

Supplementary materials

Table S1. Influences of excluding root and mycorrhizal hypha on the relative abundance of dominant species at phylum level in a subtropical Chinese fir plantation forest soil. CT, no exclusion of root or mycorrhizal hypha; NR, exclusion of root but remain mycorrhizal hypha; NRH, exclusion of root and mycorrhizal hypha. SOC, soil organic carbon; DOC, dissolved organic carbon; DON, dissolved organic nitrogen; TN, total nitrogen; AP, available phosphorus; TP, total phosphorus. Different letters indicate significant differences at $\alpha = 0.05$.

Relative abundance of species		Treatment		
		CT	NR	NRH
Bacteria	<i>*Acidobacteria</i>	0.359±0.027b	0.409±0.027ab	0.469±0.044a
	<i>*Proteobacteria</i>	0.348±0.047a	0.274±0.035b	0.25±0.015b
	<i>Chloroflexi</i>	0.059±0.014a	0.062±0.012a	0.053±0.016a
	<i>Verrucomicrobia</i>	0.039±0.006a	0.053±0.012a	0.052±0.008a
	<i>Planctomycetes</i>	0.047±0.009a	0.054±0.015a	0.045±0.009a
	<i>*Actinobacteria</i>	0.073±0.009a	0.05±0.007b	0.044±0.009b
	<i>Bacteroidetes</i>	0.018±0.006a	0.026±0.019a	0.016±0.004a
	<i>*WPS2</i>	0.016±0.002b	0.027±0.006a	0.024±0.006ab
	<i>Gemmatimonadetes</i>	0.009±0.001a	0.007±0.001a	0.007±0.002a
	<i>Chlamydiae</i>	0.004±0.001a	0.004±0.002a	0.005±0.002a
	others	0.027±0.001a	0.034±0.003a	0.034±0.005a
Fungi	<i>Ascomycota</i>	49.37±9.34a	45.37±5.93a	50.96±7.97a
	<i>Mortierellomycota</i>	12.9±13.04a	14.05±8.51a	12.07±11.97a
	<i>Basidiomycota</i>	15.72±8.57a	14.12±4.78a	8.41±1.3a
	Unassigned	14.29±2.26a	12.61±1.22a	15.72±1.43a
	<i>*Rozellomycota</i>	2.41±0.29b	6.2±3.13ab	6.92±2.06a
	<i>Mucoromycota</i>	3.58±1.86a	3.4±1.58a	2.58±0.3a
	<i>Chytridiomycota</i>	0.57±0.3a	2.17±1.75a	1.18±0.59a
	unidentified	0.77±0.22a	1.02±0.27a	0.95±0.34a
	<i>*Glomeromycota</i>	0.37±0.28b	1.04±0.32a	1.15±0.34a
	<i>Ciliophora</i>	0.003±0.005a	0.015±0.017a	0±0a
	others	0.001±0.001a	0.006±0.005a	0.05±0.095a

Table S2. Information of microbial functional genes involved in carbon or nitrogen degradation and fixation in this study.

KEGG orthology number	Gene	Encode protein
Carbon degradation		
K00705	<i>malQ</i>	4-alpha-glucanotransferase
K01187	<i>malZ</i>	alpha-glucosidase
K01179	<i>celF</i>	endoglucanase F
K01183	<i>chi</i>	chitinase
K01710	<i>rfbB</i>	phosphomannomutase
K01805	<i>xylA</i>	xylose isomerase
K05343	<i>treS</i>	maltose alpha-D-glucosyltransferase I alpha-amylase
K05349	<i>bglX</i>	beta-glucosidase
K05350	<i>bglB</i>	beta-glucosidase
K01209	<i>ablA</i>	alpha-L-arabinofuranosidase
Carbon fixation		
K01962	<i>accA</i>	acetyl-CoA carboxylase carboxyl transferase subunit alpha
K01895	<i>facA</i>	acetyl-CoA synthetase
K00031	<i>icd</i>	isocitrate dehydrogenase
K00174	<i>korA</i>	2-oxoglutarate ferredoxin oxidoreductase subunit alpha
K00175	<i>korB</i>	2-oxoglutarate ferredoxin oxidoreductase subunit beta
K01938	<i>fhs</i>	formyltetrahydrofolate synthetase
K03520	<i>coxL</i>	carbon monoxide dehydrogenase large subunit
K03519	<i>coxM</i>	carbon monoxide dehydrogenase medium subunit
K03518	<i>coxS</i>	carbon monoxide dehydrogenase small subunit
Nitrogen fixation		
K04487	<i>nifS</i>	Nitrogenase metalloclusters biosynthesis protein
Nitrogen degradation		
K00372	<i>nasA</i>	assimilatory nitrate reductase catalytic subunit
K00362	<i>nirB</i>	Nitrite reductase (NADH) large subunit
K01428	<i>ureC</i>	Urease subunit alpha
K15371	<i>GDH2</i>	NAD-specific glutamate dehydrogenase

Fig. S1. The dominant factors that contribute to microbial community diversity after removal of root and mycorrhizal hypha in a subtropical Chinese fir plantation forest soil. SOC, soil organic carbon; DOC, dissolved organic carbon; DON, dissolved organic nitrogen; TN, total nitrogen; AP, available phosphorus; TP, total phosphorus. * and ** indicate significant level at 0.05 and 0.01, respectively.

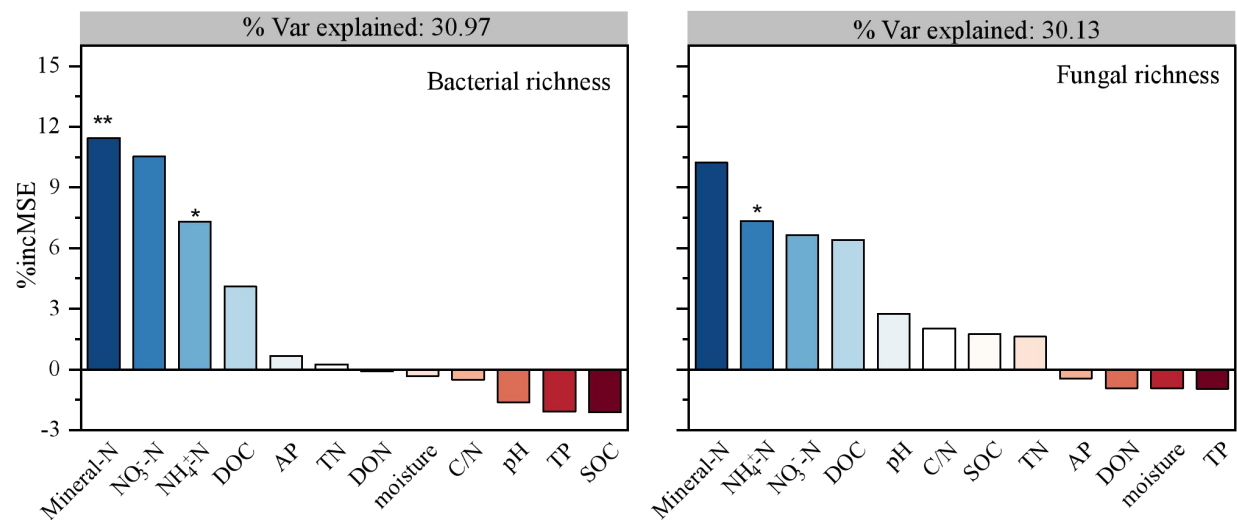


Fig. S2. Correlations between the relative abundance of dominant microbial species and soil properties in a subtropical Chinese fir plantation forest soil. SOC, soil organic carbon; DOC, dissolved organic carbon; DON, dissolved organic nitrogen; TN, total nitrogen; AP, available phosphorus; TP, total phosphorus. *, **, *** indicate significant level at 0.05, 0.01, and 0.001, respectively.

