Unveiling the critical role of opportunistic bacteria in post-wildfire phosphorus cycling in tropical peat forests

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Abstract

Although wildfires are known to significantly influence soil phosphorus (P) dynamics in forest ecosystems, the mechanisms through which bacterial subgroups with distinct life-history strategies respond to wildfire disturbances and regulate inorganic phosphorus (Pi) remain poorly understood. To address this knowledge gap, we collected soil samples from wildfire-affected tropical peat forests and oil palm agroforests to investigate how bacterial subgroups regulate phosphorus cycling. Results showed that although wildfire led to an overall decline in bacterial communities, including reductions in diversity and absolute abundance, soil Pi content increased significantly. This increase may be linked to shifts in bacterial life-history strategies. Following the classification of the community into opportunistic (r-strategists), sensitive, and tolerant (K-strategists) taxa, we observed that wildfire enhanced soil moisture, which in turn significantly increased the relative abundance of opportunistic taxa. Following wildfire, these r-strategists showed higher speciation rates, greater dormancy potential, stronger dispersal limitation (favoring local habitat colonization), and greater number of keystone species in networks. These traits provided opportunistic taxa with a competitive advantage, enabling rapid proliferation after wildfires. Additionally, they enhanced the expression of organic P-mineralization genes, particularly *phnA*, *phnW*, and *phoN*, accelerating the release and accumulation of Pi. This study for the first time revealed how bacteria with different life-history strategies influence P cycling, particularly highlighting the role of opportunistic taxa. This finding offers new insights into post-fire P dynamics driven by microbial communities in tropical forests and peatlands.

Keywords: Wildfire; Tropical peatlands; Bacterial community; Life-history strategies; Opportunistic taxa; Organic phosphorus mineralization; Inorganic phosphate

1. Introduction

Phosphorus is a critical nutrient that supports plant and microbial growth in tropical ecosystems. It fundamental in life processes such as photosynthesis and respiration (Lambers, 2022), and strongly affects biomass accumulation and community assembly. However, P cycling in forest soil is increasingly threatened. Climate change has driven a rise in the frequency of extreme wildfires, which have increased by 2.2 times over the past two decades (Cunningham et al., 2024). The global annual burned forest area is projected to increase by 29% by the end of the 21st century (Senande-Rivera et al., 2022). Wildfires not only disturb surface soil ecosystems directly but also contribute to climate change by releasing particulate aerosols and greenhouse gases. In the tropical regions of Southeast Asia, many lowland, coastal forest soils are composed of organic-rich peat, which is highly flammable. Fires on Southeast Asian peatlands have resulted in significant greenhouse gas emissions (c. 0.1 Gt C eq yr^{-1}) (Hooijer et al., 2010). Yet there remains a significant gap in literature related to processes which occur post fire. Specifically, fires may also trigger biogeochemical decoupling of nutrient cycles (Shen et al., 2025). This characteristic heightens the vulnerability of P cycling to wildfire disturbances. Understanding of microbial assemblage structure and its role in mediating nutrient availability within tropical lowland peatlands, remains virtually unexplored (Too et al., 2018). Further, the impact of fire on microbial communities in tropical peats is completely unknown and represents a major gap in our understanding of post-fire ecosystem function. Investigating post-fire P dynamics is, therefore, crucial for assessing the stability of P cycling in impacted tropical peatlands. This is a relevant phase in considerations of soil processes under global change.

Bacterial communities play a central regulatory role in soil P cycling through key biological processes such as solubilization, mineralization, and transport (Chu and Ma, 2024). However, forest wildfires have been shown to exert highly detrimental effects on soil microbiota. One meta-analysis study revealed that wildfires reduced soil bacterial biomass, abundance, and diversity to 90%, 96%, and 93% of the pre-fire levels, respectively (Pressler et al., 2018). The primary cause is that high temperatures directly inactivate enzymes and damage cellular structures, resulting in widespread mortality. Additionally, wildfires diminish the complexity of soil bacterial co-occurrence networks (Li et al., 2024; Yang et al., 2024). Such effects may indicate potentially negative impacts on Pi enrichment, given that the diversity and network complexity of bacterial communities are strongly associated with the multifunctionality of soil ecosystems (Delgado-Baquerizo et al., 2016; Zhai et al., 2024; Xiao et al., 2025). Notably, some studies suggest that soil Pi may increase following wildfires—a phenomenon potentially more widespread than previously recognized (Shen et al., 2024; Wu et al., 2024; Zhou et al., 2025). This increase has been commonly attributed to heat-induced mineralization and short-term input from ash deposition. However, this explanation overlooks the potential and sustained role of bacterial communities. For example, wildfires may stimulate the expression of organic P-mineralization genes and the secretion of phosphatases by bacteria, thereby facilitating the conversion of organic P into plant-available Pi (Shen et al., 2025). As such, given the global importance of peatlands, it is critical that the functional alteration of these systems associated with anthropogenic disturbance, be fully understood. Nevertheless, the post-fire dynamics of soil Pi in tropical peatlands remain unclear, and the underlying microbial mechanisms require further investigation.

Soil moisture is recognized as a key driver of global soil biodiversity and ecosystem functioning (Zhang et al., 2023) and is a fundamental driver of the functionality of peatlands; with water table heights and associated moisture content of peat soils controlling both carbon storage and sequestration rates (Evers et al., 2017). Alterations in soil moisture, under limiting conditions especially, can profoundly influence various ecological processes mediated by soil biota. Wildfires are intricately connected to the hydrological cycle. In the immediate aftermath of a wildfire, surface soil is often covered by a layer of highly porous ash that is rich in organic and inorganic matter (Abrantes et al., 2025), the loss of vegetation reduces evapotranspiration (Belongia et al., 2023), thereby increasing the proportion of precipitation that infiltrates into the soil. However, in tropical regions, the greater exposure of the peat surface to sunlight and heat, often increases evaporation rates and reducing moisture content (Harrison et al., 2024). Fire can also change the physiochemical properties of peat, promoting water repellence of burnt peat (Doerr et al., 2000) via alteration of soil particle size (Balfour, 2015), increase subsidence and associated compaction, and an overall reduced water storage capacity and infiltration rate (Wösten et al., 2006). In contrast, peat fires can burn to significant depth, often removing >50cm of height from the soil surface, exposing deeper reserves of recalcitrant peat material to oxidation.

During these events, the soil surface drops, driving it closer to the water table height, thereby enhancing the soil moisture content of the peat post fire (Lupascu et al., 2020). Consequently, the decline in soil moisture negatively influences P solubilization and diffusion; while excess soil moisture (caused by short-term spikes or poor drainage) can reduce soil aeration and create anaerobic conditions. Anaerobiosis alters bacterial community composition and metabolic activity, thereby indirectly influencing P cycling rates. Nevertheless, despite these observations, the extent to which wildfire-induced alterations in soil moisture affect bacterial community structure and function, as well as their subsequent roles in P cycling, remains insufficiently understood.

Understanding how soil bacteria respond to wildfire and how soil moisture influences this response, can enhance predictions of degraded tropical peat recovery and long-term impacts of both degraded and intact peatlands under global climate change. Bacterial taxa can be classified according to life-history strategies to assess their resistance to wildfire and capacity for post-disturbance recovery. These strategies represent suites of functional traits that have evolved in response to environmental disturbances and resource competition (e.g., resource allocation, reproduction, survival mechanisms, and stress tolerance), and confer competitive advantages under specific environmental conditions (Malik et al., 2020). For example, in highly variable moisture conditions, communities may become enriched with stress-tolerant taxa showing metabolic plasticity. In contrast, in environments with consistently high moisture, bacteria tend to optimize resource utilization either through enhanced decomposition of organic matter or by reducing metabolic rates to maintain competitive advantages within their niches (Evans and Wallenstein, 2014). These contrasting adaptive strategies often give rise to three distinct ecological groups within bacterial communities: opportunistic, sensitive, and tolerant taxa (Coyle et al., 2017). As r-strategists, opportunistic taxa flourish in response to resource pulses and demonstrate high growth rates and metabolic versatility. Sensitive taxa depend on stable environments, exhibit slow growth, and possess low tolerance to stress, which makes them potentially poorly adapted to habitat disturbances. Tolerant taxa, typically with high biomass and persistence, act as K-strategists and play critical role in maintaining community stability and functional continuity during recovery (Rojas-Tirado et al., 2017; Lavallee et al., 2024). Given their distinct functional traits, these three taxonomic groups may assume different roles in regulating soil Pi levels. A key scientific question is whether Pi enrichment after wildfires is primarily driven by a specific bacterial strategy. Do these taxa possess sufficient functional advantages to sustain phosphorus cycling under reduced community diversity? Investigating the role of bacteria with specific life-history strategies in P cycling is important for predicting ecosystem recovery, and the availability of Pi post fires. Specifically, understanding these changes has significance towards vegetation recovery and land management decisions.

Here, we focus on tropical forest peatlands in Malaysia, where frequent wildfires occur due to drainage of the peatlands and the reduced associated soil moisture, seasonal drought, lightning strikes, and agricultural development (driving wildfires to spread from slash and burn activities). We hypothesize that wildfire disturbance exerts selective pressure on bacterial communities by altering soil moisture and nutrient balance, preferentially enriching r-strategist taxa (e.g., opportunistic taxa), rather than uniformly affecting the entire community structure. These bacteria, due to their high growth rates and enhanced expression of organic P-mineralization genes, may drive the accumulation of soil Pi after wildfire. The objectives of this study are: 1) to investigate the effects of wildfire on soil physicochemical properties, bacterial taxa with different life-history strategies, and P-cycling functional genes; and 2) to clarify the potential mechanisms by which bacterial taxa with distinct life-history strategies influence soil Pi levels post wildfire disturbance.

2. Materials and methods

2.1. Study site and sampling

The study sites were located in Southern Selangor, Malaysia (2.69 – 2.88 °N, 101.51 – 101.64 °E), within mosaic landscapes of remnant peat swamp forests surrounding the Kuala Langat north and south peat swamp forest reserves. The peatlands are characterized by acidic peat deposits, and the peat soils sit on marine clay. The area experiences a tropical climate, with a mean annual temperature of 28°C and precipitation exceeding 2,000 mm. Seasonal rainfall patterns are distinct: the dry season (May – September) has an average monthly rainfall of 146 mm, while the wet seasons (October – April) receive approximately 295 mm monthly. Agricultural expansion has caused land conversion into four distinct ecosystems: young oil palm, mature oil palm, secondary forests, and drained forests. The secondary forests represent relic primary vegetation with mixed historical logging, though perimeter drainage and illegal encroachment has meant none of the forest sites were pristine.

Wildfires in the area typically occur during the dry season. We conducted soil sampling as soon as possible after the fire was extinguished during August 2020. During fieldwork, we selected two land cover classes representing the dominant land uses of the areas: secondary forest (F) and the mature oil palm (OP) plantation. At each site, we established both burned and control plots (denoted: BF/BOP for burned, and CF/COP for control, respectively). However the overwhelming differences between post fire and unburnt, compared to variation within land cover class meant that soil samples from F and OP land classes were combined into 'Control' and 'Burnt' for downstream analyses. Sampling was conducted at 12 locations (see Fig. S1). At each location, soil samples were collected at three depths (0 – 10 cm, 20 – 30 cm, and 40 – 50 cm) along the soil cores, covering the main oxic and anoxic zones. Four replicates were taken per location, resulting in a total of 144 soil samples. All samples were kept refrigerated and promptly transported to the laboratory for further analysis.

2.2. Physicochemical analysis

All samples were lyophilized. Soil moisture content was calculated from the weight difference before and after drying. The dried soils were mixed with ultrapure water, shaken thoroughly, and centrifuged at 6,800 g for 10 min. The resulting supernatant was used for pH measurement. The supernatant was filtered through a 0.22 μm membrane before analyzing anion concentrations (PO_4^{3-}, NH_4^+, and NO_3^-) using anion chromatography (ICS-600, Thermo Fisher Scientific, Waltham, MA), PO_4^{3-} was used as the indicator of soil Pi content (Li et al., 2025). Total nitrogen (TN), total organic carbon (TOC), and C/N ratios were determined using an elemental analyzer

(Vario MACRO cube, Elementar, Germany). Dissolved organic matter (DOM) in the supernatant was quantified with a three-dimensional fluorescence spectrometer (Fluoro Max 4, HORIBA Jobin Yvon, Edison, NJ). Its composition was qualitatively assessed using fluorescence indices: fluorescence index (FI), biological index (BIX), and humification index (HIX) (Wang et al., 2017).

2.3. DNA extraction, PCR amplification, and sequencing

Total DNA was extracted from the soil samples using the DNeasy PowerSoil Kit (12888-100; Qiagen, Hilden, Germany) following the manufacturer’s protocol. The V3–V4 region of the bacterial 16S rRNA gene was amplified using primers 338F/806R, and sequenced on an Illumina MiSeq PE250 platform (Chen et al., 2025). Absolute gene copy numbers of the 16S rRNA gene were quantified via real-time quantitative PCR (qPCR) using the CFX96 system (Bio-Rad, USA). Each 20 μL qPCR reaction contained 1 μL of template DNA, 10 μL of TB Green^{TM} Premix Ex Taq II (RR820A; TaKaRa, Kyoto), 0.5 μL each of forward and reverse primers, 3.2 μL of 25 mM $MgCl_2$, and 4.8 μL of RNase-free water. Thermocycling conditions were as follows: initial denaturation at 95 °C for 30 s; 40 cycles of 95 °C for 5 s and 60 °C for 30 s; followed by melting curve analysis to assess amplification specificity. Primer sequences and detailed methods were provided in previous research (Tettamanti Boshier et al., 2020).

2.4. Data processing

Raw sequence data were processed in QIIME 2. Primer sequences were trimmed from paired-end reads using Cutadapt, and DADA2 was used for quality filtering, denoising, chimera removal, and generation of amplicon sequence variants (ASVs) along with their representative sequences. Taxonomic assignment was performed against the SILVA 138 16S rRNA gene reference database. To standardize sequencing depth across samples, all datasets were rarefied to 16,335 sequences per sample. Functional prediction of the bacterial communities was inferred using PICRUSt2, with predicted gene families annotated against the Kyoto Encyclopedia of Genes and Genomes (KEGG) database (Douglas et al., 2020). Specifically, we focused on the relative abundances of genes associated with dormancy and P cycling.

2.5. Statistical analysis

We assessed differences between control and burned soils using t-tests. STAMP analysis was employed to identify between-group differences in bacterial abundance at the phylum level and genus level. To capture divergent bacterial life-history strategies in response to wildfire, ASVs were categorized into three subgroups based on their relative abundance shifts between burned and control soils: (1) opportunistic taxa, defined as ASVs whose relative abundances significantly increased after burning; (2) sensitive taxa, defined as ASVs whose abundances significantly decreased in burned soils; and (3) tolerant taxa, defined as ASVs that showed no significant change in abundance between treatments. Spearman's rank correlation was applied to evaluate the relationships between the variables, and to evaluate the influence of environmental drivers on bacterial subgroups. To further investigate the community assembly mechanisms, we applied the iCAMP framework to quantify the relative contributions of ecological assembly processes via the *iCAMP* package (Ning et al., 2020). Finally, we used the Binary State Speciation and Extinction (BiSSE) model to estimate rates of speciation, extinction, and state transitions of opportunistic and sensitive taxa (He et al., 2023).

Ecological co-occurrence networks were constructed in R software (version 4.4.2) using the Hmisc package to compute Spearman correlations among ASVs and igraph to assemble the network from significant associations ($r > 0.06$, $p < 0.05$). Network visualizations were performed using Gephi software (version 0.10.1). We then extracted site-specific subnetworks for each sampling location and evaluated their topological metrics in relation to soil moisture. Keystone species were identified using *Zi-Pi* analysis based on within-module connectivity and among-module connectivity, methodological details were described in previous research (Shi et al., 2016). ASVs classified as Module hubs, Network hubs, or Connectors were collectively designated as keystone species. To identify the bacterial genera most strongly associated with soil PO_4^{3-} content, we employed a random forest regression model and ranked genera based on their variable importance scores (Liao et al., 2024). Finally, we used structural equation modeling (SEM) to assess the direct and indirect effects of soil moisture, the three bacterial life-history strategy subgroups, and P-cycling gene abundances on soil PO_4^{3-} content (Dai et al., 2020).

3. Results

3.1. Wildfire increased soil moisture and PO_4^{3-} content

Wildfire significantly increased average PO_4^{3-} levels from 6.92 mg/kg to 14.72 mg/kg and raised soil moisture from 62.75% to 70.40% (Fig. 1). A significant positive correlation was observed between mean soil moisture and PO_4^{3-} (Fig. S2). NH_4^+ concentration also rose markedly, from 10.89 mg/kg to 90.22 mg/kg, and FI from increased 1.34 to 1.46. In contrast, NO_3^- decreased from 26.90 mg/kg to 12.59 mg/kg, TN dropped from 1.08% to 0.90%, TOC declined from 42.70% to 37.59%, and BIX fell from 0.18 to 0.16. However, wildfire had no significant effect on pH, C/N ratio, or HIX, which averaged 4.16, 41.17, and 15.89, respectively.

Insert Fig. 1 in here

3.2. Wildfire reduced the overall bacterial diversity and abundance

Bacterial Shannon diversity decreased significantly from 6.86 to 6.01 after the wildfire, with concurrent reductions in niche breadth (from 61.33 to 36.91) and absolute abundance (from 1.90×10^9 to 7.10×10^8 copies g^{-1} DW) (Fig. 2a). At the phylum level, *Actinomycetota* (average relative abundance: 32.58%) and *Pseudomonadota* (28.70%) were dominant (Fig. 2b). Wildfire significantly increased the relative abundance of *Bacillota* alone, from 2.47% to 27.61%, while other phyla decreased to varying extents (Fig. S4a).

At the genus level, *Acidothermus* (16.66%) and *Sulfobacillus* (6.55%) were dominant (Fig. S3). *Sulfobacillus* and *Alicyclobacillus*, both belonging to Bacillota, showed the largest relative abundance increases after wildfire, rising from 0.16% to 12.94% and from 0.44% to 6.92%, respectively. Conversely, wildfire significantly decreased the relative abundances of *Acidothermus* (21.11% to 12.20%), Subgroup_*2* (6.25% to 1.96%), and WPS-2 (3.08% to 0.53%) (Fig. S4b).

Insert Fig. 2 in here

3.3. Bacterial subgroups with different life-history strategies showed distinct responses to wildfire

We identified bacterial taxa with distinct wildfire response strategies to explore those potentially contributing to soil PO_4^{3-} enrichment, especially under varying soil moisture. Opportunistic, sensitive, and tolerant taxa accounted for 17.04%, 24.25%, and 58.71% of the community, respectively. Among opportunistic taxa, *Bacillota* showed the highest relative abundance (8.65%). *Pseudomonadota* (10.02%) and *Actinomycetota* (8.96%) were predominant phyla among the sensitive taxa, while *Actinomycetota* (20.53%) and *Pseudomonadota* (14.81%) were dominated among the tolerant taxa (Fig. 3a). Compared with sensitive taxa, opportunistic and tolerant taxa had greater dormancy potential, which increased significantly after wildfire (Fig. 3b). Soil moisture was positively correlated with opportunistic and tolerant taxa, but negatively with sensitive taxa (Fig. 3c). In contrast, TN, NO_3^-, and BIX were positively associated with sensitive taxa but negatively with opportunistic and tolerant taxa (Fig. S5).

The iCAMP model showed that drift was the main driver of soil bacterial community assembly, contributing 51.12% on average, followed by dispersal limitation (28.45%) and homogeneous selection (15.41%). Wildfire increased the contribution of dispersal limitation to the assembly of opportunistic taxa from 8.45% to 34.64%, while reducing the influence of homogeneous selection and drift by 12.11% and 11.14%, respectively. For sensitive taxa, wildfire increased the contribution of drift from 45.46% to 75.31%, while reducing homogeneous selection and dispersal limitation by 11.99%

and 18.45%, respectively. In contrast, the assembly of tolerant taxa was minimally affected by wildfire (Fig. 3d). According to BiSSE model estimates, the speciation rate of opportunistic taxa was 1.7 times higher than that of sensitive taxa, while their extinction rate was 2.6 times higher. Moreover, opportunistic taxa were predicted to transition to sensitive taxa at a rate five times higher than the reverse (Fig. 3e).

Insert Fig. 3 in here

3.4. Wildfire enhanced the network complexity and stability of opportunistic taxa

Wildfire significantly increased the proportion of opportunistic taxa in the network by 17.68%, while reducing those of sensitive and tolerant taxa by 13.23% and 4.45%, respectively (Fig. 4a). Subnetworks were constructed for each bacterial subgroup based on sampling locations (Fig. S6), and their topological features were correlated with soil moisture. All topological features of the opportunistic taxa subnetworks were positively correlated with soil moisture, while no significant correlations were observed for sensitive or tolerant taxa (Fig. 4b).

The *Zi-Pi* analysis revealed the impact of wildfire on keystone species within the bacterial networks (Fig. 4c), with their taxonomic identities and topological roles detailed in Table S1. Notably, only the number of keystone species belonging to the opportunistic taxa increased after wildfire, while those associated with sensitive and tolerant taxa declined (Fig. 4d).

Insert Fig. 4 in here

3.5. Opportunistic taxa promoted soil PO_4^{3-} enrichment

Peat PO_4^{3-} content was significantly positively correlated with the relative abundance of opportunistic taxa, but not with that of sensitive or tolerant taxa (Fig. 5). This suggests that opportunistic taxa may promote soil PO_4^{3-} enrichment.

A random forest model further identified *Methylovirgula* (1.08%), *Lysinibacillus* (0.06%), and *Candidatus* Koribacter (0.07%) as the key genus-level opportunistic taxa significantly associated with PO_4^{3-} enrichment ($p < 0.05$) (Fig. S7, Table S2).

Insert Fig. 5 in here

Genes involved in organic P-mineralization (e.g., *phnA*, *phnW*, and *phnX*), P-starvation response (*phoB*, *phoR*), inorganic P-dissolution (*ppx*), and P-transport (e.g., *pstABC*) were significantly more abundant in burned soil (Fig. 6a). These results indicate that changes following the wildfire activated P-cycling genes. Furthermore, the abundance of opportunistic taxa was significantly positively correlated with P-starvation response genes (*phoB*, *phoR*), organic P-mineralization genes (*phnA*, *phnW*, *phoN*, and *phnX*), and P-transport genes (*ugpA*, *ugpB*, *ugpE*, and *pstB*) (Fig. 6b). Only three organic P-mineralization genes (*phnA*, *phnW*, and *phoN*) were significantly positively correlated with soil PO_4^{3-} content (Fig. 6c). These results suggest that wildfire enhanced the coupling between opportunistic taxa and organic P-mineralization genes, promoting their expression and facilitating the sustained enrichment of soil PO_4^{3-}.

A conceptual model based on SEM illustrates the potential mechanism by which wildfire promotes peat PO_4^{3-} enrichment (Fig. 7). Wildfire drops peat surface level, bringing it closer to the water table and increased soil moisture, which subsequently significantly promoted opportunistic taxa and suppressed sensitive taxa but had no notable effect on tolerant taxa. Opportunistic taxa enhanced the expression of organic P-mineralization genes (*phnA*, *phnW*, and *phoN*) by increasing their relative abundance, thereby elevating soil PO_4^{3-} levels. In contrast, sensitive and tolerant taxa did not contribute to PO_4^{3-} accumulation.

Insert Fig. 6 in here

4. Discussion

4.1. The wildfire anomaly: overall decline in soil communities and Pi enrichment

Wildfires represent a significant ecological threat to tropical peat forests. As observed in this study, wildfire within the tropical peatland context significantly reduced the Shannon diversity, niche breadth, and absolute abundance of soil bacterial communities (Fig. 2), suggesting a substantial decline in the integrity of these microbial communities following fire disturbance. Similar trends have also been reported in soils from subtropical and coniferous forest ecosystems (Nelson et al., 2022; Shi et al., 2024). Typically, a decrease in bacterial diversity is associated with a decline in ecosystem functions (or nutrient availability) (Cardinale et al., 2012; Wagg et al., 2014; Wagg et al., 2019) such as the reductions in TN and TOC observed after wildfire (Fig. 1). Given that P is often a key limiting nutrient for forest productivity (Cui et al., 2025), it is likely that soil Pi would decrease after wildfire. However, contrary to predictions derived from the diversity-ecosystem function theory, our findings reveal that the loss of overall bacterial diversity did not impair P mineralization processes; rather, it coincided with an unexpected increase in Pi accumulation (Fig. 1). This paradox suggests that wildfire does not uniformly inhibit all bacterial subgroups. In contrast, it functions as an environmental filter that selectively eliminates sensitive taxa while promoting the growth of opportunistic taxa with higher potential for organic P mineralization. The relatively rapid P mineralization performed by these opportunistic taxa likely provides critical Pi nutrients, which play a crucial role in supporting early vegetation recovery after wildfire. Mineralization may also release P in soil drainage and thereby enhance eutrophication effects in receiving water ways. Additionally, alteration to peat nutrient status is likely to have implications for the significant GHG emissions associated with degraded peatlands (Hooijer et al., 2012).

https://bg.copernicus.org/articles/9/1053/2012/

Insert Fig. 7 in here

4.2. Establishment of opportunistic taxa dominance in peat forest soils under wildfire disturbance

In response to wildfire disturbance, forest soil microbial communities often shift from K-strategist to r-strategist dominance, as the latter exhibit faster growth rates and higher nutrient utilization efficiency (Qin et al., 2025). However, the underlying mechanisms of this functional shift have remained poorly understood. Our study extends current knowledge by providing detailed mechanistic insights: (i) As typical r-strategists, opportunistic taxa exhibited speciation and extinction rates 1.7 and 2.6 times higher, respectively, than those of sensitive taxa (Fig. 3e). This high turnover rate enabled them to rapidly reproduce and diversify, allowing swift occupation of newly created post-fire niches. (ii) Microorganisms can enter dormancy—a low-metabolic state—to survive unpredictable environmental stress (Lennon and Jones, 2011). Under wildfire disturbance, opportunistic taxa showed a higher potential for deploying dormancy strategies than sensitive or tolerant taxa (Fig. 3a). For example, *Bacillota*, a dominant phylum among opportunistic taxa, can form multi-layered protective endospores to enhance stress resistance (Hashimi and Tocheva, 2024). (iii) The high temperatures of wildfires can disrupt the compact structure of forest soil aggregates (Jordán et al., 2011), increasing soil porosity and habitat fragmentation. This enhances the role of dispersal limitation in driving the colonization of opportunistic taxa (Fig. 3d), enabling them to establish locally and thereby reduce direct competition with tolerant taxa (Walters et al., 2022). (iv) Wildfire increased both the relative abundance and number of keystone species of opportunistic taxa in co-occurrence networks, while those of sensitive and tolerant taxa declined (Fig. 4). This suggests that opportunistic taxa play more central functional roles in the restructured bacterial communities, potentially accelerating short-term nutrient cycling in peat soils. These findings elucidate the ecological mechanisms underlying the increased dominance of opportunistic taxa after wildfire events.

We found that soil moisture in peat soils increased significantly after wildfire (Fig. 1). This was also observed in post-fire observations by Lupascu et al., 2020. The clear drop in surface level associated with the frequently deep burn scars, contributed to bringing the peat surface closer to the water table height, thereby enhancing peat moisture content. Reduced plant transpiration and enhanced rainfall infiltration may also have contributed to this. Similarly, a study of boreal shrub wetlands reported that 13 years post wildfire, soil moisture had increased at least 26% (Li et al., 2023), indicating that fire-induced poor drainage may have long-lasting effects. Soil moisture correlated significantly positively with the relative abundances of opportunistic and tolerant taxa but negatively with sensitive taxa (Fig. 3c). Soil moisture was also positively correlated with the topological features of opportunistic taxa in the co-occurrence network (Fig. 4b). These findings collectively suggest that moisture is a key driver linking fire disturbance to bacterial community responses in warm and humid tropical peatlands (secondary forests and agricultural plantations). Adequate soil moisture facilitates the dissolution and transport of nutrients and metabolites (Smith et al., 2023), thereby promoting the rapid proliferation of r-strategist microbes. Moreover, increased soil moisture can revive the dormant spores of opportunistic taxa (Imminger et al., 2024), further enhancing their abundance. This aligns with r/K selection theory, which suggests that increased moisture may create transient resource-rich conditions favorable to r-strategists (Li et al., 2015). However, prolonged high-moisture conditions may be unfavorable for some aerobic bacteria. For example, *Acidothermus*, an aerobic genus, showed one of the most notable declines in relative abundance after wildfire (Fig. S4b). Overall, increased soil moisture appears to serve as a critical “trigger” for the rise of opportunistic taxa during the early stages of post-fire ecosystem recovery.

4.3. Organic P-mineralization genes and Pi accumulation: driven by opportunistic taxa

The relative abundance of opportunistic taxa was positively correlated with both organic P-mineralization gene abundance (*phnA*, *phnW*, and *phoN*) and soil Pi content (Figs. 5, 6, 7). This highlights the crucial role of opportunistic taxa in the wildfire-induced Pi enrichment. Previous global-scale studies have suggested that wildfires can increase soil P through mechanisms such as enhanced mechanical weathering of rocks and plant ash deposition (Zhou et al., 2025). The present study further reveals the critical bacterial contribution: by increasing soil moisture, wildfire not only stimulated the proliferation of opportunistic taxa but may also have enhanced phosphatase activity (Margalef et al., 2021), thereby accelerating the mineralization of organophosphorus compounds. In fact, the abundance of both opportunistic taxa and organic P-mineralization genes (*phnA*, *phnW*, and *phoN*) increased in parallel (Figs. 6, 7), indicating that wildfire strengthened the coupling between r-strategist microbes and P mineralization functions. Thus, opportunistic taxa may promote Pi accumulation by upregulating community-level organic P-mineralization genes. This coupling may be transient and ecologically fragile because shifting soil moisture regimes (e.g., moisture loss due to long-term declines in water-holding capacity of soil aggregates) could disrupt this microbial process in tropical peat forests under climate change. These results therefore reinforce the need to raise water tables and rewet degraded peatlands to restore ecological functionality.

5. Conclusions

Our investigation of tropical peatland revealed that although wildfire reduced the overall diversity and abundance of bacterial communities, they significantly increased soil moisture and Pi level. This suggests that fire dose not uniformly suppress all bacterial taxa. Based on life-history strategies, we classified bacteria into opportunistic, sensitive, and tolerant taxa, and revealed the central role of opportunistic taxa. Wildfire initially elevated soil moisture, which in turn enhanced the relative abundance of opportunistic taxa while reducing that of sensitive ones. After the fire disturbance, opportunistic taxa demonstrated increasing speciation rates, greater dormancy potential, stronger dispersal limitation, and an increased number of keystone species in co-occurrence networks. Meanwhile, wildfire intensified the coupling between these taxa and key P-mineralization genes (*phnA*, *phnW*, and *phoN*), thereby promoting the accumulation of Pi. This study, for the first time, uncovered a sequential ecological mechanism—from environmental disturbance to community reorganization, functional response, and ultimately nutrient cycling—highlighting the pivotal role of bacterial communities in sustaining soil nutrient dynamics and ecosystem stability under escalating wildfire frequency and global climate change.

Acknowledgment

This study was jointly funded by Nation Natural Science Foundation of China (91951208, 42402308), the Natural Science Foundation of Hubei Province, China (2024AFD383), Postdoctoral Fellowship Program of CPSF (GZB20230678), China Postdoctoral Science Foundation (2023M743286), and State Key Laboratory of Geomicrobiology and Environmental Changes, China University of Geosciences (No. GBL12403, GKZ25Y660). Fieldwork was funded by The Royal Geographical Society (RGS) Environment and Sustainability Research Grant: 'How do tropical peatland greenhouse gas emissions respond in the immediate aftermath of a fire?' and Liverpool John Moores University internal funding.

CRediT authorship contribution statement

Pengfei Gao: Conceptualization, Formal analysis, Visualization and Writing – original draft. **Xiaoyu Cheng**: Methodology, Conceptualization, Funding acquisition, and Writing – review and editing. **Wen Tian**: Investigation. **Xiaoyan Liu**: Methodology. **Olli H Tuovinen**: Writing – review and editing. **Stephanie L. Evers**: Investigation, Funding acquisition, Writing – review and editing. **Thomas E.L. Smith**: Investigation, Funding acquisition. **Hongmei Wang**: Conceptualization, Funding acquisition, Resources, and Writing – review and editing.

Data accessibility

The raw sequence data reported in this paper have been deposited in the Genome Sequence Archive in National Genomics Data Center, China National Center for Bioinformation/Beijing Institute of Genomics, Chinese Academy of Sciences, under BioProject accession No. PRJCA043095 and are publicly accessible at https://ngdc.cncb.ac.cn/gsa.

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Figure captions

Fig. 1 Effects of wildfire on physicochemical parameters of soil samples collected from Kuala Lumpur, Malaysia. Different letters (*a*, *b*) above the boxes indicate significant differences in physicochemical parameters. Control, CF/COP; Burned, BF/BOP; FI, fluorescence index; BIX, biological index; HIX, humification index.

Fig. 2 Shannon diversity, niche breadth and absolute abundance of soil bacterial communities in response to wildfire (a). Different letters above the boxes indicate significant differences between groups. Bacterial community composition at the phylum level in the control and burned soils (b).

Fig. 3 Impacts of wildfire on bacterial subgroups with different life-history strategies. Relative abundance of dominant phyla within the three bacterial subgroups (a). Effects of wildfire on the relative abundance of sporulation genes in the three subgroups (b). Different letters above the boxes indicate significant differences between groups. Relationship between bacterial subgroup abundance and soil moisture (c), * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Ecological assembly mechanisms of the three bacterial subgroups in response to wildfire (d). Evolutionary traits of opportunistic and sensitive taxa based on the BiSSE model estimates (e).

Fig. 4 Changes in soil bacterial co-occurrence networks between control and burned peat. Relative abundances of the three bacterial subgroups in the networks (a). Relationships between soil moisture and network topological features for the three bacterial subgroups (b), * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. *Zi-Pi* analysis showing wildfire effects on the keystone species in bacterial networks (c), and changes in the keystone species numbers across the three subgroups (d).

Fig. 5 Relationships between soil PO_4^{3-} content and the abundances of bacterial subgroups, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

Fig. 6 P cycling processes and differences in P-cycling gene abundances between control and burned soils (a), genes in red indicate significantly higher abundance in burned soil, and genes in blue indicate significantly higher abundance in control soil. The P-cycling functions corresponding to each gene are shown in Table S3. Correlations between the abundance of opportunistic taxa and P-cycling genes involved in P-starvation response, organic P-mineralization, and P-transport (b). Only significantly correlated genes are shown. Correlations between P-cycling gene abundance and soil PO_4^{3-} content (c). Only significantly correlated genes are shown. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

Fig. 7 SEM revealed causal relationships among soil moisture, three bacterial subgroups, organic P-mineralization genes (*phnA*, *phnW* and *phoN*), and soil PO_4^{3-} levels. Goodness of fit index is 0.767. Colors of bacteria in the central circle indicate different life-history strategies: red (opportunistic), yellow (sensitive), and blue (tolerant). Red lines indicate significant positive effects; black lines, significant negative effects; and dashed lines, nonsignificant effects. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

Supplementary materials

Fig. S1 Locations of soil sampling sites.

Fig. S2 Spearman correlation between soil moisture and PO_4^{3-} content. *** $p < 0.001$.

Fig. S3 Genus-level composition of bacterial communities in control and burned soils.

Fig. S4 Effects of wildfire on the relative abundance of bacterial taxa at the phylum (a) and genus (b) levels based on STAMP analysis. Taxa showing significant differences between control and burned soils are highlighted.

Fig. S5 Spearman correlation between environmental parameters and the three bacterial subgroups (opportunistic, sensitive, and tolerant taxa). * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

Fig. S6 Subnetworks of the three bacterial subgroups (opportunistic, sensitive, and tolerant taxa) constructed based on sampling locations.

Fig. S7 Importance ranking of bacterial genera (belonging to the three life-history strategy subgroups) in predicting soil PO_4^{3-} content based on random forest model. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

Table S1 Taxonomic information and topological roles of keystone species between control and burned soils.

Table S2 Relative abundance of genus-level bacteria affecting soil PO43-enrichment in three survival-strategy bacterial subgroups.

Table S3 Phosphorus cycling functions associated with P-cycling genes.