Supplementary Materials

Inconsistent Responses of Rhizosphere Microbial Community Structure and Extracellular Enzyme Activity to Short-Term Nitrogen and Phosphorus Additions in Chinese Fir (*Cunninghamia lanceolata*) Plantations

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Table S1. The fatty acids detected in this study.

Category	Subgroup	Fatty acid
Bacteria	Gram-positive	15:0 anteiso, 15:0 iso, 16:0 iso, 17:0 anteiso, 17:0 iso, 17:1 iso w9c, 18:0 iso,
	Gram-negative	15:1 w5c, 16:1 w7c, 17:0 cyclo w7c, 17:1 w8c, , 18:1 w5c, , 18:1 w7c, 19:0 cyclo w7c,
	Other bacteria	17:0,15:0
Fungi	Fungi	16:1 w5c, 18:1 w9c, 18:2 w6c, 18:2 w9c
	AM Fungi	16:1 w5c
Actinomycete		16:0 10-methyl, 17:0 10-methyl, 17:1 w7c 10-methyl, 18:0 10-methyl, 18:1 w7c 10-methyl, 19:1 w7c 10-methyl
Other PLFAs		14:0, 16:0, 18:0, 20:0

Tian, D.; Jiang, L.; Ma, S.; Fang, W.J.; Schmid, B; Xu, L.C., et al. Effects of nitrogen deposition on soil microbial communities in temperate and subtropical forests in China. *Sci. Total Environ.* **2017**, 607, 1367-1375.

Shen, F.F.; Wu, J.P.; Fan, H.B.; Liu, W.F.; Guo, X.M.; Duan, H.L.; Hu, L.; Lei, X.M.; Wei, X.H. Soil N/P and C/P ratio regulate the responses of soil microbial community composition and enzyme activities in a long-term nitrogen loaded Chinese fir forest. *Plant Soil* **2019**, 436, 91-107.

Table S2. General site and soil characteristics (0–10 cm soil depth) in Chinese fir plantation sites at the Huitong National Forest Ecosystem Research Station used in the present study.

Stand types	Chinese fir
Tree DBH (cm)	8.26 (0.49)
Tree height (m)	6.42 (0.62)
pH	4.28 (0.03)
SWC (%)	32.83 (0.54)
SOC (g/kg)	25.15 (0.92)
TP (g/kg)	0.15 (0.00)
DOC (mg/kg)	391.2 (15.98)
NH_4^+–N (mg/kg)	9.49 (3.13)
NO_3^-–N (mg/kg)	6.26 (1.26)
DON (mg/kg)	22.6 (1.26)
AP (mg/kg)	7.72 (0.52)

Table S3. Summary statistics (F statistic and probability level) of a one-way ANOVA on the effects of N addition and P addition on soil nutrients properties, soil enzymes and relative abundance PLFAs (mol %) in rhizosphere soil of Chinese fir plantations.

Parameters	**N addition**		**P addition**	
	F	***p***	**F**	***p***
SWC	0.51	0.7	2.57	**0.083**
pH	5.19	**0.007**	5.28	**0.008**
SOC	3.01	**0.052**	1.36	0.2
TN	9.65	**0.000**	4.06	**0.019**
Inorganic N	2.54	**0.082**	6.62	**0.002**
NH_4^+–N	2.39	**0.096**	3.01	**0.051**
NO_3^-–N	1.09	0.39	3.73	**0.026**
TP	5.69	**0.005**	2.64	**0.075**
AP	2.39	**0.096**	3.57	**0.030**
SOC:TN	0.70	0.5	3.99	**0.021**
SOC:TP	2.17	0.1	8.73	**0.000**
TN:TP	2.33	0.1	1.61	0.2
BG	50.18	**0.000**	5.69	**0.005**
NAG+LAP	9.53	**0.000**	3.16	**0.045**
ACP	8.91	**0.000**	6.71	**0.002**
CBH	27.64	**0.000**	10.23	**0.000**
BX	9.95	**0.000**	5.71	**0.005**
AG	47.06	**0.000**	9.92	**0.000**
BG:(NAG+LAP)	2.59	**0.078**	3.40	**0.035**
BG:ACP	18.61	**0.000**	0.57	0.6
(NAG+LAP):ACP	6.74	**0.002**	0.35	0.8
Vector length	3.19	**0.043**	2.67	**0.072**
Vector angle	21.12	**0.000**	0.64	0.6
Total PLFAs	0.89	0.4	1.79	0.1
Bacteria	1.47	0.2	3.91	**0.022**
Fungi	4.57	**0.012**	4.18	**0.018**

Actinobacteria	2.46	**0.090**	14.71	**0.000**
AMF	3.81	**0.024**	0.81	0.5
G+	2.75	**0.067**	3.58	**0.030**
G-	2.73	**0.068**	1.56	0.2
Other bacteria	1.96	0.1	1.52	0.2
F:B	4.30	**0.016**	4.51	**0.013**
G+:G-	2.96	**0.054**	1.52	0.2

Significant differences between different nutrient addition are shown in bold ($p < 0.1$).

Figure S1. Effects of N and P additions on rhizosphere soil properties and microbial community structure (indicated by relative abundance of individual PLFAs). Values are means ± SE (n = 4). Different lowercase letters indicate significant difference among the levels of N or P addition ($p < 0.05$). CK, 0 kg N ha^{-1} a^{-1}+0 kg P ha^{-1} a^{-1}; N1, 25 kg N ha^{-1} a^{-1}; N2, 50 kg N ha^{-1} a^{-1}; N3, 100 kg N ha^{-1} a^{-1}; N4, 200 kg N ha^{-1} a^{-1}; P1, 25 kg P ha^{-1} a^{-1}; P2, 50 kg P ha^{-1} a^{-1}; P3, 75 kg P ha^{-1} a^{-1}; P4, 100 kg P ha^{-1} a^{-1}.

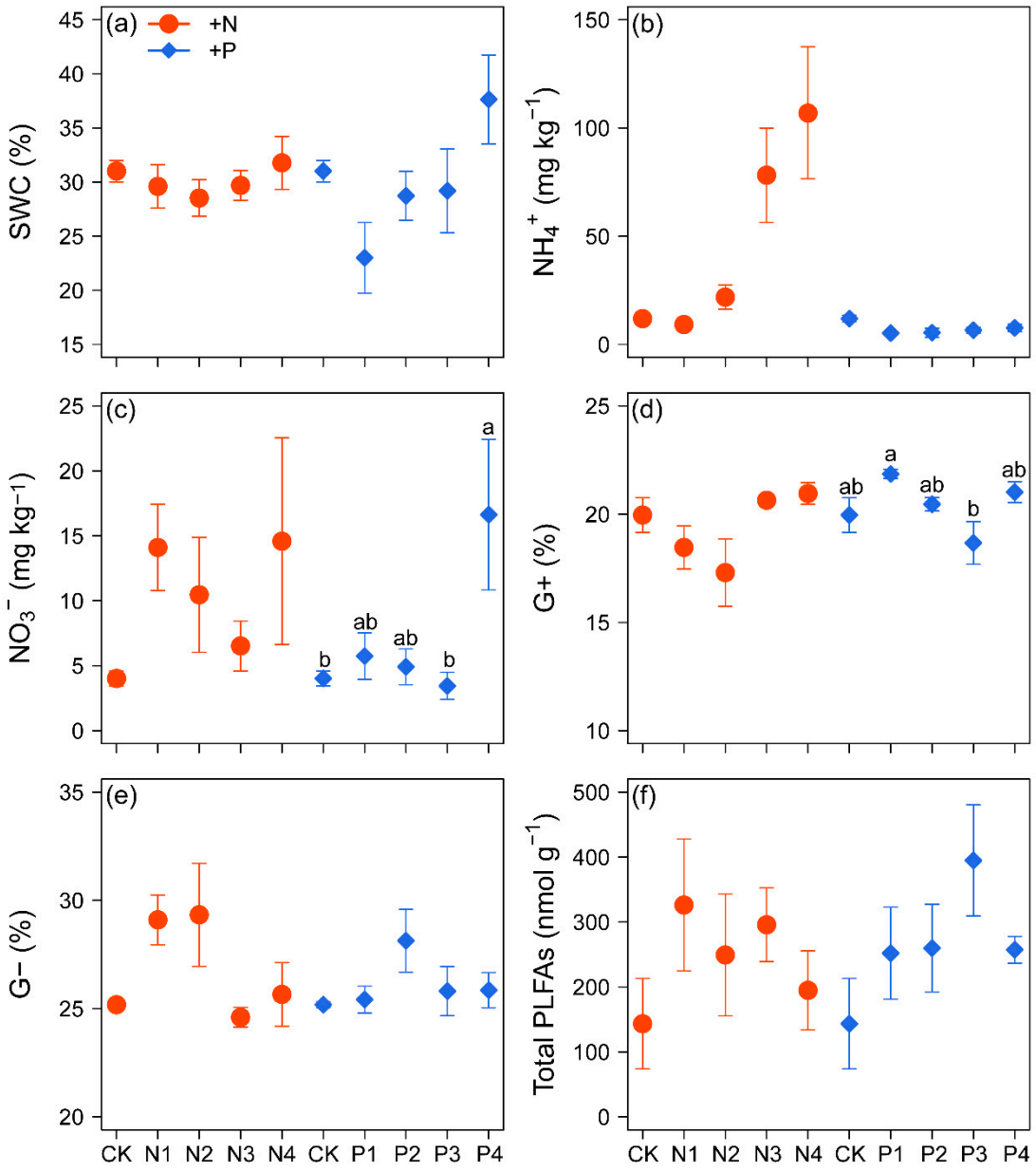


Figure S2. The correlation between soil properties and microbial groups, enzyme activities, stoichiometric ratio of enzymes, vector angle in the rhizosphere. Other B%, relative abundance of other bacteria. B%, relative abundance of bacteria. F%, relative abundance of fungi. AMF%, relative abundance of arbuscular mycorrhizal fungi. Act%, relative abundance of actinobacteria. G+%, relative abundance of Gram-positive bacteria. G-%, relative abundance of Gram-negative bacteria.* $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$.

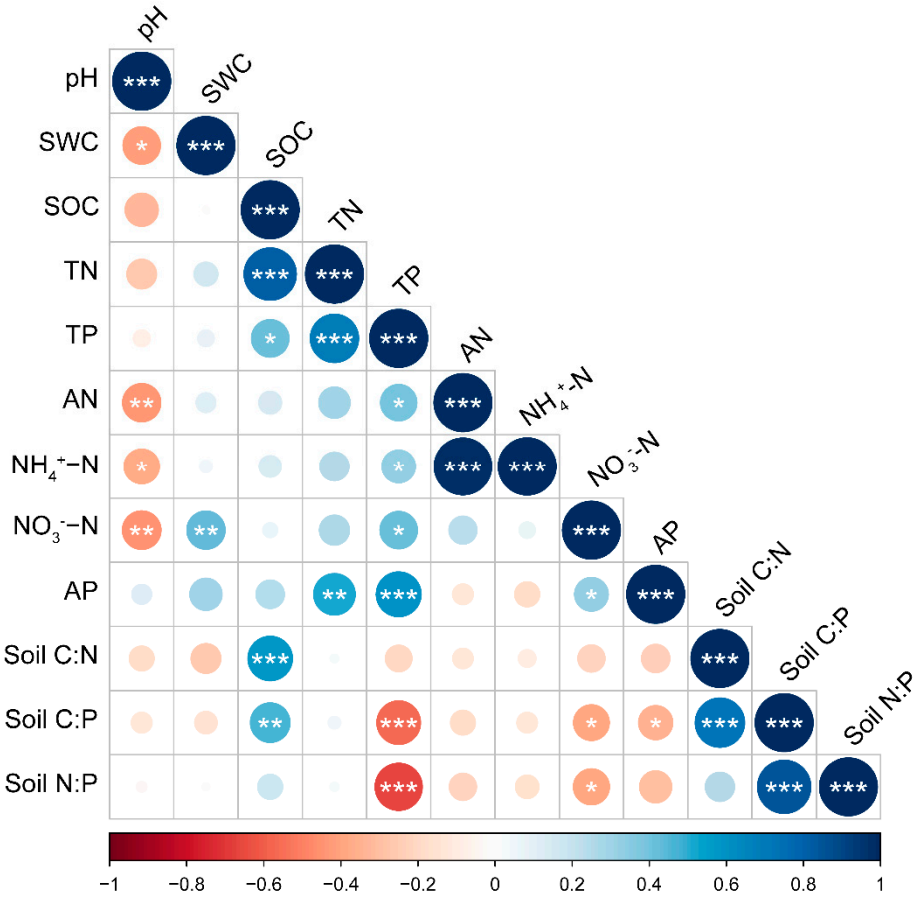


Figure S3. The correlation among microbial groups, enzyme activities and stoichiometric ratio of enzymes in the rhizosphere. F%, relative abundance of fungi. Enzyme PC1, the first principal component of enzyme profiles according to seven rhizosphere enzymes. PLFA PC1, the first principal component of the entire microbial community structure according to relative abundance of individual PLFAs. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$.

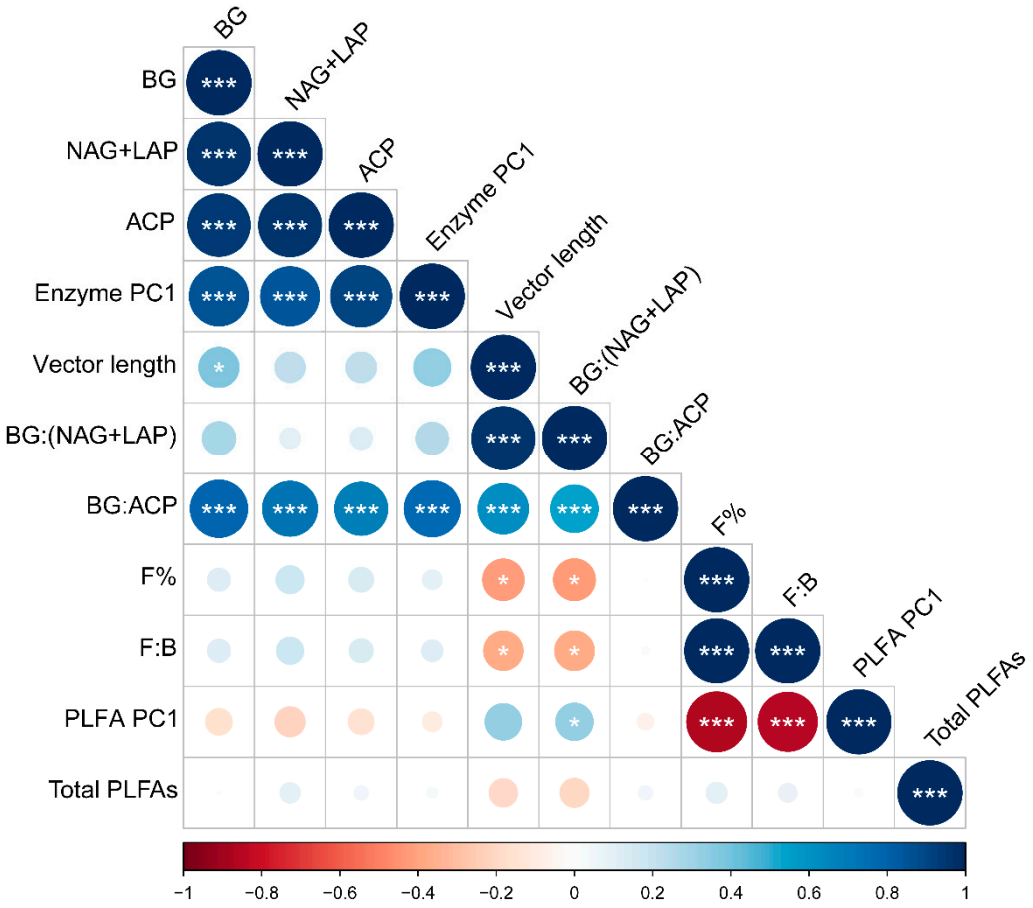
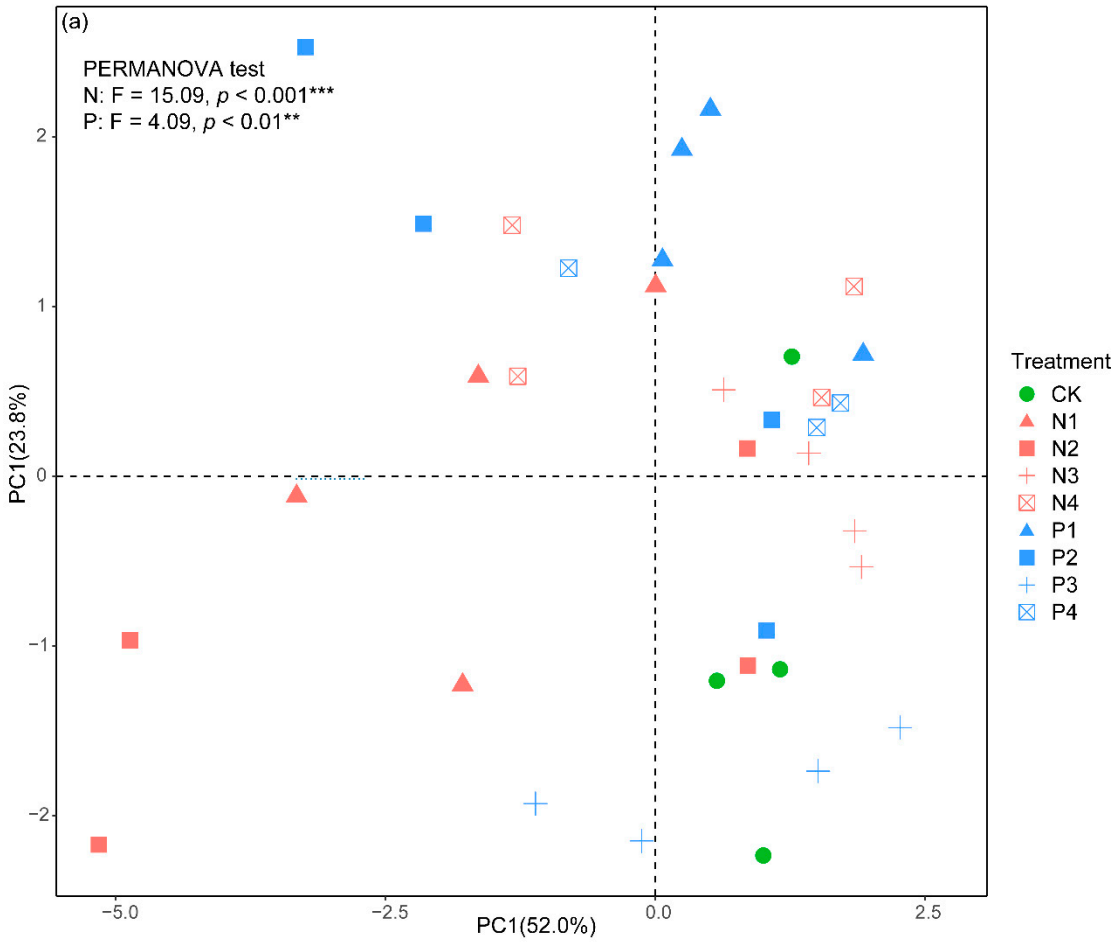
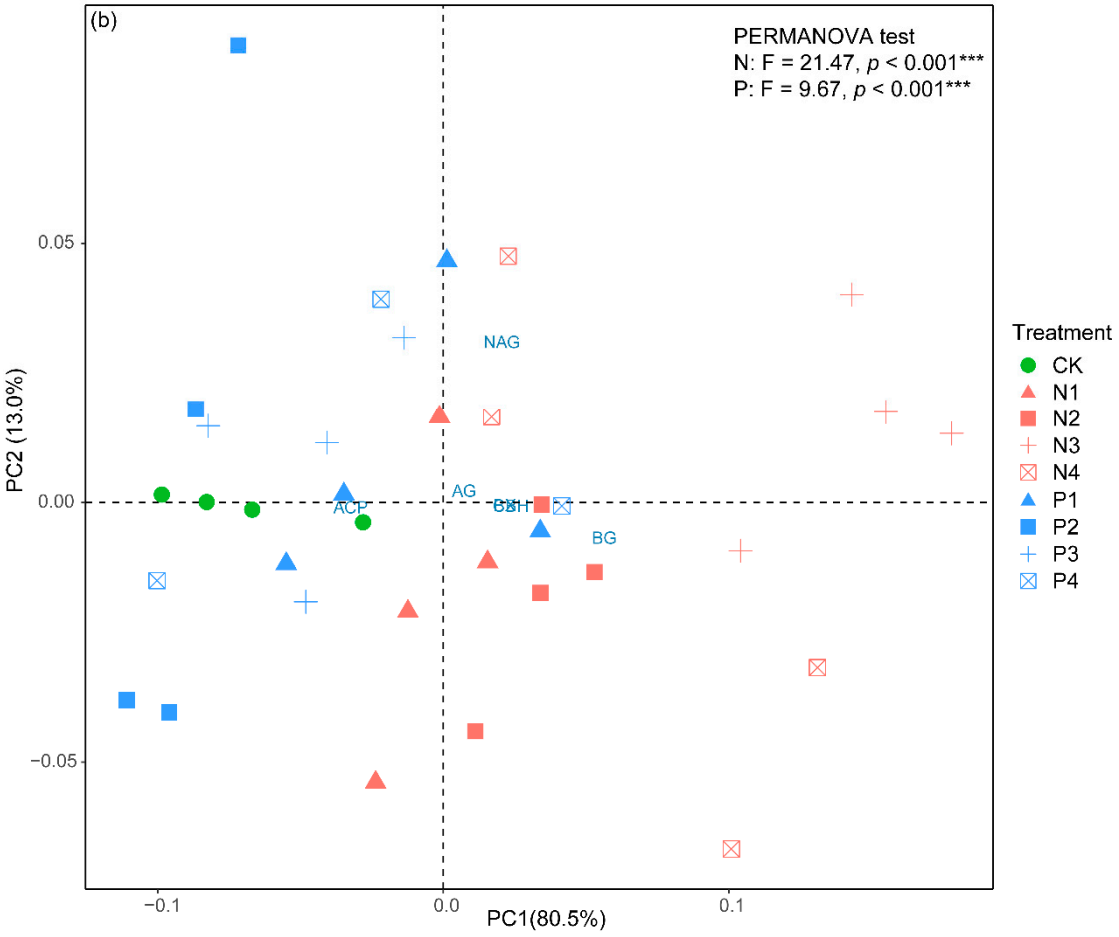


Figure S4. Principal component analysis (PCA) for rhizosphere microbial community structure (a), in which PC1 explains 52% and PC2 explains 23.8% of total variations. PCA for rhizosphere extracellular enzyme actives (b), in which PC1 explains 80.5% and PC2 explains 13% of total variations. PERMANOVA statistics refer to significant N and P treatment effects. CK, 0 kg N ha^{-1} a^{-1}+0 kg P ha^{-1} a^{-1}; N1, 25 kg N ha^{-1} a^{-1}; N2, 50 kg N ha^{-1} a^{-1}; N3, 100 kg N ha^{-1} a^{-1}; N4, 200 kg N ha^{-1} a^{-1}; P1, 25 kg P ha^{-1} a^{-1}; P2, 50 kg P ha^{-1} a^{-1}; P3, 75 kg P ha^{-1} a^{-1}; P4, 100 kg P ha^{-1} a^{-1}.




(b)
PERMANOVA test
N: F = 21.47, p < 0.001***
P: F = 9.67, p < 0.001***
0.05
0.00
−0.05
PC2 (13.0%)
−0.1
0.0
0.1
PC1(80.5%)
NAG
AG
ACP
BG
Treatment
CK
N1
N2
N3
N4
P1
P2
P3
P4