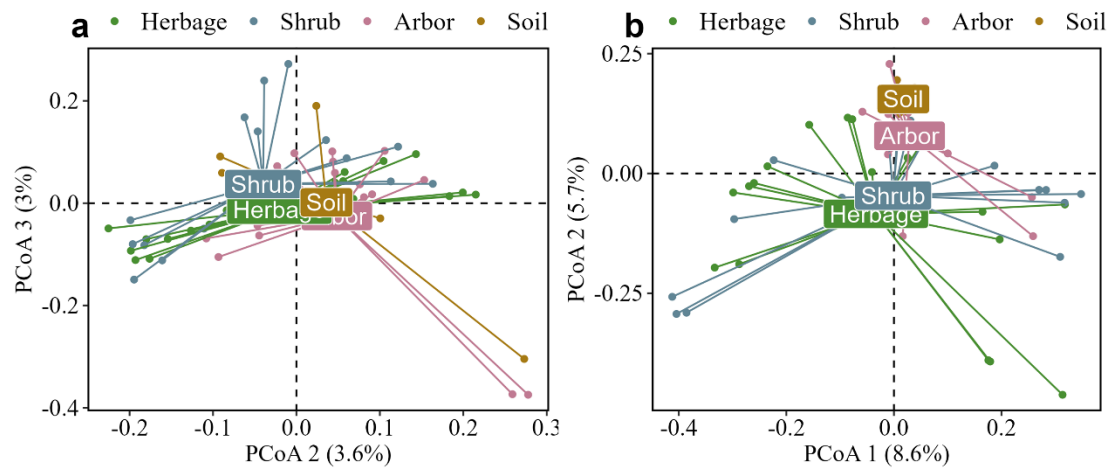


FIGURE S5. Principal component analysis (PCA) of the bacteria (a) fungus (b) among the samples. There was no significant grouping of fungus and bacteria in the four plant types.

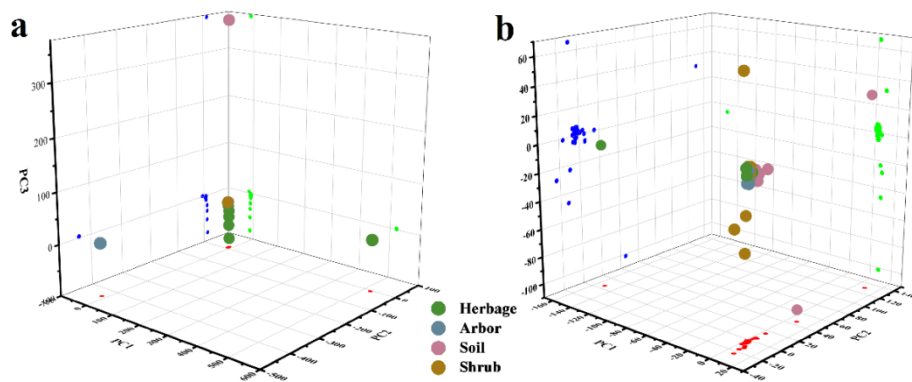


FIGURE S6. Principal coordinate analysis (PCoA) of the bacteria (a) fungus (b) between samples from two sampling locations.

