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Soil microbial diversity and network complexity promote phosphorus transformation – a case of long-term mixed plantations of *Eucalyptus* and a nitrogen-fixing tree species

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Table S1 Main characteristics in PPs and MPs.

Stand type	Altitude (m)	Gradient (°)	Age (a)	SD (trees·hm^{-2})	DBH (cm)	TH (m)
PPs	224	24	17	595±28	20.11±0.27	23.88±0.38
MPs	227	21	17	610±12	19.61±0.50	23.16±0.47
Eucalyptus urophylla	—	—	—	310±17	22.26±0.28	25.83±0.40
Acacia mangium	—	—	—	300±18	16.13±1.20	19.62±0.65

PPs: pure plantations; MPs: mixed plantations; SD: stand density; D.B.H.: diameter at breast height; TH: tree height.

Table S2. Details of the various soil extracellular enzymes and associated substrates.

Enzyme Type	Enzyme	International Classification Number	Abbreviation	Substrate
N-acquiring enzyme	β-1,4-N-acetylglucosaminidase	EC 3.2.1.30	NAG	4-MUB-N-acetyl-β-D-glucosaminide (200 μM)
	Leucine aminopeptidase	EC 3.4.11.1	LAP	L-Leucine-7-amino-4-methylcoumarin (200 μM)
P-acquiring enzyme	Acid phosphatase	EC 3.1.3.2	ACP	4-MUB-phosphate (200 μM)

EC: Enzyme Commission number describing enzymatic function in increasing level of detail (the first number distinguishes 1-oxireductases, 2-transferases, 3- hydrolases, 4-lyases, 5-isomerases, and 6-ligases)

Table S3 Quantitative real-time PCR primers for nitrogen and phosphorus cycling function genes**.**

Gene type	Target gene	Primer	Sequence (5'- 3')
Nitrogen cycle	*nifH*	Pol-F	TGCGAYCCSAARGCBGACTC
		Pol-R	ATSGCCATCATYTCRCCGGA
	AOB-amoA	amoA-1F	GGGGTTTCTACTGGTGGT
		amoA-2R	CCCCTCKGSAAAGCCTTCTTC
	narG	narG-f	TAYGTSGGGCAGGARAAACTG
		narG-r	CGTAGAAGAAGCTGGTGCTGT
	nirK	nirk876	ATYGGCGGVCAYGGCGA
		nirk1040	GCCTCGATCAGRTTRTGGTT
	nirS	Nirs-Cd3aF	GTSAACGTSAAGGARACSGG
		Nirs-R3cdR	GASTTCGGRTGSGTCTTGA
	nosZ	nosZ2F	CGCRACGGCAASAAGGTSMSSGT
		nosZ2R	CAKRTGCAKSGCRTGGCAGAA
Phosphorus cycle	*phoC*	phoc-A-F1	CGGCTCCTATCCGTCCGG
		phoc-A-R1	CAACATCGCTTTGCCAGTG
	phoD	ALPS-F730	CAGTGGGACGACCACGAGGT
		ALPS-R1101	GAGGCCGATCGGCATGTCG
	BPP	bpp-F	GACGCAGCCGAYGAYCCNGCNITNTGG
		bpp-R	CAGGSCGCANRTCIACRTTRTT
	pqqC	Fw	AACCGCTTCTACTACCAG
		Rv	GCGAACAGCTCGGTCAG
Bacteria	16S rRNA	338F	ACTCCTACGGAGCGCA
		806R	GGACTACHVGGGTWTCTAAT
Fungi	ITS	ITS1F	CTTGGTCATTTAGAGGAAGTAA
		ITS2R	GCTGCGTTCTTCATCGATGC

Table S4 Statistical table of bacterial and fungi species in both 0−10 cm and 10−20 cm soil layers in PPs and MPs.

Microbial type	Soil layer (cm)	Stand type	Phylum	Class	Order	Family	Genus	OTU
Bacteria	0−10	PPs	20	50	112	155	229	1435
		MPs	21	62	131	187	283	1760
	10−20	PPs	20	47	108	155	224	1315
		MPs	20	58	126	179	268	1695
	Total	—	21	64	140	201	311	1869
Fungi	0−10	PPs	8	18	41	57	73	693
		MPs	8	21	45	73	93	723
	10−20	PPs	8	18	41	52	56	651
		MPs	8	19	43	64	87	654
	Total	—	8	24	62	104	157	1128

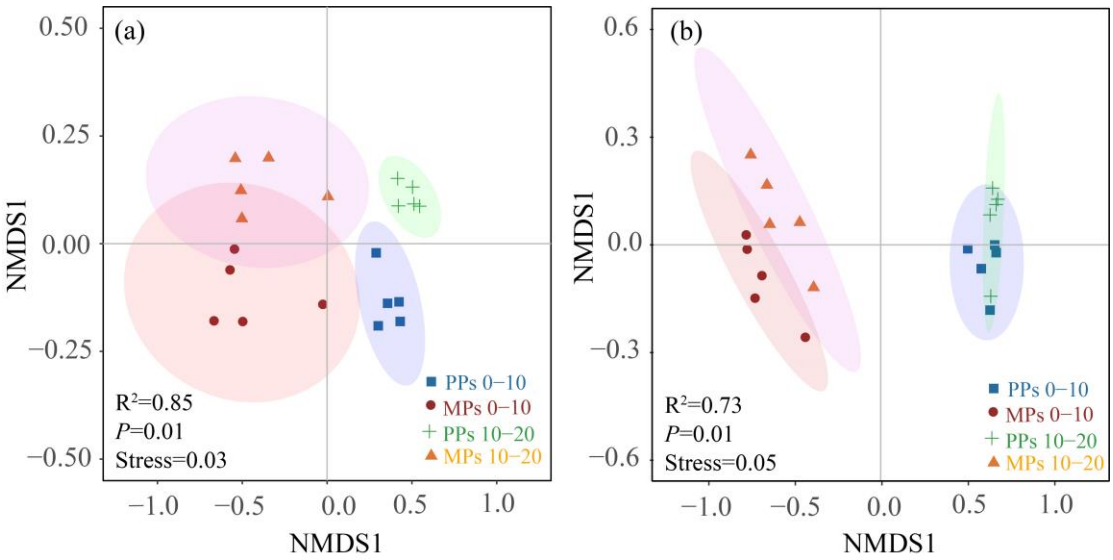

Fig. S1 Nonmetric multidimensional scaling analysis of (a) bacterial and (b) fungal, based on Bray-Curtis similarity in both 0−10 cm and 10−20 cm soil layers in PPs and MPs.

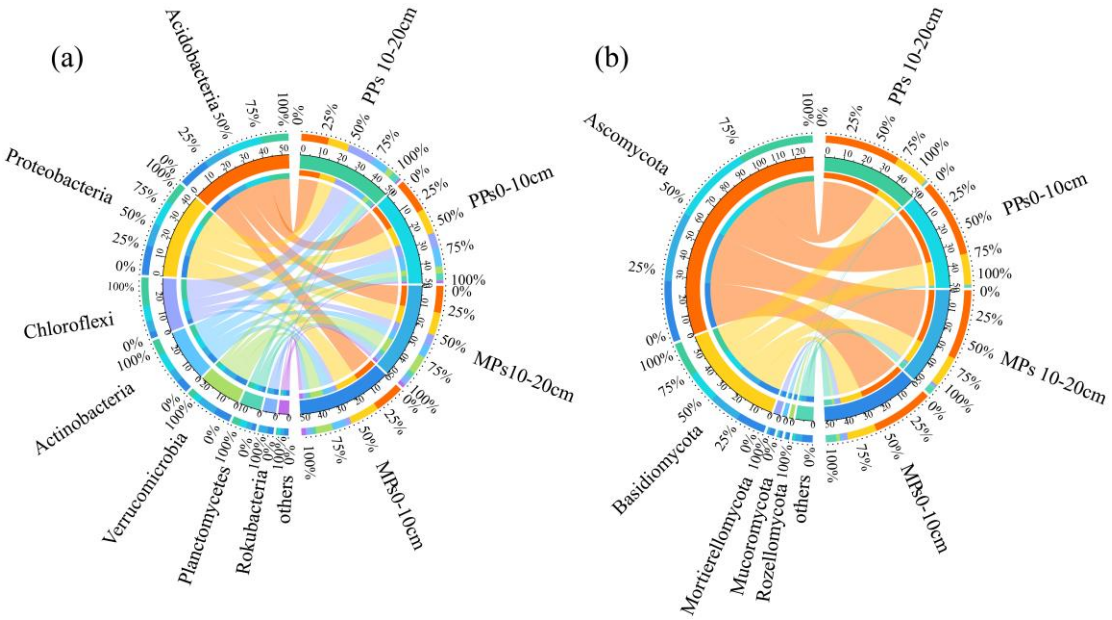

Fig. S2 Chord diagrams showing the bacterial (a) and fungal (b) community composition (at the relative abundance >1% phylum level). The outer circle scale represents the percentage information of relative abundance of OTU in the sample; The inner circle scale represents the absolute abundance information of OTU in the sample (unit: 1000).

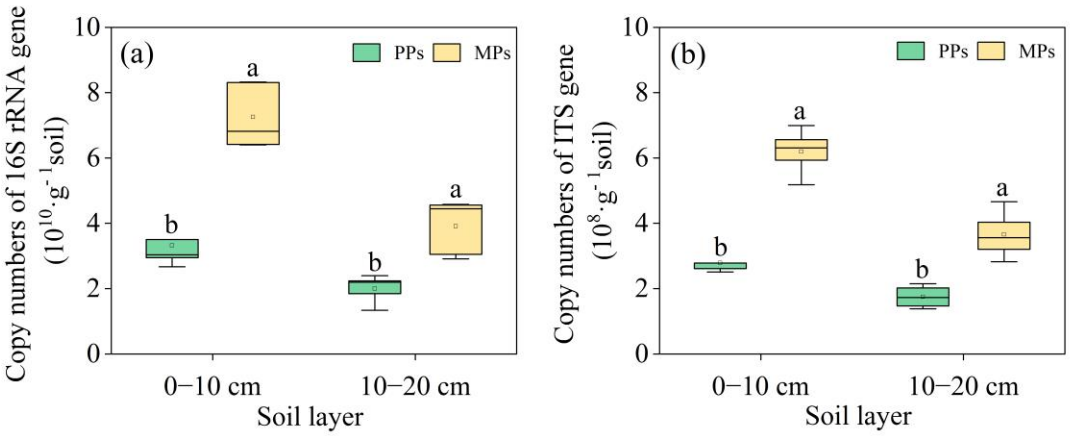

Fig. S3 Comparisions copy number of (a) 16SrRNA and (b) ITS in both 0−10 cm and 10−20 cm soil layers in PPs and MPs.

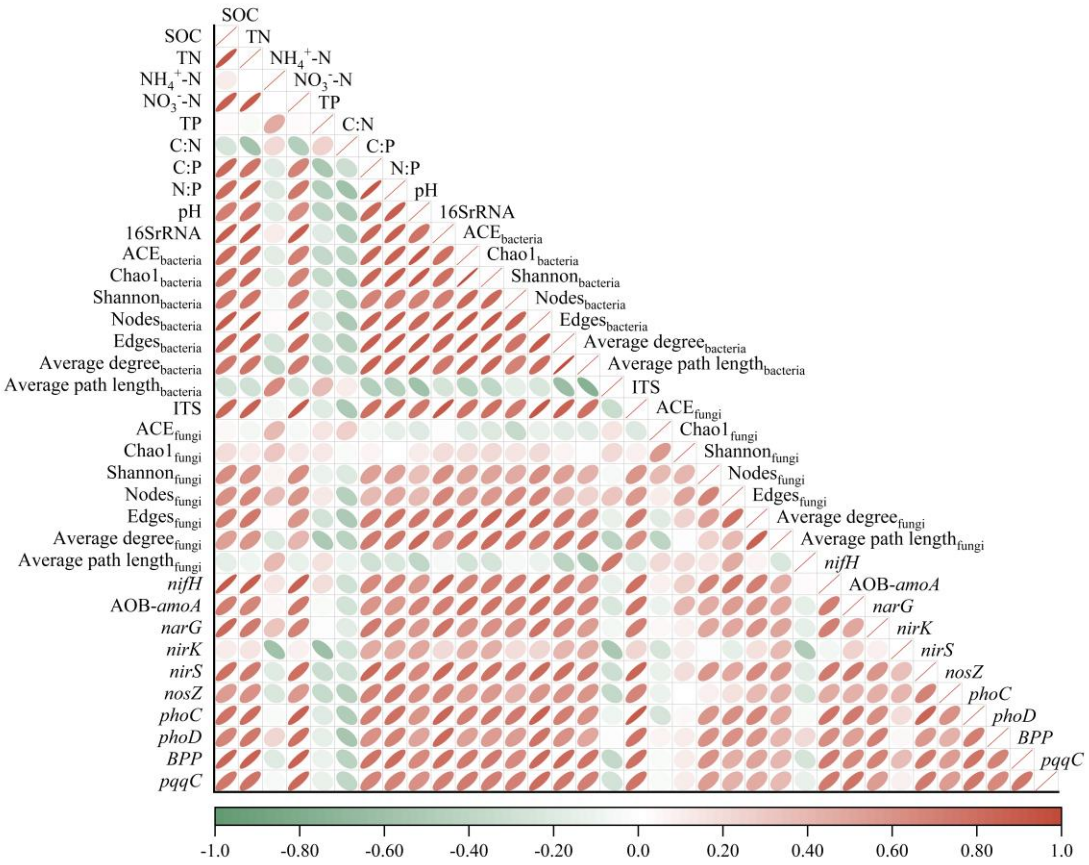

Fig. S4 Correlative relationships between soil physico-chemical properties, microbial diversity and complexity, and soil physico-chemical properties.