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

Jiyin Li [a, 1], Yeming You [a, b, 1], Wen Zhang [c], Yi Wang [d], Yuying Liang [a], Haimei Huang [a], Hailun Ma [a], Qinxia He [a], Angang Ming [b, e], Xueman Huang [a, b, *]

[a] Guangxi Key Laboratory of Forest Ecology and Conservation, Guangxi Colleges and Universities Key Laboratory for Cultivation and Utilization of Subtropical Forest Plantation, College of Forestry, Guangxi University, Nanning, Guangxi 530004, China

[b] Guangxi Youyiguan Forest Ecosystem National Observation and Research Station, Youyiguan Forest Ecosystem Observation and Research Station of Guangxi, Pingxiang 532600, Guangxi, China

[c] Jinggangshan Institute of Red Soil, Jiangxi Academy of Agricultural Sciences, Ji'an Jiangxi 343016, China

[d] Institute of Resources and Environment, Key Laboratory of National Forestry and Grassland Administration/Beijing for Bamboo & Rattan Science and Technology, International Centre for Bamboo and Rattan, Beijing, 100102, China

[e] Experimental Centre of Tropical Forestry, Chinese Academy of Forestry, Pingxiang 532600, China

[*] Corresponding author. Tel.: +86 13667881541; E-mail address: huangxm168168@163.com (X. Huang)

[1] These authors contributed equally to this work.

**Deleted:** :

**Deleted:** -species

**Deleted:** with

**Formatted:** Font: Italic

**Deleted:** a

**Deleted:** Promoted phosphorus transformation by increasing soil microbial diversity and network complexity- A case of long-term mixed-species plantations of *Eucalyptus* with N-fixing tree species…

**Formatted:** None

## Abstract

Increased nitrogen (N) availability influences soil phosphorus (P) cycling through multiple pathways. Soil microorganisms are essential facilitating a wide range of ecosystem functions. However, the impact of mixed plantations of *Eucalyptus* and N-fixing tree species affect P transformation and microbiota interactions remains unknown. Therefore, we conducted a 17-year field experiment comparing pure *Eucalyptus* plantations (PPs) and mixed plantations (MPs) with *Eucalyptus* and a N-fixing tree species to assess their effects of soil P transformation, using data collected from two soil layers (0–10 cm and 10–20 cm). The results showed that α-diversity indices (ACE and Chao1 and Shannon indices) were significantly higher in MPs than in PPs for both bacteria and fungi. Furthermore, MPs exhibited significantly higher relative abundances of bacterial phyla *Proteobacteria* (0–10 cm), *Verrucomicrobia*, and *Rokubacteria*, as well as fungal phyla *Mortierllomycota*, *Mucoromycota*, and *Rozellomycota*. Conversely, MPs showed lower abundances of the bacterial phyla *Chloroflexi*, *Actinobacteria*, and *Planctomycetes* and fungal phylum *Ascomycota*. Gene copy numbers of functional genes were also elevated in MPs, including 16S rRNA, internal transcribed spacer (ITS), N functional genes [*nifH* (0–10 cm), AOB-*amoA*, *narG*, *nirS*, and *nosZ* (0–10 cm)], and P functional genes [*phoC*, *phoD* (0–10 cm), *BPP*, and *pqqC*]. The findings indicated that MPs can enhance soil microbial diversity, network complexity, and the relative abundance of functional genes which involved N- and P- transformation by optimizing soil nutrient levels and pH, thereby facilitating P transformation. Therefore,

**Deleted:** ¶

**Formatted:** Indent: First line: 2 ch

**Deleted:** mixed

**Deleted:** ture…d plantations of *Eucalyptus* and N-fixing tre

**Deleted:** ed

**Deleted:** ture…d plantations (MPs) of

**Deleted:** s

**Deleted:** the effects of soil P transformation, with…sing da

**Deleted:** in mixed plantations (MPs) of *Eucalyptus* and N-fixing trees species…

**Deleted:** for

**Deleted:** bacteria

**Deleted:** as well asand Shannon indices) index for both

**Deleted:** S

**Deleted:** in of MPs than in PPs were determined for

**Deleted:** and for the …ungal phyla *Mortierllomycota*,

**Formatted:** Font: Not Italic

**Deleted:** associated involved with …- and P- transformatio

MPs of *Eucalyptus* and N-fixing tree species may represent a promising forest management strategy to improve ecosystem P benefits.

**Keywords:** Co-occurrence network; functional gene; mixed plantation; N-fixing species; phosphorous transformation

## 1. Introduction

Phosphorus (P) a vital macronutrient for plant and microbial growth (Turner et al., 2018), while the availability of P serves as a key indicator of soil fertility and quality (Peng et al., 2021). In most ecosystems particularly in tropical and subtropical forests, P bioavailable in soil is often limited due to intense weathering and the presence of aluminium (Al) ions and free iron (Fe) (Soltangheisi et al., 2019; Du et al., 2020). Therefore, these P reserves cannot be accessed directly by plants (Fan et al., 2019). However, plants and microorganisms have developed various strategies for access P from inorganic (Pi) and organic (Po) reservoirs and rendering it available for biological processes (including, e.g., assimilation by phosphate-solubilizing microorganisms and mineralization of enzymes) (Lu et al., 2022). Consequently, it is crucial to implement strategies for the sustainable management of soil P to enhance its utilization by plants, preserve soil quality, and mitigate the risk of P loss.

Soil microorganisms serve as both a reservoir and a source of phosphate ions, significantly influencing the availability of P. In addition, microorganisms play a role in maintaining soil functions such as nutrient cycling, biological activity, and plant growth, all of which are crucial for sustaining soil quality and fertility (Bünemann et al., 2008; Zhou et al., 2018; Sun et al., 2022). Microorganisms facilitate the P transformation by participating in the processes of P mineralization, solubilization, and cycling, converting P into bioavailable forms for plant uptake (Pastore et al., 2020). Specifically, the mineralization of Po is facilitated by the extracellular presence of phosphatases, which are mainly produced principally by soil microorganisms (Nannipieri et al., 2012). It is thus of both extracellular acid (ACP) and alkaline (ALP)

**Deleted:** constitutes
**Deleted:** crucial
**Deleted:**
**Formatted:** Not Highlight
**Deleted:** ,
**Deleted:** factor influencing the plant-microbe-soil interactions within forest ecosystems within forest ecosystems
**Deleted:** within forest ecosystems
**Deleted:** Richardson and Simpson, 2011
**Deleted:** supply
**Deleted:** frequently
**Deleted:** is
**Deleted:** strong
**Deleted:** supply
**Deleted:** free iron (Fe)
**Deleted:** aluminium (Al) ions
**Deleted:** because gaseous P compounds in the atmosphere
**Deleted:** , such that P cycling occurs mainly between plants
**Deleted:** T
**Deleted:** Rodríguez and Fraga 1999;
**Deleted:** microbes
**Deleted:** several
**Deleted:** recovering
**Deleted:** organic (Po)
**Deleted:** inorganic (Pi)
**Deleted:** use
**Deleted:** mineralization of enzymes,
**Deleted:** assimilation by phosphate-solubilizing
**Deleted:** essential
**Deleted:** Microorganisms are critical for the processes of P
**Deleted:** (Pastore et al., 2020). This is particularly true whe
**Deleted:** catalyzed
**Deleted:** the

phosphatase activities are commonly used as the indicators to assess the mineralization of Po to bioavailable Pi (Luo et al., 2019). Furthermore, P transformation is influenced by the α-diversity, structure, and composition of soil microbial communities, with pH being considered a key determinant in shaping microbial diversity and community composition (Jin et al., 2019). Microbiome co-occurrence networks are prevalently employed to scrutinize the interrelationships within microbial communities, and network attributes (e.g., the mean degree, edge quantity, and node amount) can be utilized to appraise the reciprocal ties among these communities and their reactions to modifications in cultivation paradigms (Faust, 2021; Qiu et al., 2021). Microbial network analysis can uncover the complex interactions between microorganisms, such as competition, cooperation, and antagonism, while also shedding light on important ecological processes and functional relationships that are not fully captured by microbial diversity analysis alone. For instance, it can reveal processes like the transformation and cycling of key soil nutrients (e.g., P and N), which are often overlooked in traditional diversity assessments (Yao et al., 2024). Thus, gaining insight into the relationship between microbial diversity, microbial network complexity, and the transformation and cycling of P is crucial for improving soil functions and enhancing soil fertility.

The studies on genes involved in P cycling also emphasizes the contribution of microbes in enhancing plant P uptake and efficiency (Dai et al., 2020). The P cycle cluster includes genes that stimulate the mineralization of Po (e.g., *phoD*, *phoC*, and *BPP*) (Cao et al., 2022; Khan et al., 2023) and solubilization of Pi (e.g., *pqqC*) (Meyer

**Deleted:** have

**Deleted:** been

**Deleted:** a

**Deleted:** proxy

**Deleted:** evaluate

**Deleted:** organic

**Deleted:** inorganic

**Deleted:** Nannipieri et al., 2012;

**Deleted:** Furthermore, Thethe α-diversity, structure, and composition of soil bacterial and fungal communities…are are extremely sensitive to P transformation

**Deleted:** are extremely sensitive to P transformation

**Deleted:**

**Deleted:** ¶

**Formatted:** Not Highlight

**Deleted:** The complexity of microbial networks, defined as the strength of microbial interactions, predicts ecosystem function, including the transformation and cycling of soil nutrients such as P and nitrogen (N).

**Deleted:** Therefore, network complexity is closely linked to multifunctionality (Yang et al., 2023).

**Deleted:** Thus, understanding the interplay between microbial diversity and microbial networks is essential for improving forest soil management and enhancing soil

**Deleted:** Thus, understanding the interplay between microbial diversity and microbial networks is crucial for developing forest management strategies aimed at enhancing soil fertility and optimizing ecosystem functionality.¶

**Deleted:** Functional gene markers are frequently used to examine the diversity and abundance of the microbial communities involved in elemental transformations. …

**Deleted:** organic P

**Deleted:** inorganic P

et al., 2011). The genes *phoD*/*phoC* encode phosphatases, which are capable of mineralizing Po compounds into Pi (Fraser et al., 2015). N is a fundamental element for plant growth and development, typically coupled with P in biogeochemical cycles. The N cycle group consists of genes responsible for microbially driven nitrification (e.g., AOB-*amoA*), N fixation (e.g., *nifH*), and denitrification (e.g., *nirS*). Improved interaction networks among soil microbial functional groups contribute to increasing nutrient availability and enhancing the nutrient acquisition of host plants (Shi et al., 2020; Qin et al., 2024). In addition, given that both N and P are essential elements for microorganisms, an increase in N content can influence soil pH, which subsequently alters the composition of soil microbial communities and impacts the abundance of phosphatase-coding genes (*phoC* and *phoD*) (Widdig et al., 2020). Furthermore, the presence of N-fixing plants also affects P uptake by enhancing litter decomposition rates and the release of organic acids from microbial biomass, thereby accelerating nutrient cycling and improving soil fertility (Li et al., 2021). Therefore, studying the coupling of N and P cycling in soil is crucial for understanding of the diversity and mechanisms of microbially driven biogeochemical cycles.

*Eucalyptus* is characterized by their straight trunks, well-developed horizontal root systems, and high adaptability. They are prevalent in subtropical and tropical regions, where they have significant economic and ecological value (Zhang and Wang, 2021). However, monocultures and short-term rotation management of *Eucalyptus* plantation have led to soil degradation, reductions in plant-available soil nutrient effectiveness (e.g., the availability of nutrients such as N, and P in forms that can be absorbed and utilized by plants), and soil microbial function and diversity, as well as other adverse

**Deleted:** Additionally,

**Formatted:** Font: Italic

**Formatted:** Font: Italic

**Deleted:** the gene *phoD* encodes a non-specific alkaline phosphatase (ALP) that exhibits enhanced activity in acidic soil (Fraser et al., 2015).

**Deleted:** also

**Deleted:** n

**Deleted:** essential

**Deleted:** ,

**Deleted:** ,

**Deleted:** ,

**Deleted:** Enhanced interaction networks between soil microbial functional groups account for promoting nutrient availability and acquisition of host plants (

**Deleted:**

**Deleted:** Although increased N availability enhances primary production, an optimal N: P ratio is needed to ensure P uptake and utilization, , thus maintaining the balanced nutrient availability that drives sustained growth (Tessier and Raynal 2003; Menge and Field, 2007). A…

**Deleted:** -

**Deleted:** However

**Deleted:** improving

**Deleted:** Perring et al., 2008;

**Deleted:** b

**Deleted:** impact of N availability on soil

**Deleted:** es is needed to assess P transformation in soil.

**Deleted:** are

**Deleted:** -

**Deleted:** b

**Deleted:** -

**Deleted:** i.e

**Deleted:** nitrogen

**Deleted:** phosphorus

**Deleted:** , and potassium

ecological effects. Mixed-species forests exert a strong positive impact on soil fertility and nutrient cycling by regulating the microbiome, including its diversity and structure (Pereira et al., 2019, Li et al., 2024). Recently, incorporating N-fixing trees species such as *Acacia* as a substitute for N fertilization has become widely acknowledged as one of the most effective silvicultural practices for enhancing tree N uptake and woody production in *Eucalyptus* plantations (Koutika and Mareschal, 2017; Zhang et al., 2023). In addition, mixing with N-fixing tree species improves N availability, P accumulation, microbial diversity, and forms a more complex and interconnected microbial network compared to pure plantations (Li et al., 2022; He et al., 2024; Yao et al., 2021). So far, the effect of N-fixing tree species on P cycling has mainly been addressed by investigating organic or inorganic P accumulation in soil from either pure or mixed stands of non - N-fixing tree species and N-fixing tree species (Yao et al., 2024).

*Acacia mangium*, one of the N-fixing trees species that is widely planted in many parts of the world, has clear benefits in forestry and agroforestry ecosystems (Epron et al., 2013; Koutika and Richardson, 2019). Key reasons for the widespread planting of *Acacia mangium* in pure or mixture plantations with other tree species with infertile soils, are its capacity to change soil faunal, microbial communities (Huang et al., 2014; Pereira et al., 2017), improve soil fertility (Tchichelle et al., 2017), and stimulate tree growth and forest productivity (Paula et al., 2015). Nevertheless, the effects of mixing N-fixing trees species on regulating the correlations between microbial diversity and network of P transformation is still poorly understood. Phosphomonoesterase (e.g., ACP) mineralization is an essential strategy for P transformation (Luo et al., 2019; Yu et al., 2022; Wang et al., 2023), so we employed soil ACP activity to analyse the dynamics of P transformation. Here, we aimed to (1) compare the variations in the

**Deleted:** In recent years

**Deleted:** the introduction of

**Deleted:** n

**Deleted:** alternative

**Deleted:** to

**Deleted:** gained widespread recognition

**Deleted:** favorable

**Deleted:** boosting

**Deleted:** absorption

**Deleted:** Epihov et al., 2021; Gomez-Gonz ´ alez ´ et al., 2022; …

**Formatted:** Don't adjust right indent when grid is defined, Don't snap to grid

**Formatted:** Font: Not Italic

**Deleted:** Planting *Eucalyptus* in a mixture with other trees has been demonstrated to enhance nutrient cycling efficiency, soil fertility, and overall productivity (Koutika and Mareschal, 2017; Epihov et al., 2021). *Acacia* are widely planted in South China because they require less or nofewer exogenous N from the soil, due to their N-fixing capacity (Räsänen et al., 2001). Mixed plantations that include N-fixing trees such as *Acacia* can significantly boost productivity and enhance organic carbon sequestration, thereby improving soil fertility and contributing to climate change mitigation (Marron and Epron, 2019; Zhang et al., 2023). Neverthe

**Deleted:** the mechanism through which microorganisms regulate …

**Deleted:**

**Deleted:** remains little understood

structure, diversity, and stability of soil microbial communities after mixing *Eucalyptus* with N-fixing tree species, and (2) elucidate the mechanisms through which fungal and bacterial communities, along with genes associated with N and P transformation processes, regulate P transformation. We hypothesized that (1) mixed-species plantations of *Eucalyptus* and N-fixing tree species would alter the composition of soil microbial communities and improve microbial community diversity and network complexity in the soil; (2) introduction of N-fixing tree species may cause imbalance in soil properties (e.g., SOC, pH and so on), microbial diversity and networks complexity, and related functional genes which co-regulated the P transformation with differential roles. Our findings will provide more new insights into sustainable management practices for plantations.

## 2. Materials and methods

### *2.1. Site description*

The study was conducted in the Shaoping Experimental Field at the Experimental Center for Tropical Forestry, which is affiliated with the Chinese Academy of Forestry (106°56′E, 22°03′N). The area has a subtropical climate, with approximately 1,400 mm of rainfall annually and maintaining an average yearly temperature of 21.2°C. The landscape is characterized by low mountains and hills along with acidic red soil. Forests in this area are primarily composed of commercially managed plantations, as either pure or mixed stands.

### *2.2. Plot design and sampling*

In this study, the pure (monoculture) *Eucalyptus urophylla* plantations (PPs) and adjacent mixed plantations (MPs) of *Eucalyptus urophylla* and *Acacia mangium* (N-fixing tree species) were established in 2004 on the logging tracks of *Pinus massoniana* plantations that were established in 1977. The MPs were planted at a 1:1

**Deleted:** introducing

**Deleted:** -

**Deleted:** into *Eucalyptus* plantation

**Deleted:** increase

**Deleted:** ing

**Deleted:** after the long-term mixed planting of *Eucalyptus* and N-fixing tree species remains unclear. We put forward the hypothesized that (1) introducing N-fixing tree species into *Eucalyptus* plantationmixing would alter the composition of soil microbial communities and increase microbial diversity and network complexity in the soil; (2) the soil P transformation driven by N-fixing tree speciestree species mixing may be positively regulated by microbial diversity and network complexity.(1) the diversity and composition of soil microorganisms would be changed in the mixed plantations, that (2) mixed plantations intensify the response to the beneficial impacts of N-fixing tree, thereby strengthening the correlation between the genes associated with N and P cycling, and that (3) N-fixing tree would lead to higher diversity and network complexity in mixed plantations. Our findings will provide more new insights into sustainable management practices for plantations.¶

**Deleted:** The primary aims of this study (1) were to evaluate the changes in the structure, diversity, and stability of soil microbial communities after mixing *Eucalyptus* with N-fixing tree species, and (2) to elucidate the mechanisms through which bacterial and fungal communities, along with genes involved inassociated with N and P cycling processes, regulate P transformation. ¶
<#>¶

**Formatted:** Don't adjust right indent when grid is defined, Don't snap to grid

**Deleted:** ,

**Deleted:** ¶

**Deleted:**

mixing ratio with inter-row planting, consisting of one row of *Eucalyptus urophylla* and one row of *Acacia mangium*. In the first two consecutive years post-planting, both plantations were subjected to a similar stand management regime, which included practices such as weed control and fertilization, subsequently allowing them to proceed with their natural stand development. The experimental design is described in the study conducted by Huang et al. (2017). In 2021, taking into account the differences in plantation layout and topography, five 20 m × 20 m sample plots were randomly established in each stand (PPs and MPs), ensuring that adjacent plots maintained at a distance greater than 200 m to mitigate edge effects. The diameter at breast height, height, and stand density of every tree within each plot were assessed. Detailed information on the plantations is provided in Table A1.

Soil samples were carried out in early August 2021. Soil samples were gathered from eight different points within each plot, located at 5 m intervals from the center, along angles of 0°, 45°, 90°, 135°, 180°, 225°, 270°, and 315°. Previous studies only examine a single soil layer (usually the upper 0–10 cm) (Waithaisong et al., 2022; Chen et al., 2024). More study on the P transformation and mechanisms underlying soil microbial and biochemical interactions in different soil layers is needed to determine whether the variation of P cycle is dependent on depth. Therefore, soil samples in our study were obtained from the depth intervals of 0−10 cm and 10−20 cm following the removal of extraneous materials such as little stones, and dead leaves. Eight undisturbed samples from each soil layer were amalgamated into a composite sample and transported to the laboratory on ice. Each composite sample was partitioned into two aliquots: one designated for the analysis of physicochemical properties, and the other reserved for genomic DNA extraction.

### *2.3. Soil properties and soil enzyme activity*

**Deleted:** -

**Deleted:** -

**Deleted:** s

**Deleted:** -

**Deleted:** Soil samples were obtained from

Soil pH was measured using a 1:2.5 soil-to-water ratio method, and soil organic carbon (SOC) was quantified using the $K_2Cr_2O_7$-$H_2SO_4$ oxidation method. The total nitrogen (TN) content of soil was determined using an Auto Analyzer III in an extract obtained by digestion of the sample with $H_2SO_4$ and a catalyst ($CuSO_4$:$H_2SO_4$ = 10:1). The levels of nitrate N ($NO_3^-$-N) and ammonia N ($NH_4^+$-N) were determined by $CaCl_2$ extraction, followed by quantitative analysis using an AutoAnalyzer III (Tsiknia et al., 2014). Total P (TP) was quantified using the molybdenum blue colorimetric method following extraction of the samples with $HClO_4$-$H_2SO_4$ (Murphy and Riley, 1962).

N and P metabolised by soil extracellular enzyme activity (EEA), e.g., β-1,4-N-acetylglucosaminidase (NAG) and leucine aminopeptidase (LAP) activity are involved in N acquisition and acid phosphomonoesterase is associated with P mineralization, were quantified in a fluorescence assay conducted in a 96-well microplate (Yan et al., 2022). Soil EEA was calculated from the fluorescence readings of the enzyme after its reaction with the appropriate substrate. The assay was conducted using 200 µL of a soil suspension prepared by weighing 1.25 g of fresh soil to which sodium acetate buffer (pH 4.5) was added, and stirred for 1 min to ensure consistent extraction conditions and effective solubilization of the soil constituents. Eight replicates per sample were tested. The samples were incubated in darkness at 25°C for 3 h, after which the reaction was terminated by adding NaOH. Fluorescence was then immediately measured within the wavelength range of 365–450 nm by using a fluorescence microplate reader. Information on the substrates of the three EEA can be found in Table A2.

**Deleted:**

**Deleted:**

**Deleted:**

**Deleted:**

**Deleted:**

**Formatted:** Not Superscript/ Subscript

**Deleted:** and available P (AP)

**Deleted:** ere

**Formatted:** Not Superscript/ Subscript

**Deleted:** and HCl-$H_2SO_4$, respectively

**Deleted:** i.e

**Deleted:** for

**Deleted:** (ACP)

**Deleted:** activity for

**Deleted:**

**Deleted:** -

**Deleted:** soil extracellular enzymes

### *2.4. Soil DNA extraction and sequencing*

Microbial genomic DNA was obtained from soil samples utilizing the PowerSoil DNA isolation kit (MN NucleoSpin 96 Soi) for subsequent analysis and measurements. The primers employed were 338F and 806R for the amplification of the V3–V4 hypervariable region of the 16S rRNA gene (Mori et al., 2014; Parada et al., 2016), while ITS1F and ITS2R were employed to amplify the ITS1 region of fungal rRNA gene loci (Adams et al., 2013; Dong et al., 2021) (Table A3). Sequencing data were processed by filtering the raw reads using Trimmomatic v0.33, removing the primers using Cutadapt v1.9.1, assembling the clean reads by overlap with Usearch v10, and removing chimeras with UCHIME v4.2 to ensure data validity. After the removal of potential chimeras, 1,600,678 and 1,550,033 high-quality bacterial and fungal reads were obtained, respectively.

The genetic potential of the soil microorganisms was assessed by real-time fluorescence quantitative PCR (qPCR) to quantitatively determine the gene copy numbers of bacteria (16S rRNA) and fungi (ITS). The genetic potential of N cycling processes was evaluated based on the abundance of functional genes involved in nitrogen fixation (*nifH*), nitrification (AOB-*amoA*), and denitrification (*narG*, *nirS*, *nirK*, and *nosZ*). Similarly, the genetic potential of P cycling processes was assessed using the abundance of functional genes involved in organic phosphorus hydrolysis (*phoC*, *phoD*, *BPP*) and Pi hydrolysis (*pqqC*). These functional genes are well-established biomarkers of the biochemical pathways essential for nutrient cycling in various ecosystems. The qPCR amplification efficiencies ranged from 90%

**Deleted:** (5′-ACTCCTACGGAGCGCA-3′)

**Deleted:** (5′-GGACTACHVGGGTWTCTAAT-3′)

**Deleted:** additionally

**Deleted:** ,

**Deleted:** (5′-CTTGGTCATTTAGAGGAAGTAA-3′)

**Deleted:** (5′- GCTGCGTTCTTCATCGATGC-3′)

**Deleted:** utilized

**Deleted:** -

**Formatted:** Font: Italic

**Formatted:** Font: Italic

**Formatted:** Font: Italic

**Formatted:** Font: Italic

**Formatted:** Font: Italic

**Formatted:** Font: Italic

**Formatted:** Font: Italic

**Formatted:** Font: Italic

**Deleted:** To evaluate the ability of genes to support N and P cycle processes, we analyzed the abundances of the functional genes *nifH*, AOB-*amoA*, *narG*, *nirS*, *nirK*, and *nosZ* as representatives of the N cycle. Similarly, we analyzed the genetic potential of *phoC*, *phoD*, *BPP*, and *pqqC* as representatives of the P cycle. These functional genes are

**Formatted:** Font: Italic

**Deleted:** -

to 110%. The primers and references for the functional genes are reported in Table A3.

*2.5. Network construction*

Networks for bacteria and fungi were constructed by dividing the 20 samples into four groups, consisting of two soil layers for PPs and MPs, respectively. First, sample operational taxonomic units (OTUs) were filtered, discarding those that appeared in fewer than three samples within each group (3 out of 5 replicates) (Hu et al., 2023). OTUs with a relative abundance exceeding 1% in the bacterial and fungal communities were selected for further correlation analysis (Fan et al., 2018). The network was built according to thresholds of Pearson correlation coefficient > 0.6 and $P < 0.05$, assessed using the *Hmisc* package in R v4.0.5. We adjusted the *P* values according to the Hochberg false discovery rate test (Benjamini et al., 2006), with a cut-off of adjusted $P < 0.05$. Network properties were computed utilizing the *igraph* R package, and visualized using Gephi (https://gephi.org/). In all figures, bacterial and fungal phyla exhibiting a relative abundance greater than 1% within the network are represented by distinct colors.

**Deleted:** Spearman's

**Deleted:** -

Keystone species were identified by utilizing the connectivity within modules (Zi) and between modules (Pi). Microorganisms were classified into four categories depending on intra-module degree (Z-score) and participation coefficient (C-score) thresholds, into network hubs, module hubs, connectors, and peripherals (Poudel et al., 2016). Network hubs refer to nodes with a high degree of connectivity both globally and within individual modules; module hubs are nodes with significant connectivity

**Deleted:** -

**Deleted:** z

**Deleted:** z

**Deleted:** c

**Deleted:** c

restricted to a single module; connectors are nodes that facilitate strong connections between different modules, and peripheral nodes are those with few connections to other nodes (Poudel et al., 2016). Network hubs, module hubs, and connectors occupy critical positions within the network and are classified as keystone topological features. These characteristics are essential for sustaining the stability of microbial communities (Delmas et al., 2019). Consequently, OTUs associated with these nodes were designated as keystone species.

### *2.6. Data analyses*

Microbial diversity (Shannon index) and richness (Chao1 and ACE), which were both calculated using phyloseq with default setting by Mothur (v 1.30.2) software (Schloss et al., 2009). Soil physicochemical properties, microbial community indices, such as the ACE and Shannon and Chao1 indices, as well as functional genes and enzyme activity, were analyzed in independent samples t-tests using SPSS v24.0. This statistical approach was applied to evaluate differences attributable to stand type (monoculture or mixed). Differences in soil microorganisms across stand types and soil layers were analyzed using non-metric multidimensional scaling (NMDS) with Bray–Curtis dissimilarity and analysis of similarity (ANOSIM), implemented using the *vegan* package in R (Oksanen et al., 2013; Knowles et al., 2019). Random forest analysis based on Pearson correlation analysis and the best multiple regression model was used to evaluate the contributions of soil properties, microbial characteristics, and functional genes involved in the N and P cycles to the variation in nitrogen and phosphorus transformation enzyme activities, and to identify the major predictors

**Formatted:** Level 2

**Deleted:** Alpha

**Deleted:** index analyses including ACE, Chao1 and Shannon indices were

**Deleted:** performed

**Deleted:** -

**Deleted:** Pearson correlation coefficients were used to analyze the relationships among soil characteristics, microbial characteristics, genes associated with N and P cycling, N and P transformation, with the results visualized in a heat map generated in Origin 2024. …

based on their importance. Computation and visualization were carried out in R software (Jiao et al., 2020). Correlation analysis and visualization of soil properties, microbial characteristics, and functional genes related to N and P cycling were performed in Origin 2024. A redundancy analysis (RDA) was employed to explore the multivariate associations between soil physicochemical characteristics and microorganisms. The most important soil physicochemical properties affecting bacterial and fungal phyla were identified in the RDA and visualized using CANOCO v5. A partial least squares path model (PLS-PM) was constructed using R software to assess the direct and indirect effects of mixed planting of *Eucalyptus* and *Acacia* on P transformation. A PLS-PM can reveal causal connections between observed and latent variables, and its superiority for small sample sizes has been demonstrated in simulation studies, in which path modeling estimation was shown to be reliable (Monecke and Leisch, 2012; Sanchez, 2013). The goodness-of-fit statistic was used to assess the adequacy of the PLS-PM fit, with a value > 0.7 indicating good model fit (Tenenhaus et al., 2004; Sanchez, 2013).

## 3. Results

### *3.1. Soil properties*

Significant ($P < 0.05$) higher of SOC, TN, $NO_3^-$-N, C:P, N:P, and pH were determined in both two investigated soil layers in MPs than those in PPs (Table 1); however, TP (10–20 cm) was significantly lower in MPs than in PPs ($P < 0.05$ (Table 1).

**Table 1** Soil physicochemical properties in both 0−10 cm and 10−20 cm soil layers in PPs and

**Deleted:** Henseler and Sarstedt, 2013

**Deleted:** (Henseler and Sarstedt, 2013)

**Deleted:** increases in

**Deleted:** (0-10cm: t=-6.970, $P$<0.001; 10-20cm: t=-5.790, $P$<0.001)…

**Deleted:**

**Deleted:**

**Deleted:**

**Deleted:**

**Deleted:** soil layers of the MPs and PPs

**Deleted:** soil layer

**Deleted:** ,

MPs.

| **Soil physicochemical properties** | **Stand type** | **M±SE** | **t** | ***P*** | **M±SE** | **t** | ***P*** |
|---|---|---|---|---|---|---|---|
| | | **0–10 cm** | | | **10–20 cm** | | |
| SOC | PP | 12.98±0.90b | -5.790 | $P < 0.001$ | 10.31±0.79b | -4.189 | $P < 0.001$ |
| | MP | 21.18±1.10a | | | 14.45±0.59a | | |
| TN | PP | 1.15±0.04b | -6.658 | $P < 0.001$ | 0.83±0.02b | -5.551 | $P < 0.001$ |
| | MP | 2.17±0.15a | | | 1.33±0.09a | | |
| $NH_4^+$-N | PP | 18.92±1.49a | 1.402 | $P < 0.001$ | 13.84±0.83a | 2.262 | $P = 0.001$ |
| | MP | 15.14±2.25a | | | 11.71±0.44a | | |
| $NO_3^-$-N | PP | 4.86±0.06b | -13.372 | $P = 0.198$ | 3.05±0.05b | -33.443 | $P = 0.054$ |
| | MP | 13.90±0.67a | | | 5.39±0.05a | | |
| TP | PP | 0.31±0.02a | 0.520 | $P < 0.001$ | 0.32±0.03a | 3.458 | $P < 0.001$ |
| | MP | 0.30±0.02a | | | 0.22±0.01b | | |
| C:N | PP | 11.38±0.96a | 1.497 | $P = 0.167$ | 12.37±0.89a | 1.182 | $P = 0.009$ |
| | MP | 9.82±0.39a | | | 10.98±0.76a | | |
| C:P | PP | 42.04±3.18b | -4.887 | $P = 0.173$ | 32.73±2.47b | -8.865 | $P = 0.271$ |
| | MP | 72.75±5.35a | | | 64.63±2.62a | | |
| N:P | PP | 3.74±0.25b | -7.173 | $P = 0.001$ | 2.67±0.17b | -6.093 | $P < 0.001$ |
| | MP | 7.37±0.44a | | | 6.00±0.52a | | |
| pH | PP | 4.28±0.04b | -6.970 | $P < 0.001$ | 4.21±0.05b | -5.824 | $P < 0.001$ |
| | MP | 5.09±0.11a | | | 5.04±0.13a | | |

SOC: Soil Organic Carbon; TN: Total Nitrogen; $NH_4^+$-N: Ammonium Nitrogen; $NO_3^-$-N: Nitrate Nitrogen; TP: Total Phosphorus; C:N: Carbon: Nitrogen ratio; C:P: Carbon: Phosphorus ratio; N:P: Nitrogen: Phosphorus ratio; pH: Soil pH Value; Value = Mean ± Standard Error; Different lowercase letters in the table represent significant differences between PPs and MPs ($P < 0.05$), the same below.

### 3.2. Bacterial and fungal community diversity and composition

In both soil layers, the bacterial ACE (0–10 cm: t = -5.164, $P = 0.001$; 10-20 cm: t = -7.305, $P < 0.001$), Chao1 (0–10 cm: t = -5.039, $P = 0.001$; 10-20 cm: t = -6.387, *P*

**Deleted:** ¶

**Deleted:** ¶

**Deleted:** Soil layer¶
(cm)

**Deleted:**

**Deleted:**

**Deleted:**

$< 0.001$), and Shannon (0–10 cm: t = -3.478, $P = 0.008$; 10-20 cm: t = -3.772, $P < 0.005$) indices of α-diversity were significantly higher in MPs than in PPs (Fig. 1a–c). Fungal Shannon (t = -3659, $P = 0.006$) index in the 0–10 cm was also significantly higher in MPs than in PPs (Fig. 1f). The composition of bacterial and fungal community exhibited significant differences between the two plantation types and soil layers, except for the fungal communities in PPs, which did not differ between the surface and deeper soil layers ($P < 0.05$, ANOSIM: $R^2 = 0.85$, $P = 0.01$, stress = 0.03 and $R^2 = 0.73$, $P = 0.01$, stress = 0.05, respectively, Fig. A1).

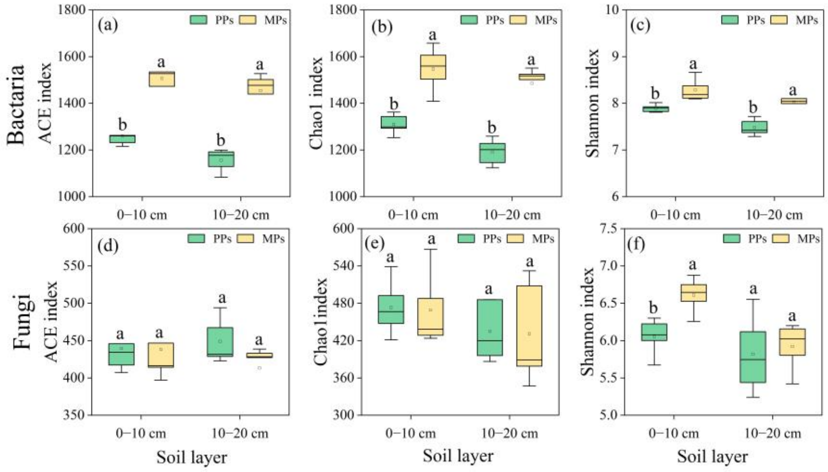


**Fig. 1** Comparisions of (a-c) bacterial and (d-f) fungal community, by α diversity index in two soil layers in PPs and MPs. Different lowercase letters in the table represent significant differences between PPs and MPs ($P < 0.05$), the same below.

After clustering at a 97.0% similarity level, a total of 1,869 OTUs were obtained for bacteria, which revealed 21 phyla, 64 classes, 140 orders, 201 families, and 311 genera. For fungi, a total of 1,128 OTUs were obtained, showing 8 phyla, 24

**Deleted:** $P < 0.05$,

**Deleted:** soil layer

**Deleted:** P < 0.05,

**Deleted:**

**Deleted:**

**Deleted:**

**Deleted:**

**Deleted:**

**Deleted:**

**Deleted:**

**Deleted:**

**Deleted:**

**Deleted:**

**Deleted:**

**Deleted:**

**Formatted:** Centered

classes, 62 orders, 104 families, and 157 genera (Table A4). The most abundant bacterial phyla (relative abundance > 1%) in both PPs and MPs were *Acidobacteria* (26.83%), *Proteobacteria* (22.46%), *Chloroflexi* (13.95%), *Actinobacteria* (13.62%), *Verrucomicrobia* (11.16%), *Planctomycetes* (5.6%), and *Rokubacteria* (3.5%), which represented 94.08% of the total bacterial community in the 0–10 cm layer (Figs. 2a, b and A2a). The most abundant fungal phyla (relative abundance >1%) in both PPs and MPs were *Ascomycota* (63.25%), *Basidiomycota* (28.14%), *Mortierellomycota* (1.77%), *Mucoromycota* (1.18%), and *Rozellomycota* (1.06%), which represented 95.40% of the total fungal community (Figs. 2c, d and A2b). The introduction of N-fixing tree species resulted in changes in the relative abundance and composition of these microbial communities, although these changes were not always statistically significant (Fig. 2).

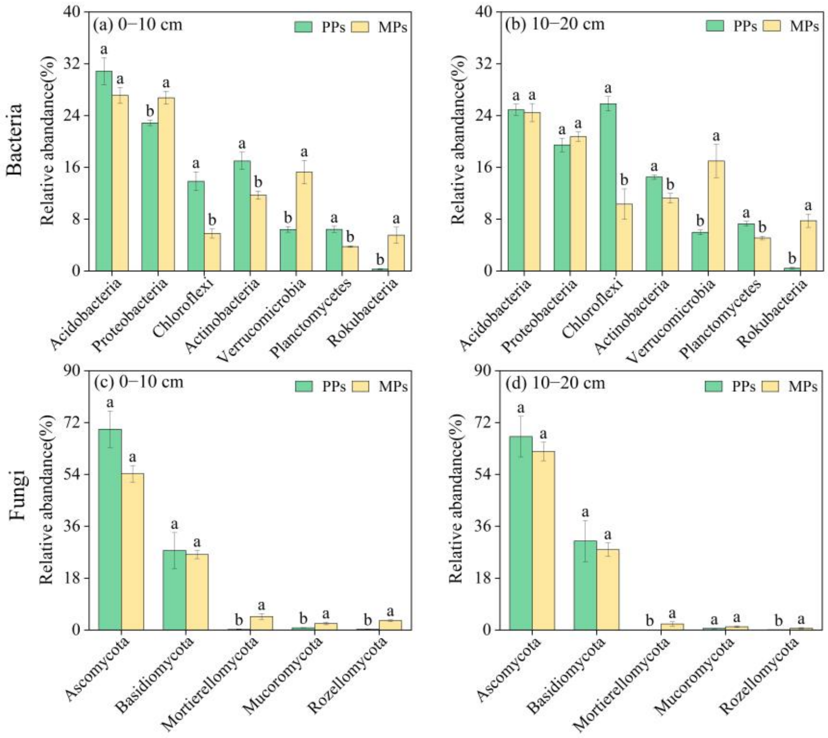


**Fig. 2** Abundance difference of (a-b) bacterial and (c-d) fungal and based on relative abundance > 1% at phylum level.

We used RDA to determine the linkage between soil microbial phyla and the specific soil physicochemical factors. The first two components of RDA axes explained 80.87% and and 47.75% of the total variance in the relationship between soil bacterial and fungal communities and nine selective soil physicochemical factors, respectively (Fig. 3a, b). Forward selection of the nine soil physicochemical factors in the RDA ordinations showed that the bacterial communities were primarily influenced by pH, TN, and SOC (Fig. 3a), and the fungal communities were primarily influenced by pH ($P < 0.05$) (Fig. 3b).

**Deleted:** 66.76

**Deleted:** 14.11

**Deleted:** tion

**Deleted:** variation in

**Deleted:** ,

**Deleted:** For the fungal communities, the first two RDA axes explained 38.05% and 9.7% of the total variation, with …

**Deleted:** as the major regulating factor

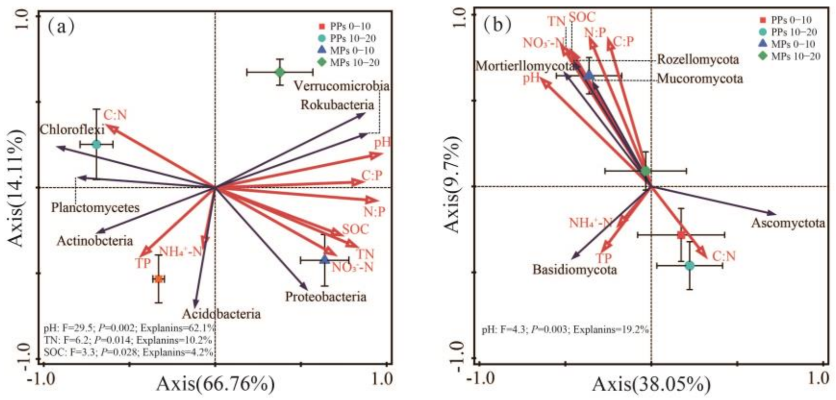


**Fig. 3** RDA plot showing significant factors affecting bacterial (a) and fungal (b) communities.

### *3.3. Microbial network complexity and stability*

Microbial species with an average abundance of at least 1% in the 0–10 and 10–20 cm of PPs and MPs were selected for network analysis. Significant differences in microbial network structure were found between PPs and MPs in both soil layers (Fig. 4a, b). In the bacterial and fungal networks, there were significantly more nodes in MPs than in PPs (Table 2). Therefore, compared to PPs, MPs significantly stimulated the complexity of the co-occurrence network, particularly in the 0–10 cm. Positive correlations (bacterial networks: ranging = 0.665–0.712, fungal networks: ranging = 0.754–0.849) were determined for both PPs and MPs (Table 2). Compared with PPs, the average path lengths in MPs were shorter (except for the fungal network in the 10–20 cm) and the network diameter was smaller (except for the bacterial network in the 10–20 cm) and had a higher average degree for both the bacterial and the fungal networks in both soil layers (Table 2).

**Deleted:** soil layers

**Deleted:** soil layer

**Deleted:**

**Deleted:** soil layer

**Deleted:** soil layer

The Zi–Pi plot showed that network hubs were absent from the bacterial and fungal networks, with keystone species instead concentrated in connectors and module hubs (Fig. 4c, d). Bacterial keystone OTUs were primarily found in the top three phyla, *Proteobacteria*, *Acidobacteriota*, and *Actinobacteriota* (Fig. 4c). Fungal keystone OTUs were likewise concentrated in the top three phyla, *Ascomycota*, *Basidiomycota*, and *Mucoromycota* (Fig. 4d).

**Table 2** Co-occurrence network parameters of bacterial and fungal community at OTU level

| Species type | Soil layer (cm) | Stand type | Number of nodes | Number of edges | positive edges | negative edges | Average path length | Network diameter | Average degree |
|---|---|---|---|---|---|---|---|---|---|
| Bacteria | 0–10 | PPs | 529 | 2498 | 1661 | 837 | 13.58 | 38 | 9.44 |
|  |  | MPs | 667 | 7930 | 5403 | 2527 | 7.79 | 26 | 23.6 |
|  | 10–20 | PPs | 447 | 2509 | 1786 | 723 | 9.41 | 27 | 11.2 |
|  |  | MPs | 581 | 6342 | 4257 | 2085 | 8.51 | 30 | 21.8 |
| Fungi | 0–10 | PPs | 298 | 642 | 484 | 158 | 6.47 | 22 | 4.31 |
|  |  | MPs | 344 | 859 | 722 | 137 | 5.80 | 20 | 4.99 |
|  | 10–20 | PPs | 260 | 511 | 421 | 90 | 3.00 | 12 | 3.93 |
|  |  | MPs | 304 | 779 | 661 | 118 | 5.04 | 15 | 5.13 |

**Formatted:** Font: Italic

**Formatted:** Font: Italic

**Formatted:** Font: Italic

**Formatted:** Font: Italic

**Formatted:** Font: Italic

**Formatted:** Font: Italic

**Formatted:** Font: 10.5 pt

**Formatted:** Font: 10.5 pt

**Deleted:** Bactaria

**Formatted:** Font: 10.5 pt

**Formatted:** Font: 10.5 pt

**Formatted:** Font: 10.5 pt

**Formatted:** Font: 10.5 pt

**Formatted:** Font: 10.5 pt

**Formatted:** Font: 10.5 pt

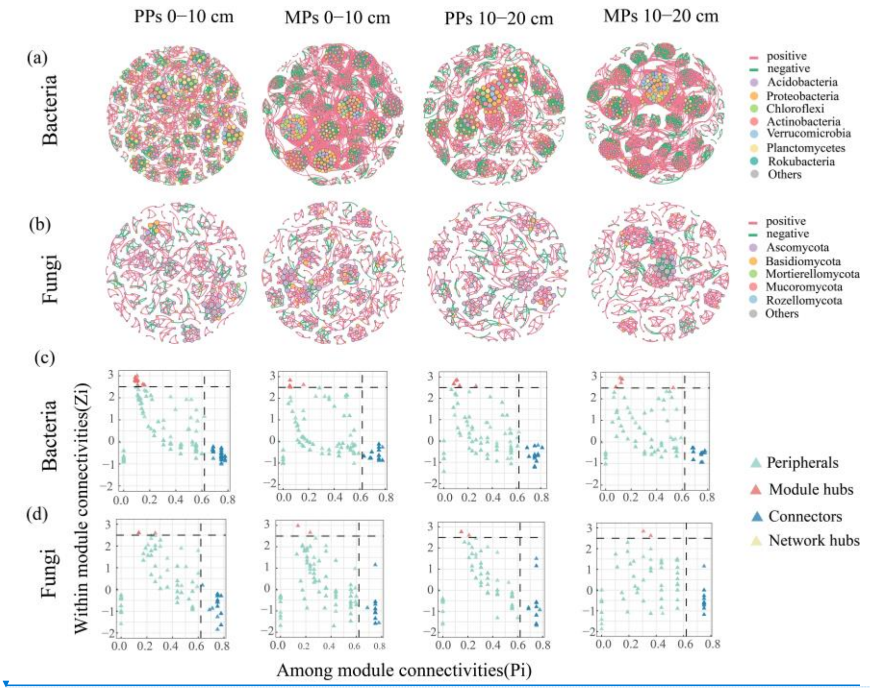
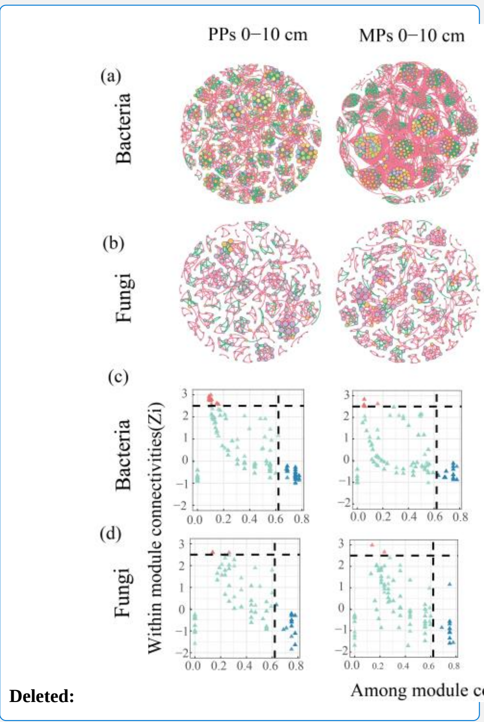


**Fig. 4** Co-occurrence network characteristics of (a) bacterial and (b) fungal communities. The node color represents the phyla with relative abundance greater than 1%, and the node size represents the degree. The Zi-Pi plot (c-d) predicts keystone OTUs in (c) bacterial and (d) fungal networks.

### *3.4. Microbial functional genes involved in N and P transformation and enzyme activity*

Introducing *Acacia mangium* into the *Eucalyptus urophylla* plantation increased the abundances of functional genes involved in N and P transformation (Figs. 5 and 6). Specifically, the abundances of the N-related functional genes *nifH* (t = -4.218, *P* = 0.003), AOB-*amoA* (t = -3.648, *P* = 0.003), *narG* (t = -2.518, *P* = 0.036), *nirS* (t = -3.876, *P* = 0.005), and *nosZ* (t = -2.613, *P* = 0.031) in the 0–10 cm and of



**Deleted:**

**Formatted:** Justified

**Deleted:** The node color node size represent the relative abundance >1% phyla and degree, respectively…

**Deleted:** -

**Deleted:** soil layer

AOB-*amoA* ($t = -2.466$, $P = 0.039$), *narG* ($t = -2.482$, $P = 0.038$), and *nirS* ($t = -4.477$, $P = 0.002$) in the 10–20 cm were significantly higher in MPs than in PPs (Fig. 5a–f).

The abundances of the P functional genes *phoC* (0–10 cm: $t = -4.316$, $P = 0.003$; 10–20 cm: $t = -4.177$, $P = 0.003$), *phoD* (0–10 cm: $t = -2.906$, $P = 0.020$), *BPP* (0–10 cm: $t = -6.373$, $P < 0.001$; 10–20 cm: $t = -2.956$, $P = 0.018$), and *pqqC* (0–10 cm: $t = -3.746$, $P = 0.006$; 10–20 cm: $t = -4.403$, $P = 0.002$) in both soil layers were significantly higher in MPs than in PPs, with the exception of *phoD* in the 10–20 (Fig. 6).

**Deleted:** soil layer

**Deleted:** $P < 0.05$,

**Deleted:** ($P < 0.05$)

**Deleted:** soil layer

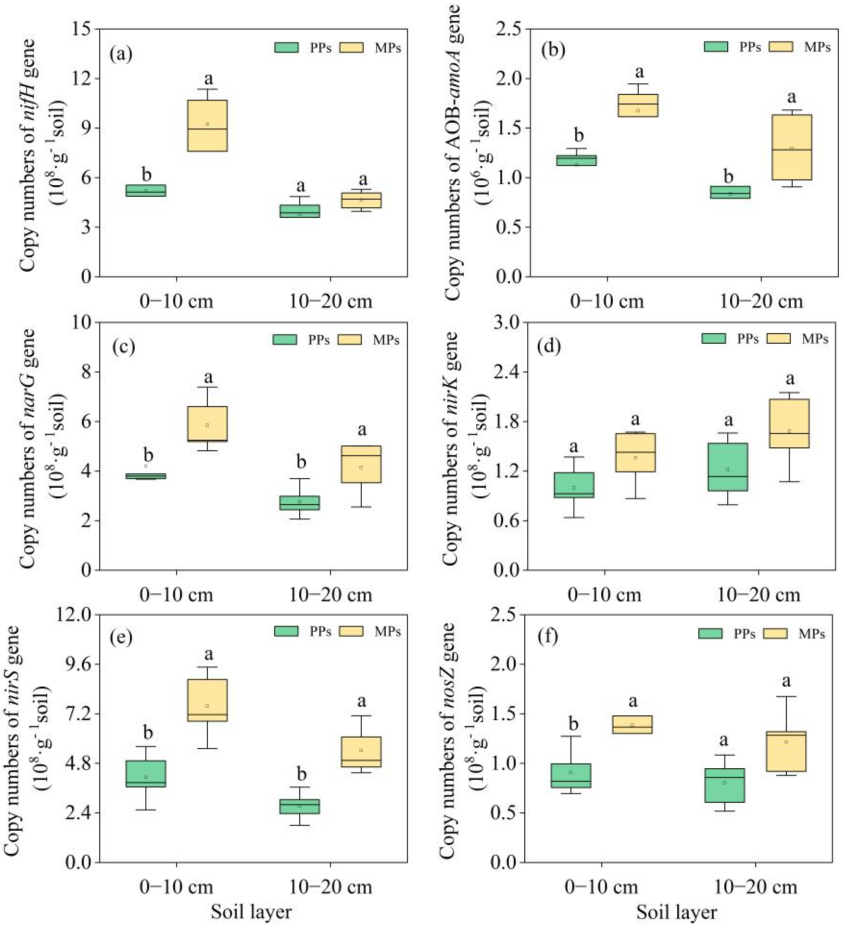


**Fig. 5** Comparison of the abundance of functional genes involved in nitrogen fixation (*nifH*) (a), nitrification (AOB-*amoA*) (b), and denitrification [*narG* (c), *nirK* (d), *nirS* (e), and *nosZ* (f)] in two soil layers in PPs and MPs.

**Deleted:** Comparisions nitrogen cycle functional genes of (a) *nifH*, (b) AOB-*amoA*, (c) *narG*, (d) *narK*, (e) *nirS*, and (f) *nosZ* in two soil layers in PPs and MPs.…

**Formatted:** Font: Italic

**Formatted:** Font: Italic

**Formatted:** Font: Italic

**Formatted:** Font: Italic

**Formatted:** Font: Italic

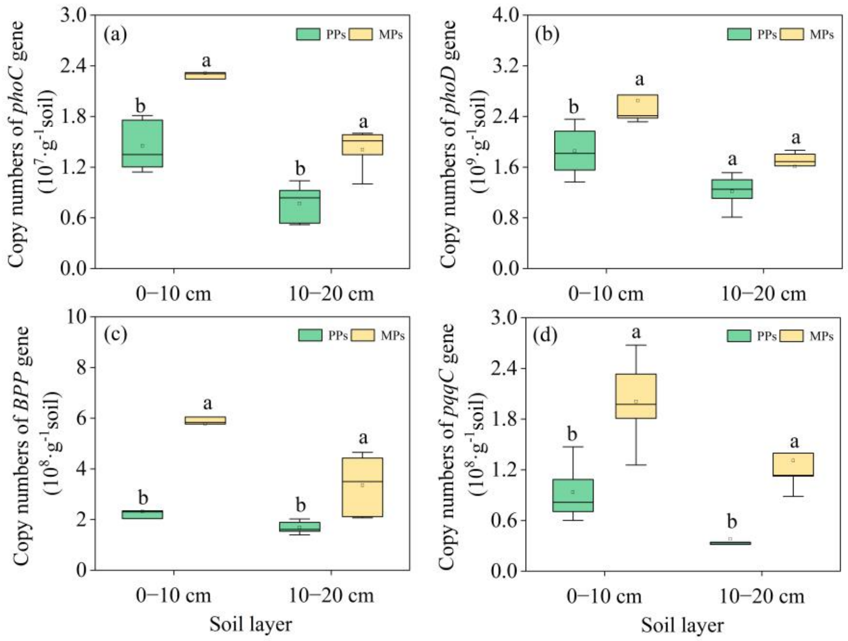


**Fig. 6** Comparison of the abundance of functional genes involved in Po hydrolysis [*phoC* (a), *phoD* (b), *BPP* (c)] and Pi hydrolysis (*pqqC*) (e) in two layers in PPs and MPs.

The EEA analysis results showed that NAG (t = -13.435, *P* < 0.001), LAP (t = -2.528, *P* = 0.035), and ACP (t = -5.291, *P* = 0.001) in the 0–10 cm were significantly higher in MPs than in PPs, by 97.31%, 31.72%, and 64.35% respectively (Fig. 7). In the 10–20 cm, NAG (t = -13.435, *P* < 0.001), LAP (t = -3.239, *P* = 0.012), and ACP (t = -4.102, *P* = 0.003) were also significantly higher in MPs than in PPs, by 24.02%, 88.54%, 39.83%, and 47.72%, respectively (Fig. 7). The qPCR results showed significantly higher levels of 16S rRNA (0–10 cm: t = -7.258, *P* < 0.001; 10–20 cm: t = -4.489, *P* = 0.002) and ITS (0–10 cm: t = -10.262, *P* < 0.001; 10–20 cm: t = -5.391, *P* = 0.001) in MPs than in PPs (Fig. A3).

**Formatted:** Font: Italic

**Formatted:** Justified

**Formatted:** Font: Italic

**Formatted:** Font: Italic

**Formatted:** Font: Italic

**Deleted:** Comparisions phosphorus cycle functional genes of (a) *phoC*, (b) *phoD*, (c) *BPP*, and (d) pqqC…

**Deleted:**

**Deleted:** soil layer

**Deleted:** ($P < 0.05$)

**Deleted:** soil layer

**Deleted:** ($P < 0.05$)

**Deleted:** $P < 0.05$,

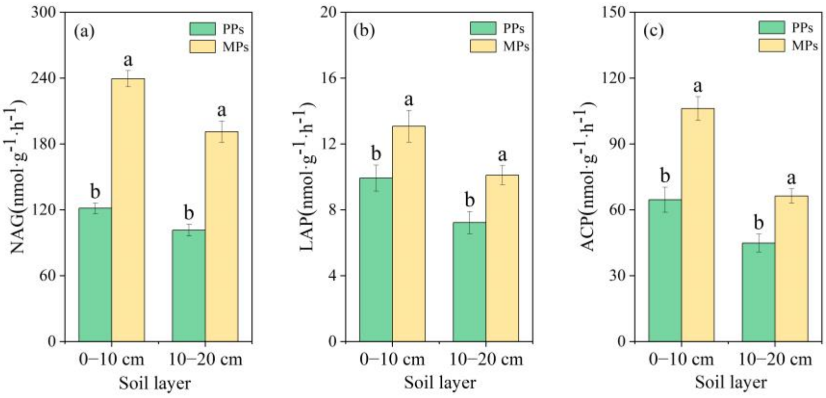


**Fig.7** Comparisions extracellular soil enzyme activity of (a) β-1,4-N-acetylglucosaminidase for chitin degradation （NAG）; (b) Leucine aminopeptidase for protein degradation, (LAP); and (c) Acid phosphatase for catalyzing the hydrolysis of phosphate monoesters, ACP in two soil layers in PPs and MPs.

**Deleted:** NAG,

**Formatted:** Justified

**Deleted:** LAP,

**Deleted:** ACP,

**Deleted:**

### *3.5. Integrating variation in microbial diversity and network complexity with P transformation*

The random forest analysis results showed that NAG, LAP, and ACP activities were explained by soil properties, microbial characteristics, and functional genes involved in the N and P cycles to 84.09%, 58.95%, and 75.51%, respectively (Fig. 8). The results showed significant positive correlations for NAG, LAP, and ACP with SOC, TN, NO$_3^-$-N, C:P, N:P, and pH; for the three enzymes with 16S rRNA, ACE$_{\text{bacteria}}$, Chao1$_{\text{bacteria}}$, Shannon$_{\text{bacteria}}$, nodes$_{\text{bacteria}}$, edges$_{\text{bacteria}}$, and average degree$_{\text{bacteria}}$ ($P < 0.05$); for NAG, LAP, and ACP with ITS, Shannon$_{\text{fungi}}$, edges$_{\text{fungi}}$, and average degree$_{\text{fungi}}$; for LAP and ACP with nodes$_{\text{fungi}}$; for NAG, LAP, and ACP with *nifH*, *AOB-amoA*, *narG*, and *nirS*; for NAG and LAP with *nosZ*; and for NAG, LAP, and ACP with *phoC*, *phoD*, *BPP*, and *pqqC* (all $P < 0.05$). In addition, NAG was

**Deleted:** PearsonSpearman correlation

**Deleted:** analysis

**Deleted:** (Fig. 8)

**Deleted:**

**Deleted:**

significantly negatively correlated with average path length$_{bacteria}$ ($P$ < 0.05). Soil physicochemical properties (SOC, TN, $NO_3^-$-N), bacterial community diversity and network complexity, as well as functional genes involved in the N (*nifH*) and P (*phoC*) cycles are strong positive predictors of the variation in EEA.

**Formatted:** Font: 12 pt

**Formatted:** Font: 12 pt, Subscript

**Formatted:** Font: 12 pt, Superscript

**Formatted:** Font: 12 pt

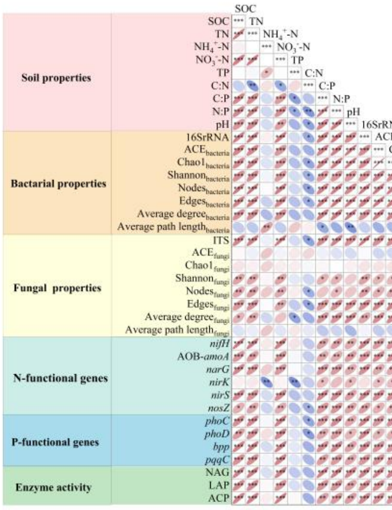
**Formatted:** Font: 12 pt, Italic

**Formatted:** Font: 12 pt

**Formatted:** Font: 12 pt, Italic

**Formatted:** Font: 12 pt

**Deleted:** ¶



**Deleted:**

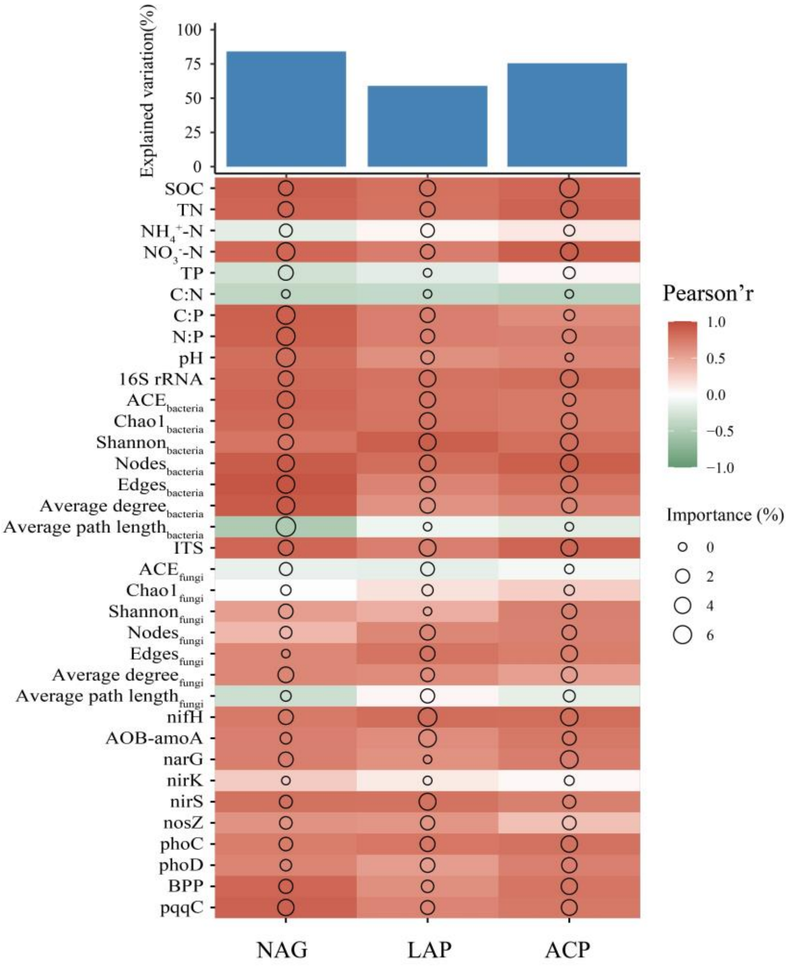


**Fig. 8** The potential biological contributions of soil properties, microbial influences, and functional genes related to N and P cycling to the activity of N and P transformation enzymes. The size of the circles represents the importance of the variables, and the color indicates the Pearson

**Formatted:** Justified

correlation

In the model of P transformation, the variance of 75.7%, 71.5%, 96.1%, 83.9%, 76.2 and 69.5% could be explained by soil properties, fungal properties, bacterial properties, N functional genes, P functional genes, and N transformation, respectively, within a goodness-of-fit index of 0.782 (Fig. 9a). N transformation and P functional genes (*phoC*, *phoD*, and *BPP*) had a strong direct influence on P transformation, with path coefficients of 0.283 and 0.605, respectively ($P < 0.01$). The diversity and complexity of the network also had favorable effects on N and P functional genes, exerting a substantial influence on P transformation. The overall influence of each factor on P transformation in soil followed the order: soil properties > P functional genes > bacterial properties > N functional genes > fungal properties > N transformation (Fig. 9b). Overall, the mixture of *Eucalyptus* with N-fixing tree species directly induces alterations in soil properties, which subsequently influence soil microbial characteristics, functional genes involved in N and P cycling, as well as P transformation, ultimately regulating P transformation.

**Deleted:** Pearson correlations of enzyme activity, soil, bacteria and fungi properties, nitrogen (N) and phosphorus (P) cycle functional genes.¶

**Formatted:** Not Highlight

**Deleted:** According to the PLS-PM analysis results (Fig. 9a),

**Deleted:** and fungal

**Deleted:** and

**Formatted:** Not Highlight

**Deleted:** strongly impacted P transformation,

**Deleted:** together accounting for

**Formatted:** Not Highlight

**Deleted:** of the variance, with a high goodness of fit

**Deleted:** for 78.20.782% of the variance, with a high

**Deleted:** strongly impacted P transformation, together accounting for 78.20.782% of the variance, with a high for 78.20.782% of the variance, with a high goodness of fit.

**Formatted:** Font: Italic

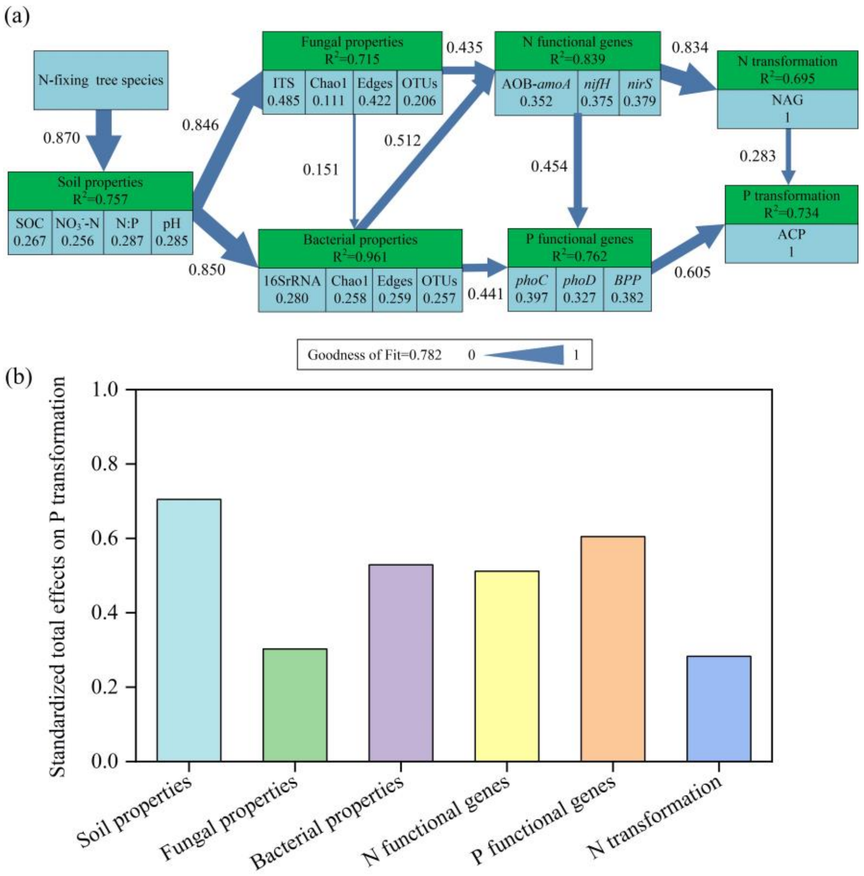


**Fig. 9** (a) Path model describing the control pathways of P transformation (ACP activity) and (b) Standardized total effects (including both direct and indirect effects) on P transformation derived from PLS-PM. The light blue in (a) represents the observation variable, the light green represents the latent variable, the number under the observation variable represents the contribution weight of the observation variable to the latent variable, the number and the width of the arrow on the arrow represent the standardized path coefficient between the latent variables, and R$^2$ represents the explanation rate of the model to the latent variable.

**Deleted:**

**Deleted:** Directed graph of the partial least squares path models (PLS-PM)…

**Deleted:** plus

**Deleted:** the partial least squares path models (

**Deleted:** -

**Deleted:** )

**Deleted:** .

**Deleted:** ,

**Deleted:**

**Deleted:** (b) Standardized total effects (direct plus indirect effects) on P transformation derived from the PLS-PM. the same below. …

## 4. Discussion

### *4.1 Soil microbial diversity and network response in a mixed plantation of Eucalyptus and N-fixing tree species*

The mixed planting of *Eucalyptus* with N-fixing species significantly impacted the soil microbial community structure, increasing microbial diversity and network complexity. With methodological advances that enable more comprehensive understanding of soil microbial diversity and network, we know that soil microorganisms are not only involved in nutrient (e.g., N and P) transformations but also shape the soil habitat by multiple biophysical and biogeochemical processes (Philippot et al., 2024). In our study, the combination of *Eucalyptus* and N-fixing *Acacia mangium* enhanced soil nutrient content and altered the stoichiometric ratios of C, N, and P (Table 1). Mixed plantations with N-fixing tree species have higher litter quantity and quality, which enhances nutrient retention and acquisition capacity (Huang et al., 2014), stimulates microbial growth, and promotes microbial aggregation and metabolism, thereby increasing microbial diversity (Guo et al., 2019) (Figs. 1 and A1). These findings align with those of a previous study, which demonstrated that the incorporation of *Eucalyptus* with N-fixing tree species increased the abundance and diversity of microorganisms, while also revealing variability in community structure across different stands (Li et al., 2023). The composition and diversity of soil microbial communities are primarily driven by C:N:P ratios (Delgado-Baquerizo et al., 2017). The availability of essential nutrients such as N, P, and Fe are controlled by the soil C supply, while the lower C:N ratio in

**Formatted:** Font: Italic

**Deleted:** The complexity and diversity of microbial communities in soil are fundamental to ecosystem persistence and resilience, as they both reinforce ecological functions and offer a robust defense against external disruptions (Guo et al., 2021). In our study, the combination of

**Formatted:** Font: Italic

**Formatted:** Font: Italic

**Deleted:** Our study demonstrated that mixed plantations improved the α- and β-diversity of soil bacteria and fungi…

**Deleted:** In our study, *Eucalyptus* mixed with N-fixing *Acacia mangium* resulted in increased SOC, TN, and $NO_3^-$-N content as well as soil C: P and N : P ratios, while decreasing the soil C : N ratio. Soil properties are key in influencing the composition of microbial communities, which serves as a vital indicator of soil health (Xia et al., 2020). The presence of N-fixing tree speciess leads to an increase in litter production, resulting in higher exogenous nutrient inputs (Huang et al., 2014; Zhang et al., 2022), which enhance bacterial and fungal α-diversity (Guo et al., 2019). …

**Deleted:**

**Deleted:**

**Deleted:** is

mixed plantations promotes the formation of various C components, thereby increasing SOC input, which subsequently influences the structure of the microbial communities and their co-occurrence patterns (Yuste et al., 2011; Qiu et al., 2021). Interestingly, in this study, the TP content in MPs was significantly lower than that in PPs (Table 1), which may be a result of increased plant uptake due to higher biomass. Additionally, the high soil N content in MPs with N-fixing tree species may positively influence plant growth, potentially stimulating P uptake (Li et al., 2016). In subtropical regions, characterized by high temperatures and heavy rainfall, P leaching is substantial; however, the introduction of N-fixing tree species increases N content, which may shift the limitation from N to P in MPs. In this context, plants are likely to recycle P more efficiently (See et al., 2015; Lang et al., 2016). Therefore, P returned to the soil through decomposition would be reduced.

In natural habitats, soil microbial communities form intricate arrays and robustly structured networks that allow adaptation to shifting environments (de Vries et al., 2018). The complexity and diversity of microbial communities in soil are fundamental to ecosystem persistence and resilience, as they both reinforce ecological functions and offer a robust defense against external disruptions (Guo et al., 2021). The complexity of the topological structure and connectivity between nodes influence the overall stability of microbial networks and their resilience to environmental disturbances (Yuan et al., 2021). The overwhelming predominance of positive over negative correlations indicated microbial adaptation to similar ecological niches through co-operation (Gao et al., 2022). Networks characterized by higher connectivity and larger numbers of interrelationships are better equipped to withstand environmental changes, thereby preserving the functional stability of the ecosystem (Cornell et al., 2023). Our study showed that N-fixing tree species mixed plantations increased the complexity of bacterial and fungal networks (Fig. 4), as demonstrated by a higher number of nodes and edges, with positive associations predominating over negative ones, indicating stronger interactions between microorganisms (Ma et al., 2020; Niraula, 2021). Random forest analysis also revealed a robust positive association between the number of nodes and the diversity of fungal and bacterial species expressing enzymes responsible for N and P transformation (Fig. 8). These results align with our hypothesis, suggesting that *Eucalyptus* mixed with N-fixing tree species increases the complexity of microbial networks (Guo and Gong, 2024). The relative abundances of *Proteobacteria*, *Rokubacteria*, and *Verrucomicrobia* in the bacterial community were also higher in MPs than in PPs (particularly in the 0–10 cm), as were the relative abundances of *Mortierllomycota*, *Mucoromycota*, and *Rozellomycota* in the fungal community. Several edaphic factors collectively influenced the structure of both communities, among which pH was the most important (Fig. 3a, b). These findings are in line with earlier research, which demonstrated that soil pH was a key determinant in shaping the structure and composition of microbial communities (Siciliano et al., 2014; Cheng et al., 2020). According to our Zi–Pi plots, the keystone species of the bacterial community were members of phyla *Proteobacteria*, *Acidobacteriota*, and *Actinobacteria*, and those of the fungal community belonged to *Ascomycota*, *Basidiomycota*, and *Mucoromycota*.

**Deleted:** Our study showed more complex bacterial and fungal networks in MPs than in PPs (Fig. 4), demonstrated by the higher number of nodes and edges and the predominance of positive over negative associations, which suggested stronger competition between microorganisms in MPs (Ma et al., 2020; Niraula, 2021).…

**Deleted:** Correlation heat maps

**Deleted:** ¶

**Deleted:** *Verrucomicrobia*

**Deleted:** *Rokubacteria*

**Deleted:** soil layer

**Deleted:** .

**Deleted:** *Verrucomicrobia* is associated with N fixation (Wertz et al., 2012) and serves as an indicator of chemical changes associated with increased soil fertility (Navarrete et al., 2015). …

The ability of leguminous plant species to establish symbiotic associations with root nodule bacteria, commonly referred to as rhizobia, is well established (e.g., Stougaard, 2000; Yang et al., 2022). The phylum *Proteobacteria* is one of the largest and phenotypically most diverse divisions, which includes gram-negative bacteria such as rhizobia. Furthermore, the N-fixing ability of rhizobia in the phylum *Proteobacteria* is a key contributor to maintaining the complexity and stability of microbial networks (Sprent and Platzmann, 2001; Fu et al., 2022). Among fungi, *Ascomycota* is the dominant phylum in soil worldwide (Egidi et al., 2019). In the present study, the relative abundance of Ascomycetes showed dominance in both PPs and MPs, but the relative abundance diminished in MPs. Although keystone taxa may not always abundant, they play a vital role in shaping microbial communities and maintaining their ecological functions, through specific regulatory pathways that affect community structure and function (Banerjee et al., 2018; Liu et al., 2022). For example, a prior study demonstrated that keystone taxa played a critical role in increasing the complexity of microbial networks, enhancing plant health and biomass, and promoting the hydrolysis of organophosphorus compounds through enzymatic activity (Qiao et al., 2024; Zeng et al., 2024).

### *4.2 Association of microbial diversity and networks with P transformation and key environmental drivers*

Our study showed that the abundance of functional genes related to N and P cycles significantly increases after intercropping with N-fixing tree species, which supports our second hypothesis (Fig. 5 and 6). In contrast to this finding, Qin et al.

**Formatted:** Font: Italic

**Deleted:** an extensive

**Deleted:** significant phylum

**Deleted:** -

**Deleted:** Rhizobia are gram-negative bacteria within the extensive and significant phylum *Proteobacteria*.…

**Deleted:** T

**Deleted:** T

**Deleted:** *Actinobacteria*

**Deleted:** *Actinobacteria*

**Formatted:** Font: Not Italic

**Deleted:** *Proteobacteria* and *Actinobacteria* include N-fixing for plants (Sprent and Platzmann, 2001) and both are critical contributors to maintaining the complexity and stability of microbial networks (Fu et al., 2022).…

**Deleted:** However, i

**Formatted:** Not Highlight

**Deleted:** although

**Deleted:** its

**Formatted:** Not Highlight

**Deleted:** P is crucial for maintaining plant health and ecological balance in terrestrial ecosystems (Du et al., 2020). Soil microorganisms possess numerous different genes involved in N and P transformation, which enable them to regulate N and P cycling by synthesizing and secreting extracellular enzymes (Dai et al., 2020). …

**Deleted:** s

(2024) reported that although planting N-fixing tree species with *Eucalyptus* enhanced the complexity and stability of N and P functional gene networks, it reduced the abundances of these genes. This discrepancy can be explained by shifts in soil microbial communities related to N and P cycles, which consequently affect the microbial functions that respond to environmental changes (Graham et al., 2016; Zhang et al., 2021). A previous study also found that the microbial community associated with a mixed plantation of *Eurograndis* and *Amangium* differed from that associated with monocultures of either species, attributable to positive effects of the mixture on soil P and nitrate levels, which enhanced the abundances of N and P functional genes (Rachid et al., 2013).

Biological N fixation is a fundamental ecosystem process that involves the conversion of atmospheric N into a form usable by plants, which, facilitated by a highly diverse group of microorganisms, significantly enhances soil fertility and promoting plant growth (Burns and Hardy, 2012; Soumare et al., 2020). All N-fixing microorganisms carry functional *nifH* genes that encode a component of nitrogenase and act as markers of the abundance and diversity of N-fixing microorganisms across various environmental contexts (Wang et al., 2018). Our results indicate that the relative abundance of P functional genes was significantly higher after the introduction of N-fixing tree species compared to pure *Eucalyptus* plantations (Fig. 6). Both *phoC* and *phoD* are functional genes that encode phosphatase activity needed for P solubilization and mineralization and are thus critically involved in promoting soil P availability (Tian et al., 2021; Cao et al., 2022). The P cycling gene *pqqC*, which

**Deleted:** a

**Formatted:** Font: Italic

**Deleted:** Furthermore, our results suggested high abundances of the P functional genes *phoC*, *BPP*, and *ppqC* in both soil layers and significantly higher abundance of *phoD* in the 0–10 cm soil layer in MPs than in PPs.…

encodes the P-mobilizing enzyme pyrroloquinoline quinone synthase, is a marker of phosphate-mobilizing bacteria (Meyer et al., 2011). The predominant bacteria containing *phoD* and *pqqC* are primarily members of the *Actinobacteria* and *Proteobacteria* (Tan et al., 2013; Hu et al., 2018), whose community structure was shown to remain unchanged with an increase in soil P pools (Ragot et al., 2015). In line with our results, a higher abundance and diversity of *phoD*-, *phoC*-, and *pqqC*-bearing soil microorganisms; higher abundances of these genes in soil were correlated with higher soil SOC and TN contents (Luo et al., 2019; Cao et al., 2022). Our study also identified significantly positive correlations between most N and P functional genes and 16S rRNA as well as the ACE, Chao1, and Shannon indexes in bacterial communities, whereas a significant positive correlation was determined only between the ITS region and the Shannon index in fungal communities (Fig. A4). This variation can be attributed to the significant positive impact that high levels of available nutrients have on the development of bacterial communities in the soil (Ming et al., 2016).

The significant positive correlations detected for the N enzymes NAG and LAP with AOB-*amoA*, *nifH*, and the denitrification genes *nirS*, *nosZ*, and *narG* determined in our study suggest that, after the introduction of N-fixing tree species, the microbial community facilitated soil N transformation by increasing the abundance of N cycling genes. Both random forest analysis and PLS-PM analyses indicated that P transformation reflected the interaction of biological and non-biological factors in ecological processes influenced by the introduction of

**Deleted:** -

**Deleted:** -

**Deleted:** *Proteobacteria*

**Deleted:** *Actinobacteria*

**Deleted:** 8

**Deleted:** *nifH*,

**Deleted:** *narG*

**Deleted:** *nirS*,

**Deleted:** *nosZ*

**Deleted:**

**Deleted:** *Acacia*

**Deleted:** correlation heat maps

**Deleted:** -

**Deleted:** -

N-fixing tree species (Figs. 8 and 9). Complex interactions between bacteria, fungi, and P cycle genes have been shown to promote microbial community stability while facilitating P transformation processes (Liu et al., 2024). *Eucalyptus* mixed with N-fixing tree species also increased soil TN and the $NH_4^+$-N content, which increased ACP activity and thus soil Po mineralization. The higher soil pH in MPs than in PPs was likely driven by exchange interactions involving Fe/Al hydroxide minerals and functional groups (Table 1), which enhanced the conversion of potentially labile Pi into plant available P via competitive adsorption (Hinsinger, 2001; Kang et al., 2021).

Together, these results indicate that forest management practices that *Eucalyptus* mixed with N-fixing tree species will improve soil physicochemical properties, microbial community diversity, and correlations between microbial N and P cycling genes, thereby promoting soil P transformation.

## 5. Conclusions

This study suggests the benefits of incorporating mixed N-fixing tree species with *Eucalyptus*, specifically highlighting their positive effects on P transformation. The presence of *Acacia* was shown to alter soil physicochemical properties, improved soil bacterial and fungal community diversity, network complexity, and the abundance of N and P cycling functional genes, ultimately driving P transformation. Increases in soil nutrient content, particularly SOC, TN, and $NO_3^-$-N, as well as the increase in pH that occurred in MPs influenced soil microbial diversity. PLS-PM analysis revealed that mixed plantations have significantly enhanced correlations between P transformation and microbial functional genes that mediate N and P cycling. Our

**Deleted:** cycle

**Deleted:** Pereira et al., 2021;

**Deleted:** organic P

**Deleted:** inorganic P

**Deleted:** -

**Formatted:** Font: Italic

**Deleted:** -

findings offer fresh insights into the predictive capacity of potential shifts in the belowground microbial communities for soil functionality within mixed plantation ecosystems involving N-fixing tree species and *Eucalyptus*.

**Deleted:**

## Appendix A

**Table A1** 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 A2**. 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 A3** 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 A4** 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 |

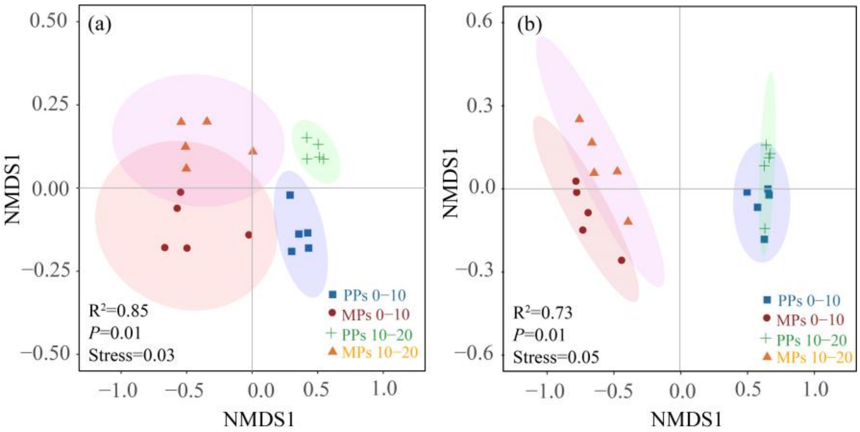


**Fig. A1** Nonmetric multidimensional scaling analysis of (a) bacterial and (b) fungal, based on Bray-Curtis similarity in both 0−10 cm and 10−20 cm soil layers in PPs and MPs.

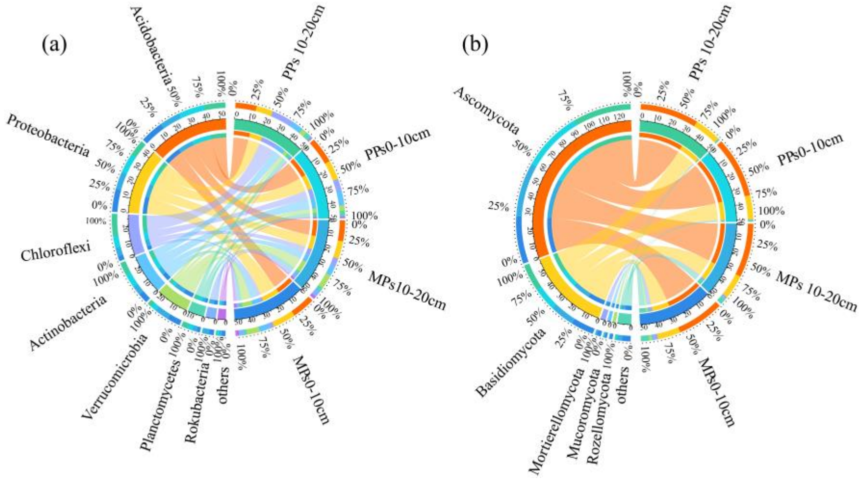


**Fig. A2** Chord diagrams showing the bacterial (a) and fungal (b) community composition (at the relative abundance >1% phylum level). The outer circle scale represents the percentage information of relative abundance of OTU in the sample; The inner circle scale represents the absolute abundance information of OTU in the sample (unit: 1000).

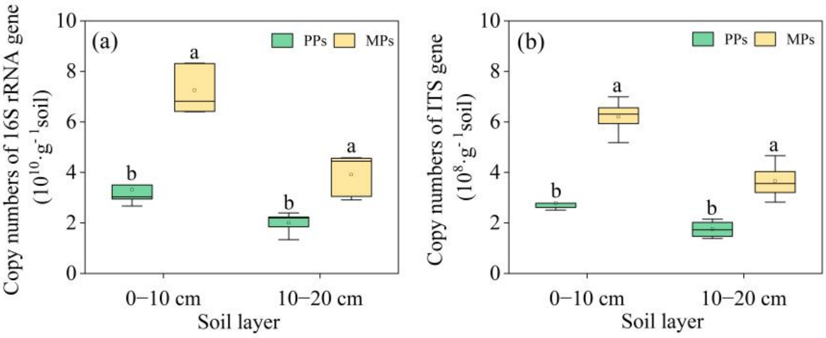


**Fig. A3** Comparisions copy number of (a) 16SrRNA and (b) ITS in both 0−10 cm and 10−20 cm soil layers in PPs and MPs.

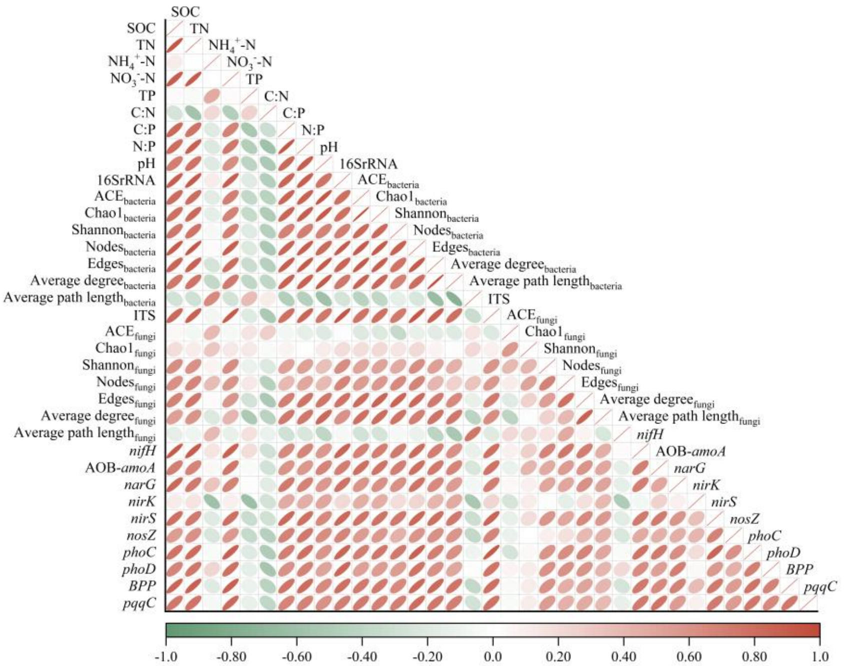


**Fig. A4** Correlative relationships between soil physico-chemical properties, microbial diversity and complexity, and soil physico-chemical properties.

## Data availability

All raw data can be provided by the corresponding authors upon request.

## Author contributions

JL, XH, and YY conceived and designed of the study. JL, XH, YY, and WZ processed and analyzed data acquisition of field experiments. JL, WZ, YL, HH, HM, and QH conducted the fieldwork. JL and WZ performed laboratory analysis. JL completed the analysis of the data and prepared the original draft of the manuscript, XH, YY, YW, and AM helped to review and edit the manuscript. All the authors gave approval for the final manuscript.

## Competing interests

The authors declare that they have no conflict of interest.

## Acknowledgments

This research was funded by grants from the National Natural Science Foundation of China (Nos. 32171755, 32101500, and 31960240), the Guangxi Natural Science Foundation (No. 2025GXNSFAA069288), and the scientific research capacity building project for Youyiguan Forest Ecosystem Observation and Research Station of Guangxi under Grant (No. 2203513003).

## References

Adams, R. I., Miletto, M., Taylor, J. W., Bruns, T. D.: Dispersal in microbes: fungi in indoor air are dominated by outdoor air and show dispersal limitation at short distances, ISME J., 7(7), 1262-1273, https://doi.org/10.1038/ismej.2013.28, 2013.

Banerjee, S., Schlaeppi, K., van der Heijden, M. G.: Keystone taxa as drivers of microbiome structure and functioning, Nat. Rev. Microbiol, 16(9), 567-576, https://doi.org/10.1038/s41579-018-0024-1, 2018.

Benjamini, Y., Krieger, A. M., Yekutieli, D.: Adaptive linear step up procedures that control the false discovery rate, Biometrika 93(3), 491-507, https://doi.org/10.1093/biomet/93.3.491, 2006.

Bünemann, E. K., Smernik, R. J., Marschner, P., McNeill, A. M.: Microbial synthesis of organic and condensed forms of phosphorus in acid and calcareous soils, Soil Biol. Biochem., 40(4), 932-946, https://doi.org/10.1016/j.soilbio.2007.11.012, 2008.

Burns, R. C., Hardy, R. W.: Nitrogen fixation in bacteria and higher plants, 2012.

Cao, N., Zhi, M., Zhao, W., Pang, J., Hu, W., Zhou, Z., Meng, Y.: Straw retention combined with phosphorus fertilizer promotes soil phosphorus availability by enhancing soil P-related enzymes and the abundance of *phoC* and *phoD* genes, Soil Till. Res., 220, 105390, https://doi.org/10.1016/j.still.2022.105390, 2022.

Cheng, J., Zhao, M., Cong, J., Qi, Q., Xiao, Y., Cong, W., Deng, Y., Zhou, J., Zhang, Y.: Soil pH exerts stronger impacts than vegetation type and plant diversity on soil bacterial community composition in subtropical broad-leaved forests, Plant Soil, 450, 273-286, https://doi.org/10.1007/s11104-020-04507-2, 2020.

Chen, S., Lin, L., Deng, Y., Yuan, S., Zhang, N.: Tree species richness and mycorrhizal types drive soil nitrogen cycling by regulating soil microbial community composition and diversity in tropical forests, Forest Ecol. Manag., 569, 122187, https://doi.org/10.1016/j.foreco.2024.122187, 2024.

Cornell, C. R., Zhang, Y., Ning, D., Xiao, N., Wagle, P., Xiao, X., Zhou, J.: Land use conversion increases network complexity and stability of soil microbial communities in a temperate grassland, ISME J., 17(12), 2210-2220, https://doi.org/10.1038/s41396-023-01521-x, 2023.

**Deleted:** ¶

**Deleted:** -

**Field Code Changed**

Dai, Z., Liu, G., Chen, H., Chen, C., Wang, J., Ai, S., Wei, D., Li, D. Ma, B., Tang, C., Brookes, P. C., Xu, J.: Long-term nutrient inputs shift soil microbial functional profiles of phosphorus cycling in diverse agroecosystems, ISME J., 14(3), 757-770, https://doi.org/10.1038/s41396-019-0567-9, 2020.

de Vries, F. T., Griffiths, R. I., Bailey, M., Craig, H., Girlanda, M., Gweon, H. S., Hallin, S., Kaisermann, A., Keith, A. M., Kretzschmar, M., Lemanceau, P., Lumini, E., Mason, K. E., Oliver, A., Ostle, N., Prosser, J. I., Thion, C., Thomson, B., Bardgett, R. D.: Soil bacterial networks are less stable under drought than fungal networks, Nat. Commun., 9(1), 3033, https://doi.org/10.1038/s41467-018-05516-7, 2018.

Delgado-Baquerizo, M., Reich, P. B., Khachane, A. N., Campbell, C. D., Thomas, N., Freitag, T. E., Al-Soud, W. A., Sørensen, S., Bardgett, R. D., Singh, B. K.: It is elemental: soil nutrient stoichiometry drives bacterial diversity, Environ. Microbiol., 19(3), 1176-1188, https://doi.org/10.1111/1462-2920.13642, 2017.

Delmas, E., Besson, M., Brice, M. H., Burkle, L. A., Dalla Riva, G. V., Fortin, M. J., Gravel, D., Guimarães, P. R., Guimarães Jr., P. R., Hembry, D. H., Newman, E. A., Olesen, J. M., Pires, M. M., Yeakel, J. D., Poisot, T.: Analysing ecological networks of species interactions, Biol. Rev., 94(1), 16-36, https://doi.org/10.1111/brv.12433, 2019.

Dong, H., Ge, J., Sun, K., Wang, B., Xue, J., Wakelin, S. A., Wu, J., Sheng, W., Xu, Q., Jiang, P., Chen, J., Qin, H.: Change in root-associated fungal communities affects soil enzymatic activities during *Pinus massoniana* forest development in subtropical China, Forest Ecol. Manag., 482, 118817, https://doi.org/10.1016/j.foreco.2020.118817, 2021.

Du, E., Terrer, C., Pellegrini, A. F., Ahlström, A., van Lissa, C. J., Zhao, X., X, N., Wu, X., Jackson, R. B.: Global patterns of terrestrial nitrogen and phosphorus limitation, Nat. Geosc., 13(3), 221-226, https://doi.org/10.1038/s41561-019-0530-4, 2020.

Egidi, E., Delgado-Baquerizo, M., Plett, J. M., Wang, J., Eldridge, D. J., Bardgett, R. D., Maestre, F. T., Singh, B. K.: A few Ascomycota taxa dominate soil fungal communities worldwide, Nat. Commun., 10(1), 2369, https://doi.org/10.1038/s41467-019-10373-z, 2019.

Epron, D., Nouvellon, Y., Mareschal, L., e Moreira, R. M., Koutika, L. S., Geneste, B., Delgado-Rojas, J, S., Laclau J, P., Sola, G., Gonçalves, J, L, M., Bouillet, J. P.: Partitioning of net primary production in *Eucalyptus* and Acacia stands and in mixed-species plantations:

**Deleted:** Epihov, D. Z., Saltonstall, K., Batterman, S. A., Hedin, L. O., Hall, J. S., van Breugel, M., Leake, J. R., Beerling, D. J.: Legume–microbiome interactions unlock mineral nutrients in regrowing tropical forests, P Natl. Acad. Sci., 118(11), e2022241118, https://doi.org/10.1073/pnas.2022241118, 2021.…

**Formatted:** Font: Italic

two case-studies in contrasting tropical environments, Forest Ecol. Manag., 301, 102-111, https://doi.org/10.1016/j.foreco.2012.10.034, 2013.

Fan, K., Weisenhorn, P., Gilbert, J. A., Chu, H.: Wheat rhizosphere harbors a less complex and more stable microbial co-occurrence pattern than bulk soil, Soil Biol. and Biochem., 125, 251-260, https://doi.org/10.1016/j.soilbio.2018.07.022, 2018.

Fan, Y., Zhong, X., Lin, F., Liu, C., Yang, L., Wang, M., Chen, G., Chen, Y., Yang, Y.: Responses of soil phosphorus fractions after nitrogen addition in a subtropical forest ecosystem: Insights from decreased Fe and Al oxides and increased plant roots, Geoderma, 337, 246-255, https://doi.org/10.1016/j.geoderma.2018.09.028, 2019.

Faust, K.: Open challenges for microbial network construction and analysis, ISME J., 15(11), 3111-3118, https://doi.org/10.1038/s41396-021-01027-4, 2021.

Fraser, T., Lynch, D. H., Entz, M. H., Dunfield, K. E.: Linking alkaline phosphatase activity with bacterial *phoD* gene abundance in soil from a long-term management trial, Geoderma, 257, 115-122, https://doi.org/10.1016/j.geoderma.2014.10.016, 2015.

Fu, L., Yan, Y., Li, X., Liu, Y., Lu, X.: Rhizosphere soil microbial community and its response to different utilization patterns in the semi-arid alpine grassland of northern Tibet, Front. Microbiol, 13, 931795, https://doi.org/10.3389/fmicb.2022.931795, 2022.

Gao, C., Xu, L., Montoya, L., Madera, M., Hollingsworth, J., Chen, L., Purdom, E., Singan, V., Vogel, J., Hutmacher, R. B., Dahlberg, J. A., Coleman-Derr, D., Lemaux, P. G., Taylor, J. W.: Co-occurrence networks reveal more complexity than community composition in resistance and resilience of microbial communities, Nat. Commun., 13(1), 3867, https://doi.org/10.1038/s41467-022-31343-y, 2022.

Graham, E. B., Knelman, J. E., Schindlbacher, A., Siciliano, S., Breulmann, M., Yannarell, A., Beman, J. M., Abell, G., Philippot, L., Prosser, J., Foulquier1, A., Yuste, J. C., Glanville, H. C., Jones, D. L., Angel, R., Salminen, J., Newton, R. J., Bürgmann, H., Ingram, L. J., Hamer, U., Siljanen, H. M. P., Peltoniemi, K., Potthast, K., Bañeras, L., Hartmann, M., Banerjee, S., Yu, R. Q., Nogaro, G., Richter, A., Koranda, M., Castle, S. C., Goberna, M., Song, B., Chatterjee, A., Nunes, O. C., Lopes, A. R., Cao, Y., Kaisermann, A., Hallin, S., Strickland, M. S., Garcia-Pausas, J., Barba, J., Kang, H., Isobe, K., Papaspyrou, S., Pastorelli, R., Lagomarsino, A., Lindström, E. S., Basiliko, N., Nemergut1, D. R.: Microbes as engines of

**Field Code Changed**

ecosystem function: when does community structure enhance predictions of ecosystem processes?, Front. Microbial, 7, 214, https://doi.org/10.3389/fmicb.2016.00214, 2016.

Guo, Q., Gong, L.: Compared with pure forest, mixed forest alters microbial diversity and increases the complexity of interdomain networks in arid areas, Microbiology Spectrum, 12(1), e02642-23, https://doi.org/10.1128/spectrum.02642-23, 2024.

Guo, Y., Hou, L., Zhang, Z., Zhang, J., Cheng, J., Wei, G., Lin, Y.: Soil microbial diversity during 30 years of grassland restoration on the Loess Plateau, China: Tight linkages with plant diversity, Land Degrad. Dev., 30(10), 1172-1182, https://doi.org/10.1002/ldr.3300, 2019.

Guo, Y., Xu, T., Cheng, J., Wei, G., Lin, Y.: Above-and belowground biodiversity drives soil multifunctionality along a long-term grassland restoration chronosequence, Sci. Total Environ., 772, 145010, https://doi.org/10.1016/j.scitotenv.2021.145010, 2021.

He, Y., Wen Y., Li, K., Ye, S., Zhang, H., He, F., Fan, R., Wu, H.: Responses of soil multifunctionality, microbial diversity, and network complexity to tree species mixing in *Eucalyptus* plantations, Ind. Crop. Prod., 225: 120575, https://doi.org/10.1016/j.indcrop.2025.120575, 2025.

Hinsinger, P.: Bioavailability of soil inorganic P in the rhizosphere as affected by root-induced chemical changes: a review, Plant soil, 237(2), 173-195, https://doi.org/10.1023/A:1013351617532, 2001.

Hu, J. P., Zhang, M. X., Lü, Z. L., He, Y. Y., Yang, X. X., Khan, A., Xiong, Y. C., Fang, X. L., Dong, Q. M., Zhang, J. L.: Grazing practices affect phyllosphere and rhizosphere bacterial communities of Kobresia humilis by altering their network stability, Sci. Total Environ., 900, 165814, https://doi.org/10.1016/j.scitotenv.2023.165814, 2023.

Hu, Y., Xia, Y., Sun, Q. I., Liu, K., Chen, X., Ge, T., Zhu, B., Zhu, Z., Zhang, Z., Su, Y.: Effects of long-term fertilization on *phoD*-harboring bacterial community in Karst soils, Sci. Total Environ., 628, 53-63, https://doi.org/10.1016/j.scitotenv.2018.01.314, 2018.

Huang, X., Liu, S., Wang, H., Hu, Z., Li, Z., You, Y.: Changes of soil microbial biomass carbon and community composition through mixing nitrogen-fixing species with *Eucalyptus urophylla* in subtropical China, Soil Biol. Biochem., 73, 42-48, https://doi.org/10.1016/j.soilbio.2014.01.021, 2014.

Huang, X., Liu, S., You, Y., Wen, Y., Wang, H., Wang, J.: Microbial community and associated

**Formatted:** Not Highlight

**Formatted:** Not Highlight

**Formatted:** Font: Italic

**Deleted:** Henseler, J., Sarstedt, M.: Goodness-of-fit indices for partial least squares path modeling. Computation, Stat, 28, 565-580, https://doi.org/10.1007/s00180-012-0317-1, 2013.¶

enzymes activity influence soil carbon chemical composition in *Eucalyptus urophylla* plantation with mixing $N_2$-fixing species in subtropical China, Plant Soil, 414, 199-212, https://doi.org/10.1007/s11104-016-3117-5, 2017.

Jiao, S., Yang, Y., Xu, Y., Zhang, J., Lu, Y.: Balance between community assembly processes mediates species coexistence in agricultural soil microbiomes across eastern China, ISME J., 14(1), 202-216. https://doi.org/10.1038/s41396-019-0522-9, 2020.

Jin, X., Liu, Y., Hu, W., Wang, G., Kong, Z., Wu, L., Ge, G.: Soil bacterial and fungal communities and the associated nutrient cycling responses to forest conversion after selective logging in a subtropical forest of China, Forest Ecol. Manag., 444, 308-317, https://doi.org/10.1016/j.foreco.2019.04.032, 2019.

Kang, L., Zhang, G., Chu, G.: Split delivering phosphorus via fertigation to a calcareous soil increased P availability and maize yield (Zea mays L.) by reducing P fixation, J. Soil. Sediment., 21, 2287-2300, https://doi.org/10.1007/s11368-021-02914-1, 2021.

Khan, A., Zhang, G., Li, T., He, B.: Fertilization and cultivation management promotes soil phosphorus availability by enhancing soil P-cycling enzymes and the phosphatase encoding genes in bulk and rhizosphere soil of a maize crop in sloping cropland, Ecotox. Environ., Safe, 264, 115441, https://doi.org/10.1016/j.ecoenv.2023.115441, 2023.

Knowles, S. C. L., Eccles, R. M., Baltrūnaitė, L.: Species identity dominates over environment in shaping the microbiota of small mammals, Ecol. Lett., 22(5), 826-837, https://doi.org/10.1111/ele.13240, 2019.

Koutika, L. S., Mareschal, L.: Acacia and eucalypt change P, N and C concentrations in POM of Arenosols in the Congolese coastal plains, Geoderma Reg., 11, 37-43, https://doi.org/10.1016/j.geodrs.2017.07.009, 2017.

Koutika, L. S., Richardson, D. M.: *Acacia mangium* Willd: benefits and threats associated with its increasing use around the world, For. Ecosyst., 6, 1-13, https://doi.org/10.1186/s40663-019-0159-1, 2019.

Lang, F., Bauhus, J., Frossard, E., George, E., Kaiser, K., Kaupenjohann, M., Krüger, J., Matzner, E., Polle, A., Pietzel, J., Rennenberg, H., Wellbrock, N.: Phosphorus in forest ecosystems: new insights from an ecosystem nutrition perspective, J. Plant Nutr. Soil Sc., 179(2): 129-135, https://doi.org/10.1002/jpln.201500541, 2016.

**Deleted:** and

**Field Code Changed**

**Formatted:** Font: Italic

**Field Code Changed**

**Formatted:** Not Highlight

**Formatted:** Not Highlight

**Deleted:** ¶

**Field Code Changed**

Li, C., Xu, Y., Wang, Z., Zhu, W., Du, A.: Mixing planting with native tree species reshapes soil fungal community diversity and structure in multi-generational eucalypt plantations in southern China, Front. Microbiol, Fro., 14, 1132875, https://doi.org/10.3389/fmicb.2023.1132875, 2023.

Li, M., You, Y., Tan, X., Wen, Y., Yu, S., Xiao, N., Shen, W., Huang, X.: Mixture of $N_2$-fixing tree species promotes Po accumulation and transformation in topsoil aggregates in a degraded karst region of subtropical China, Geoderma, 413: 115752, https://doi.org/10.1016/j.geoderma.2022.115752, 2022.

Li, N., Zhang, Y., Qu, Z., Liu, B., Huang, L., Ming, A., Sun, H.: Mixed and continuous cropping eucalyptus plantation facilitated soil carbon cycling and fungal community diversity after a 14-year field trail, Ind. Crop. Prod., 210: 118157, https://doi.org/10.1016/j.indcrop.2024.118157, 2024.

Li, Q., Lv, J., Peng, C., Xiang, W., Xiao, W., Song, X.: Nitrogen-addition accelerates phosphorus cycling and changes phosphorus use strategy in a subtropical Moso bamboo forest, Environ. Res. Lett., 16(2), 024023, https://doi.org/10.1088/1748-9326/abd5e1, 2021.

Li, Y., Niu, S., Yu, G.: Aggravated phosphorus limitation on biomass production under increasing nitrogen loading: A meta - analysis, Global Change Biol., 22(2): 934-943, https://doi.org/10.1111/gcb.13125, 2016.

Liu, S., Li, H., Xie, X., Chen, Y., Lang, M., Chen, X.: Long-term moderate fertilization increases the complexity of soil microbial community and promotes regulation of phosphorus cycling genes to improve the availability of phosphorus in acid soil, Appl. Soil Ecol., 194, 105178, https://doi.org/10.1016/j.apsoil.2023.105178, 2024.

Liu, S., Yu, H., Yu, Y., Huang, J., Zhou, Z., Zeng, J., Chen, P., Xiao, F., He, Z., Yan, Q.: Ecological stability of microbial communities in Lake Donghu regulated by keystone taxa, Ecol. Indic., 136, 108695, https://doi.org/10.1016/j.ecolind.2022.108695, 2022.

Lu, X., Wen, L., Sun, H., Fei, T., Liu, H., Ha, S., Tang, S., Wang, L.: Responses of soil respiration to phosphorus addition in global grasslands: A meta-analysis, J. Clean. Prod., 349, 131413, https://doi.org/10.1016/j.jclepro.2022.131413, 2022.

Luo, G., Sun, B., Li, L., Li, M., Liu, M., Zhu, Y., Guo, S., Ling, N., Shen, Q.: Understanding how long-term organic amendments increase soil phosphatase activities: insight into *phoD*-and

**Deleted:** .

**Deleted:** ,

**Deleted:** b

**Formatted:** Not Highlight

**Formatted:** Not Highlight

**Formatted:** Not Highlight

**Formatted:** Not Highlight

**Field Code Changed**

*phoC*-harboring functional microbial populations, Soil Biol. Biochem., 139, 107632, https://doi.org/10.1016/j.soilbio.2019.107632, 2019.

Ma, B., Wang, Y., Ye, S., Liu, S., Stirling, E., Gilbert, J. A., Faust, K., Knight, R., Jansson, J. K., Cardona, C., Röttjers, L., Xu, J.: Earth microbial co-occurrence network reveals interconnection pattern across microbiomes, Microbiome, 8(1), 1-12, https://doi.org/10.1186/s40168-020-00857-2, 2020.

Meyer, J. B., Frapolli, M., Keel, C., Maurhofer, M.: Pyrroloquinoline quinone biosynthesis gene *pqqC*, a novel molecular marker for studying the phylogeny and diversity of phosphate-solubilizing pseudomonads, Appl. Environ. Microb., 77(20), 7345-7354, https://doi.org/10.1128/AEM.05434-11, 2011.

Ming, L. I., Ming, L. I. U., Li, Z. P., Jiang, C. Y., Meng, W. U.: Soil N transformation and microbial community structure as affected by adding biochar to a paddy soil of subtropical China, J. Integr. Agr., 15(1), 209-219, https://doi.org/10.1016/S2095-3119(15)61136-4, 2016.

Monecke, A., Leisch, F.: semPLS: structural equation modeling using partial least squares, J Stat. Softw., 48, 1-32, https://doi.org/10.18637/jss.v048.i03, 2012.

Mori, H., Maruyama, F., Kato, H., Toyoda, A., Dozono, A., Ohtsubo, Y., Nagata, Y., Fujiyama, A., Tsuda, M., Kurokawa, K.: Design and experimental application of a novel non-degenerate universal primer set that amplifies prokaryotic 16S rRNA genes with a low possibility to amplify eukaryotic rRNA genes, DNA Res., 21(2), 217-227, https://doi.org/10.1093/dnares/dst052, 2014.

Murphy, J. A. M. E. S., Riley, J. P.: A modified single solution method for the determination of phosphate in natural waters, Anal. Chim. Acta, 27, 31-36, https://doi.org/10.1016/S0003-2670(00)88444-5, 1962.

Nannipieri, P., Giagnoni, L., Renella, G., Puglisi, E., Ceccanti, B., Masciandaro, G., Fornasier, F., Moscatelli, M. C., Marinari, S. A. R. A.: Soil enzymology: classical and molecular approaches, Biol. Fert. Soil., 48, 743-762, https://doi.org/10.1007/s00374-012-0723-0, 2012.

Niraula, S.: Effects of a $N_2$-Fixing Biofertilizer on the Rhizosphere Microbiome and the Influence of Biochar on Soil Fertility and Microbial Communities, The University of Texas at Arlington, 2021.

Oksanen, J., Blanchet, F. G., Kindt, R., Legendre, P., Minchin, P. R., O'hara, R. B., Solymos, P.,

**Deleted:** Marron, N., Epron, D.: Are mixed-tree plantations including a nitrogen-fixing species more productive than monocultures?, Forest Ecol. Manag., 441, 242-252, https://doi.org/10.1016/j.foreco.2019.03.052, 2019.¶
Menge, D. N., Field, C. B.: Simulated global changes alter phosphorus demand in annual grassland, Global Change Biol., 13(12), 2582-2591, https://doi.org/10.1111/j.1365-2486.2007.01456.x, 2007.¶

**Deleted:** Journal

**Deleted:** of

**Deleted:** ative

**Deleted:** Agriculture

**Field Code Changed**

**Deleted:** Navarrete, A. A., Soares, T., Rossetto, R., van Veen, J. A., Tsai, S. M., Kuramae, E. E.: Verrucomicrobial community structure and abundance as indicators for changes in chemical factors linked to soil fertility, Anton. Leeuw. Int. J. G., 108, 741-752, https://doi.org/10.1007/s10482-015-0530-3, 2015.¶

Stevens, M. H. H., Szoecs, E., Wagner, H., Barbour, M., Bedward, M., Bolker , B., Borcard, D., Carvalho, G., Chirico, M., Caceres, M. D., Durand, S., Evangelista, H. B. A., FitzJohn, R., Friendly, M., Furneaux, B., Hannigan, G., Hill, M. O., Lahti, L., McGlinn, D., Ouellette, M. H., Cunha, E. R., Smith, T., Stier, A., Braak, C. J. K. T., Weedon, J.: Package 'vegan'. Community ecology package, version, 2(9), 1-295, 2013.

Parada, A. E., Needham, D. M., Fuhrman, J. A.: Every base matters: assessing small subunit rRNA primers for marine microbiomes with mock communities, time series and global field samples, Environ. Microbiol., 18(5), 1403-1414, https://doi.org/10.1111/1462-2920.13023, 2016.

Pastore, G., Kaiser, K., Kernchen, S., Spohn, M.: Microbial release of apatite-and goethite-bound phosphate in acidic forest soils, Geoderma, 370, 114360, https://doi.org/10.1016/j.geoderma.2020.114360, 2020.

Paula, R. R., Bouillet, J. P., Trivelin, P. C. O., Zeller, B., de Moraes Gonçalves, J. L., Nouvellon, Y., Bouvet, J, M., Plassard, C., Laclau, J. P.: Evidence of short-term belowground transfer of nitrogen from *Acacia mangium* to *Eucalyptus* grandis trees in a tropical planted forest, Soil Biol. Biochem., 91, 99-108, https://doi.org/10.1016/j.soilbio.2015.08.017, 2015.

Peng, Y., Duan, Y., Huo, W., Xu, M., Yang, X., Wang, X., Wang, B., Blackwell, M. S. A., Feng, G.: Soil microbial biomass phosphorus can serve as an index to reflect soil phosphorus fertility, Biol. Fert. Soils, 57, 657-669, https://doi.org/10.1007/s00374-021-01559-z, 2021.

Pereira, A. P. D. A., Andrade, P. A. M. D., Bini, D., Durrer, A., Robin, A., Bouillet, J. P., Andreote, F, D., Cardoso, E. J. B. N.: Shifts in the bacterial community composition along deep soil profiles in monospecific and mixed stands of *Eucalyptus* grandis and *Acacia mangium*, PloS one, 12(7), e0180371, https://doi.org/10.1371/journal.pone.0180371, 2017.

Pereira, A. P. A., Durrer, A., Gumiere, T., Gonçalves, J. L. M., Robin, A., Bouillet, J. P., Wang, J., Verma, J. P., Singh, B. K., Cardoso, E. J. B. N.: Mixed *Eucalyptus* plantations induce changes in microbial communities and increase biological functions in the soil and litter layers, Forest Ecol. Manag., 433: 332-342, https://doi.org/10.1016/j.foreco.2018.11.018, 2019.

Philippot, L., Chenu, C., Kappler, A., Rillig, M. C., Fierer, N.: The interplay between microbial communities and soil properties, Nat. Rev. Microbiol., 22(4), 226-239, https://doi.org/10.1038/s41579-023-00980-5, 2024.

**Formatted:** Font: Italic

**Formatted:** Font: Italic

**Field Code Changed**

**Formatted:** Font: Italic

**Formatted:** Font: Italic

**Field Code Changed**

**Formatted:** Not Highlight

**Formatted:** Not Highlight

**Formatted:** Not Highlight

**Formatted:** Not Highlight

**Formatted:** Font: Italic

**Deleted:** Pereira, A. P. D. A., Santana, M. C., Zagatto, M. R., Brandani, C. B., Wang, J. T., Verma, J. P., Singh, B. K., Cardoso, E. J.: Nitrogen-fixing trees in mixed forest systems regulate the ecology of fungal community and phosphorus cycling, Sci. Total Environ., 758, 143711, https://doi.org/10.1016/j.scitotenv.2020.143711, 2021.¶
Perring, M. P., Hedin, L. O., Levin, S. A., McGroddy, M., De Mazancourt, C.: Increased plant growth from nitrogen addition should conserve phosphorus in terrestrial ecosystems, P. Natl. A. Sci. India., 105(6), 1971-1976, https://doi.org/10.1073/pnas.0711618105, 2008.…

**Field Code Changed**

Poudel, R., Jumpponen, A., Schlatter, D. C., Paulitz, T. C., Gardener, B. M., Kinkel, L. L., Garrett, K. A.: Microbiome networks: a systems framework for identifying candidate microbial assemblages for disease management, Phytopathology, 106(10), 1083-1096, https://doi.org/10.1094/PHYTO-02-16-0058-FI, 2016.

Qiao, Y., Wang, T., Huang, Q., Guo, H., Zhang, H., Xu, Q., Shen, Q., Ling, N.: Core species impact plant health by enhancing soil microbial cooperation and network complexity during community coalescence, Soil Biol. and Biochem., 188, 109231, https://doi.org/10.1016/j.soilbio.2023.109231, 2024.

Qin, F., Yang, F., Ming, A., Jia, H., Zhou, B., Xiong, J., Lu, J.: Mixture enhances microbial network complexity of soil carbon, nitrogen and phosphorus cycling in *Eucalyptus* plantations, Forest Ecol. Manag., 553, 121632, https://doi.org/10.1016/j.foreco.2023.121632, 2024.

Qiu, L., Zhang, Q., Zhu, H., Reich, P. B., Banerjee, S., van der Heijden, M. G., Sadowsky, M. J., Ishii, S., Jia, X., Shao, M., Liu, B., Jiao, H., Li, H., Wei, X.: Erosion reduces soil microbial diversity, network complexity and multifunctionality, ISME J., 15(8), 2474-2489, https://doi.org/10.1038/s41396-021-00913-1, 2021.

Rachid, C. T., Balieiro, F. D. C., Peixoto, R. S., Pinheiro, Y. A. S., Piccolo, M. D. C., Chaer, G. M., Rosado, A. S.: Mixed plantations can promote microbial integration and soil nitrate increases with changes in the N cycling genes, Soil Biol. Biochem., 66, 146-153, https://doi.org/10.1016/j.soilbio.2013.07.005, 2013.

Ragot, S. A., Kertesz, M. A., Bünemann, E. K.: phoD alkaline phosphatase gene diversity in soil, Appl. Environ. Microb., 81(20), 7281-7289, https://doi.org/10.1128/AEM.01823-15, 2015.

Sanchez, G.: PLS path modeling with R. Berkeley: Trowchez Editions, 383(2013), 551, 2013.

Schloss, P. D., Westcott, S. L., Ryabin, T., Hall, J. R., Hartmann, M., Hollister, E. B., Lesniewski, R. A., Oakley, B. B., Parks,D. H., Robinson, C. J., Sahl, J. W., Stres, B., Thallinger, G. G., Horn, D. J. V., Weber, C. F.: Introducing mothur: open-source, platform-independent, community-supported software for describing and comparing microbial communities, Appl. Environ. Microb., 75(23), 7537-7541, https://doi.org/10.1128/AEM.01541-09, 2009.

See, C. R., Yanai, R. D., Fisk, M. C., Vadeboncoeur, M. A., Quintero B A, Fahey T J.: Soil nitrogen affects phosphorus recycling: foliar resorption and plant–soil feedbacks in a

**Deleted:** ¶
Räsänen, L. A., Sprent, J. I., Lindström, K.: Symbiotic properties of sinorhizobia isolated from Acacia and Prosopis nodules in Sudan and Senegal, Plant and Soil, 235, 193-210, https://doi.org/10.1023/A:1011901706936, 2001.¶
Richardson, A. E., Simpson, R. J.: Soil microorganisms mediating phosphorus availability update on microbial phosphorus, Plant physiol., 156(3), 989-996, https://doi.org/10.1104/pp.111.175448, 2011.¶
Rodríguez, H., Fraga, R.: Phosphate solubilizing bacteria and their role in plant growth promotion, Biotechnol. Adv., 17(4-5), 319-339, https://doi.org/10.1016/S0734-9750(99)00014-2, 1999.¶
Sanchez, G.: PLS path modeling with R. Trowchez Editions, 2013.¶

**Formatted:** Not Highlight

**Formatted:** Not Highlight

**Formatted:** Not Highlight

**Formatted:** Not Highlight

northern hardwood forest, Ecology, 96(9): 2488-2498, https://doi.org/10.1890/15-0188.1, 2015.

Shi, Y., Delgado Baquerizo, M., Li, Y., Yang, Y., Zhu, Y. G., Peñuelas, J., Chu, H.: Abundance of kinless hubs within soil microbial networks are associated with high functional potential in agricultural ecosystems, Environ. Int., 142, 105869. https://doi.org/10.1016/j.envint.2020.105869, 2020.

Siciliano, S. D., Palmer, A. S., Winsley, T., Lamb, E., Bissett, A., Brown, M. V., van Dorst, J., Ji, M., Ferrari, B. C., Grogan, P., Chu, H., Snape, I.: Soil fertility is associated with fungal and bacterial richness, whereas pH is associated with community composition in polar soil microbial communities, Soil Biol. Biochem., 78, 10-20, https://doi.org/10.1016/j.soilbio.2014.07.005, 2014.

Soltangheisi, A., Withers, P. J., Pavinato, P. S., Cherubin, M. R., Rossetto, R., Do Carmo, J. B., da Rocha, G., C., Martinelli, L. A.: Improving phosphorus sustainability of sugarcane production in Brazil, Gcb Bioenergy, 11(12), 1444-1455, https://doi.org/10.1111/gcbb.12650, 2019.

Soumare, A., Diedhiou, A. G., Thuita, M., Hafidi, M., Ouhdouch, Y., Gopalakrishnan, S., Kouisni, L.: Exploiting biological nitrogen fixation: a route towards a sustainable agriculture, Plants, 9(8), 1011, https://doi.org/10.3390/plants9081011, 2020.

Sprent, J. I., Platzmann, J.: Nodulation in legumes (p. 146p), Kew: Royal Botanic Gardens, 2001.

Stougaard, J.: Regulators and regulation of legume root nodule development, Plant Physiol., 124(2), 531-540, https://doi.org/10.1104/pp.124.2.531, 2000.

Sun, H., Wu, Y., Zhou, J., Yu, D., Chen, Y.: Microorganisms drive stabilization and accumulation of organic phosphorus: An incubation experiment, Soil Biol. Biochem., 172, 108750, https://doi.org/10.1016/j.soilbio.2022.108750, 2022.

Tan, H., Barret, M., Mooij, M. J., Rice, O., Morrissey, J. P., Dobson, A., Griffiths, B., O'Gara, F.: Long-term phosphorus fertilisation increased the diversity of the total bacterial community and the *phoD* phosphorus mineraliser group in pasture soils, Biol. Fert. Soils, 49, 661-672, https://doi.org/10.1007/s00374-012-0755-5, 2013.

Tchichelle, S. V., Epron, D., Mialoundama, F., Koutika, L. S., Harmand, J. M., Bouillet, J. P., Mareschal, L.: Differences in nitrogen cycling and soil mineralisation between a eucalypt

**Field Code Changed**

**Field Code Changed**

**Field Code Changed**

**Deleted:** ¶

**Deleted:** ¶

**Formatted:** Not Highlight

**Deleted:** ,

plantation and a mixed eucalypt and *Acacia mangium* plantation on a sandy tropical soil, South. Forests, 79(1), 1-8, https://doi.org/10.2989/20702620.2016.1221702, 2017.

Tenenhaus, M., Amato, S., Esposito Vinzi, V.: A global goodness-of-fit index for PLS structural equation modelling, In Proceedings of the XLII SIS scientific meeting (Vol. 1, No. 2, pp. 739-742), 2004, June.

Tian, J., Ge, F., Zhang, D., Deng, S., Liu, X.: Roles of phosphate solubilizing microorganisms from managing soil phosphorus deficiency to mediating biogeochemical P cycle, Biology, 10(2), 158, https://doi.org/10.3390/biology10020158, 2021.

Tsiknia, M., Tzanakakis, V. A., Oikonomidis, D., Paranychianakis, N. V., Nikolaidis, N. P.: Effects of olive mill wastewater on soil carbon and nitrogen cycling, Appl. Microbiol. Biot., 98, 2739-2749, https://doi.org/10.1007/s00253-013-5272-4, 2014.

Turner, B., Brenes Arguedas, T., Condit, R.: Pervasive phosphorus limitation of tree species but not communities in tropical forests, Nature, 555(7696): 367-370, https://doi.org/10.1038/nature25789, 2018.

Waithaisong, K., Robin, A., l'Huillery, V., Abadie, J., Sauvage, F. X., Chemardin, P., Mareschal, L., Bouillet, J, P., Gonçalves, J, L, M., Plassard, C.: Organic phosphorus immobilization in microbial biomass controls how N$_2$-fixing trees affect phosphorus bioavailability in two tropical soils, Environmental Advances, 8, 100247, https://doi.org/10.1016/j.envadv.2022.100247, 2022.

Wang, Q., Wang, J., Li, Y., Chen, D., Ao, J., Zhou, W., Shen, D., Li, Q., Huang, Z., Jiang, Y.: Influence of nitrogen and phosphorus additions on N$_2$-fixation activity, abundance, and composition of diazotrophic communities in a Chinese fir plantation, Sci. Total Environ., 619, 1530-1537, https://doi.org/10.1016/j.scitotenv.2017.10.064, 2018.

Wang, Y., Luo, D., Xiong, Z., Wang, Z., Gao, M.: Changes in rhizosphere phosphorus fractions and phosphate-mineralizing microbial populations in acid soil as influenced by organic acid exudation, Soil Till. Res., 225: 105543, https://doi.org/10.1016/j.still.2022.105543, 2023.

Widdig, M., Heintz-Buschart, A., Schleuss, P. M., Guhr, A., Borer, E. T., Seabloom, E. W., Spohn, M.: Effects of nitrogen and phosphorus addition on microbial community composition and element cycling in a grassland soil, Soil Biol. Biochem, 151, 108041, https://doi.org/10.1016/j.soilbio.2020.108041, 2020.

**Formatted:** Font: Italic

**Field Code Changed**

**Deleted:** Tessier, J. T., Raynal, D. J.: Use of nitrogen to phosphorus ratios in plant tissue as an indicator of nutrient limitation and nitrogen saturation, J. Appl. Ecol., 40(3), 523-534, https://doi.org/10.1046/j.1365-2664.2003.00820.x, 2003.¶

**Formatted:** Subscript

**Field Code Changed**

**Deleted:** ¶
Walker, T. W., Syers, J. K.: The fate of phosphorus during pedogenesis, Geoderma, 15(1), 1-19, https://doi.org/10.1016/0016-7061(76)90066-5, 1976.¶

**Deleted:** Wertz, J. T., Kim, E., Breznak, J. A., Schmidt, T. M., Rodrigues, J. L.: Genomic and physiological characterization of the *Verrucomicrobia* isolate Diplosphaera colitermitum gen. nov., sp. nov., reveals microaerophily and nitrogen fixation genes, Appl. Environ. Microb., 78(5), 1544-1555, https://doi.org/10.1128/AEM.06466-11, 2012.¶

Yan, J., Huang, X., Su, X., Zhang, W., Gao, G., You, Y.: Introducing N$_2$-Fixing Tree Species into *Eucalyptus* Plantation in Subtropical China Alleviated Carbon and Nitrogen Constraints within Soil Aggregates, Forests, 13(12), 2102, https://doi.org/10.3390/f13122102, 2022.

Yang, J., Lan, L., Jin, Y., Yu, N., Wang, D., Wang, E.: Mechanisms underlying legume–rhizobium symbioses, J. Integr. Plant Biol., 64(2), 244-267, https://doi.org/10.1111/jipb.13207, 2022.

Yao, X., Zhang, Q., Zhou, H., Zhu, H., Nong, Z., Ye, S., Deng, Q.: Introduction of Dalbergia odorifera enhances nitrogen absorption on *Eucalyptus* through stimulating microbially mediated soil nitrogen-cycling, For. Ecosyst., 8: 1-12, https://doi.org/10.1186/s40663-021-00339-3, 2021.

Yao, X., Hui, D., Xing, S., Zhang, Q., Chen, J., Li, Z., Xu, Y., Deng, Y.: Mixed plantations with N-fixing tree species maintain ecosystem C:N:P stoichiometry: Implication for sustainable production, Soil Biol. Biochem., 191: 109356, https://doi.org/10.1016/j.soilbio, 109356, 2024.

Yuan, M. M., Guo, X., Wu, L., Zhang, Y. A., Xiao, N., Ning, D., Shi, Z., Zhou, X., Wu, L., Yang, Y., Tiedje, J. M., Zhou, J.: Climate warming enhances microbial network complexity and stability, Nat. Clim. Change, 11(4), 343-348, https://doi.org/10.1038/s41558-021-00989-9, 2021.

Yu, Q., Ma, S., Ni, X., Ni, X., Guo, Z., Tan, X., Zhong, M., Hanif, MA., Zhu, J., Ji, C., Zhu, B.: Long-term phosphorus addition inhibits phosphorus transformations involved in soil arbuscular mycorrhizal fungi and acid phosphatase in two tropical rainforests, Geoderma, 425: 116076, https://doi.org/10.1016/j.geoderma.2022.116076, 2022.

Yuste, J. C., Penuelas, J., Estiarte, M., GARCIA-MAS, J., Mattana, S., Ogaya, R., PUJOL, M., Sardans, J.: Drought-resistant fungi control soil organic matter decomposition and its response to temperature, Global Change Biol., 17(3), 1475-1486, https://doi.org/10.1111/j.1365-2486.2010.02300.x, 2011.

Zeng, Q., Peñuelas, J., Sardans, J., Zhang, Q., Zhou, J., Yue, K., Chen, C., Yang, Y., Fan, Y.: Keystone bacterial functional module activates P-mineralizing genes to enhance enzymatic hydrolysis of organic P in a subtropical forest soil with 5-year N addition, Soil Biol. and Biochem., 192, 109383, https://doi.org/10.1016/j.soilbio.2024.109383, 2024.

Zhang, M., O'Connor, P. J., Zhang, J., Ye, X.: Linking soil nutrient cycling and microbial

**Formatted:** Subscript

**Formatted:** Font: Italic

**Field Code Changed**

**Deleted:** Xia, Q., Rufty, T., Shi, W.: Soil microbial diversity and composition: Links to soil texture and associated properties, Soil Biol. Biochem., 149, 107953, https://doi.org/10.1016/j.soilbio.2020.107953, 2020.¶

**Deleted:** Yang, Y., Chai, Y., Xie, H., Zhang, L., Zhang, Z., Yang, X., Hao, S., Gai, J., Chen, Y.: Responses of soil microbial diversity, network complexity and multifunctionality to three land-use changes, Sci Total Environ., 859, 160255, https://doi.org/10.1016/j.scitotenv.2022.160255, 2023.…

**Formatted:** Not Highlight

**Formatted:** Not Highlight

**Formatted:** Font: Italic

**Formatted:** Not Highlight

**Formatted:** Not Highlight

**Formatted:** Not Highlight

**Formatted:** Not Highlight

**Field Code Changed**

**Deleted:** ¶

community with vegetation cover in riparian zone, Geoderma, 384, 114801, https://doi.org/10.1016/j.geoderma.2020.114801, 2021.

Zhang, W., You, Y., Su, X., Yan, J., Gao, G., Ming, A., Shen, W., Huang, X.: Introducing $N_2$-fixing tree species into *Eucalyptus* plantations promotes soil organic carbon sequestration in aggregates by increasing microbial carbon use efficiency, Catena, 231, 107321, https://doi.org/10.1016/j.catena.2023.107321, 2023.

Zhang, Y., Wang, X.: Geographical spatial distribution and productivity dynamic change of eucalyptus plantations in China, Sci. Rep.-UK, 11(1), 1-15, https://doi.org/10.1038/s41598-021-97089-7, 2021.

Zhou, Y., Boutton, T. W., Wu, X. B.: Soil phosphorus does not keep pace with soil carbon and nitrogen accumulation following woody encroachment, Global Change Biol., 24(5), 1992-2007, https://doi.org/10.1111/gcb.14048, 2018.

**Deleted:** a

**Deleted:** Zhang, X., Wang, L., Zhou, W., Hu, W., Hu, J., Hu, M.: Changes in litter traits induced by vegetation restoration accelerate litter decomposition in Robinia pseudoacacia plantations, Land Degrad. Dev., 33(1), 179-192, https://doi.org/10.1002/ldr.4136, 2022.¶

**Deleted:** b