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Seasonal dynamics of soil bacterial and fungal communities in Colombian tropical forests and páramo ecosystems

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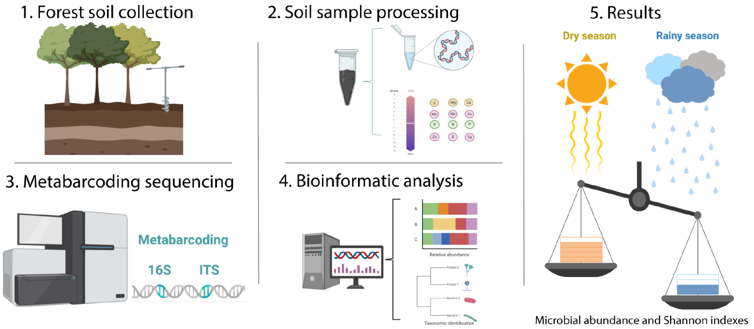
ABSTRACT

- The microbial communities in the forest soils of the studied ecosystems generally demonstrated higher abundances during the dry season sampling event in comparison to the rainy season sampling event.
- Seasonal climatic variations significantly affected the diversity of soil microbial communities in tropical forests.
- Soil chemical properties had a more pronounced influence on bacterial communities during the dry season sampling event than in the rainy season sampling event.



Understanding the dynamics of soil microbial communities and their responses to seasonal fluctuations is crucial for maintaining soil health and predicting the effects of climate change. We investigated seasonal impacts on soil microorganisms in tropical dry forests, Andean forests, and páramos. We characterized bacterial and fungal communities using 16S rRNA and ITS gene metabarcoding, complemented by soil chemical analysis. Proteobacteria, Actinobacteriota, Acidobacteriota, and Chloroflexi dominated bacterial communities. Fungi primarily comprised Ascomycota, Basidiomycota, and Mortierellomycota across all ecosystems. Bacterial Shannon diversity was significantly higher during the dry season at all sites, irrespective of ecosystem type. While fungal communities also showed higher species richness in the dry season, these differences were not statistically significant. Correlations between microbial communities and soil properties were generally stronger in the dry season, particularly in tropical dry forests. These findings suggest bacterial communities are more responsive to seasonal environmental shifts, whereas fungal communities exhibit greater structural stability. The páramo notably exhibited the greatest seasonal variability and highest proportion of unclassified reads, underscoring its ecological sensitivity and need for further research and conservation. This study provides valuable insights into the temporal dynamics of microbes in underexplored ecosystems, which are particularly vulnerable to the effects of climate change.

Keywords forest microbiome, metabarcoding, soil ecology, soil microorganisms

1 Introduction

Forests constitute one of the largest terrestrial ecosystems, covering approximately 30% of the world's total land area (Baldrian, 2017). They provide various ecosystem services such as soil and groundwater stabilization (crucial for agricultural activities), serve as the primary source of raw materials such as timber resources (Uroz et al., 2016; Li et al., 2022b) and are recognized as one of the most important biodiversity hotspots, hosting a wide variety of fauna and flora (Onyango et al., 2023). In addition to this, forest ecosystems play a crucial role as carbon sinks, storing approximately 80% of the carbon in terrestrial ecosystems (Chen et al., 2019). Consequently, forest soils become ideal habitats for diverse communities of microorganisms, including bacteria, archaea, and fungi.

Soil microorganisms are responsible for critical processes such as nutrient cycling, carbon sequestration, and maintaining soil fertility and productivity (Grosso et al., 2018). These microorganisms can respond to environmental

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changes over shorter time scales compared to other living organisms such as plants and animals (Li et al., 2018; Luo et al., 2020). Variation in seasonal climatic conditions is one of the main drivers shaping the soil microbiome. Seasonal dynamics of soil microbial communities have previously been studied, for example, it has been found that bacteria have a higher abundance in the dry season sampling event, due to variations in soil organic matter and soil pH (Luo et al., 2019). Similarly, considering that the soil microbiome is composed not only of active microorganisms but also of a dormant state (Kačergius et al., 2023), it has been observed that during the dry/warm seasons, there is an increase in diversity and higher activity, while during the rainy season sampling event, the metabolic functions of microorganisms tend to decrease (Lin et al., 2023). In contrast, it has been observed that fungal communities display an opposing behavior, compared to bacteria (Shigyo et al., 2019), showing an increase in activity during cold seasons (Voříšková et al., 2014; Ji et al., 2021). Similarly, the dominant bacterial phyla have been observed to remain relatively stable across different seasons compared to fungi, which demonstrate a greater differentiation between seasons (Ma et al., 2021; Xu et al., 2023)

To date, most studies on the seasonal dynamics of the forest soil microbiome have been conducted in northern hemisphere countries, primarily focusing on non-tropical forests (Shigyo et al., 2019; Xu et al., 2023; Fiore-Donno et al., 2024; Gazol et al., 2024). This has contributed to the limited understanding of the impact of climatic seasons on the soil microbiome associated with tropical forests, which are among the most biodiverse and carbon-rich biomes globally, storing nearly 40% of terrestrial carbon (James and Harrison, 2016). Moreover, tropical forests located in regions such as South America are highly susceptible to the impacts of the El Niño-Southern Oscillation (ENSO) phenomenon (Brugnoli et al., 2017). ENSO alters precipitation and temperature patterns in these ecosystems, with El Niño representing the warm phase and La Niña the cold phase, associated with variations in trade winds and rainfalls (Cai et al., 2021). These ENSO phases can induce extreme drought and flood conditions, which can restructure the forest ecosystem and impact the function and biodiversity of the soil microbiome (Gao et al., 2024; Maurice et al., 2024; Palácios et al., 2024). In particular, Colombian tropical forests and páramo ecosystems are ecologically strategic and highly sensitive to climate variability due to their narrow environmental thresholds and essential roles in water regulation and carbon cycling (Cresso et al., 2020). Despite their ecological significance, the seasonal dynamics of soil microbial communities in these systems remain largely unexplored. Therefore, the current study seeks to evaluate the impact of two contrasting climatic seasons on the soil microbiome of Colombian tropical forests, employing metabarcoding. The investigation encompasses three distinct ecosystem types, including tropical dry forest, Andean forest, and páramo, as defined by the Holdridge life zones classification.

2 Material and methods

2.1 Soil sampling following an elevation gradient.

Soil sampling was conducted in forest and páramo, ranging from 900 m.a.s.l. to 3800 m.a.s.l. during two distinct seasonal sampling events: dry season event 2021 (October to December 2021; average precipitation of 124 mm) and rainy season event 2022–2023 (September 2022 to March 2023; average precipitation of 183 mm) in Valle del Cauca, Colombia (Fig. 1, Table S1). The sampling sites include the Laguna de Sonso Regional Integrated Management District (RIMD, 900 m.a.s.l.), Vínculo Regional Natural Park (1000 m.a.s.l.), Mateguadua Regional Natural Park (1200 m.a.s.l.), Yotoco Forestry Reserve (1800 m.a.s.l.), Páramo del Duende Regional Natural Park (2400 m.a.s.l.), El Pailón Civil Society Reserve (2400 m.a.s.l.) and Páramo las Domínguez RIMD (3800 m.a.s.l.) (Fig. 1). The elevation gradient was composed of tropical dry forest (900–1200 m.a.s.l.), Andean forest (1800–2400 m.a.s.l.), and páramo (3800 m.a.s.l.). Within each sampling point established three plots of 10 m × 10 m, separated each other by 20 m. From each plot, three soil samples were collected from the top 25 cm for microbial analysis. From the same locations, paired samples were also taken for physicochemical characterization, resulting in a total of nine samples per analysis type at each sampling point. Microbial analysis samples were stored at –80 °C until DNA extraction.

2.2 Soil physicochemical analysis

The physicochemical analysis sampling was measured for pH, effective cation exchange capacity (ECEC), electrical conductivity (EC), soil organic matter (SOM), soil organic carbon (SOC), available nitrogen (N), available phosphorus (P), available sulfur (S), calcium (Ca), magnesium (Mg), potassium (K), sodium (Na), boron (B), iron (Fe), copper (Cu), manganese (Mn), and zinc (Zn), as well as bulk density (BD). Results were analyzed using a non-parametric Kruskal-Wallis test with Jamovi 2.2.5 (The Jamovi Project 2021) and *p*-values were adjusted using the Benjamini–Hochberg false discovery rate (FDR) method to account for multiple comparisons in Rstudio software.

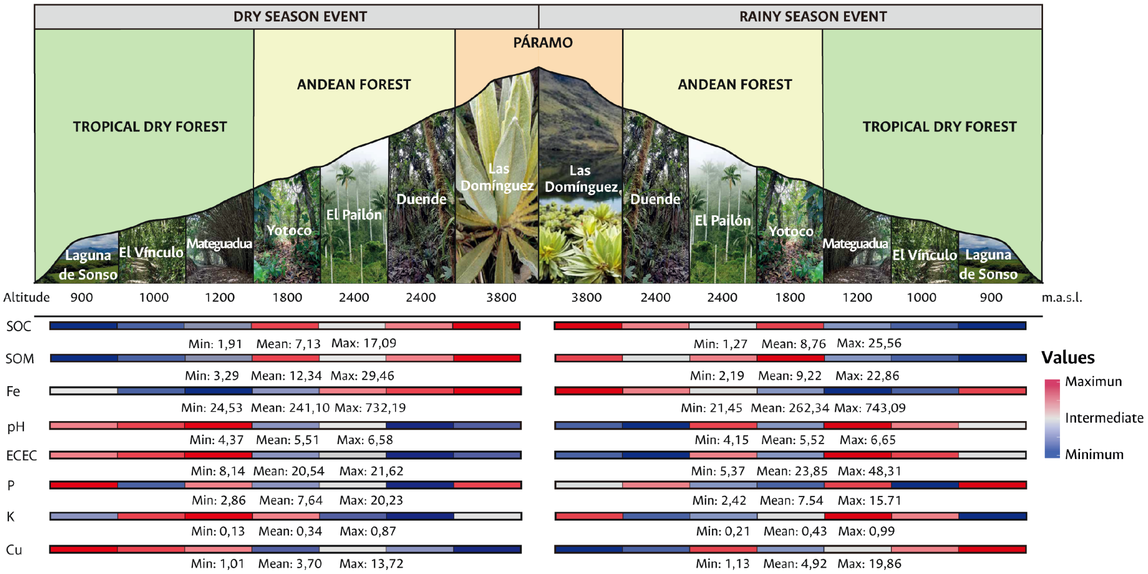

Fig. 1 Soil chemical properties across ecosystems and seasons.

2.3 Sampling processing and sequencing

DNA extractions of soil sampling were conducted using the commercial DNeasy PowerSoil Pro Kit (Qiagen, Hilden, Germany) following the protocol of the manufacturer. The products of extractions were quality evaluated using spectrophotometry (Colibri Titertek Berthold 84030) and 0.8% agarose gels. Following this, libraries were created for the V3-V4 regions of the 16S rRNA gene for bacteria and the ITS1 region for fungi. For bacterial amplification, the primers 341F (5′-CCTAYGGGRBGCASCAG-3′) and 805R (5′-GGACTACNNGGGTATCTAAT-3 ′) were used (Hjelmsø et al., 2014) and for fungal amplification, the primers ITS5-1737F (5 ′-GGAAGTAAAAGTCGTAACAAGG-3 ′) and ITS2-2043R (5′-GCTGCGTTCTTCATCGATGC-3′) were used (Bellemain et al., 2010). Sequencing was then performed using Illumina NovaSeq 6000 technology with a depth of approximately 150000 reads per sample. Raw data of reads for bacteria and fungi were deposited were deposited in the European Nucleotide Archive (ENA) under project number PRJEB61162.

2.4 Bioinformatics and statistical analyses

An initial quality control assessment was conducted using FastQC (Andrews, 2010) to ensure that all raw sequence reads met the minimum Phred score threshold (Phred ⩾ 20). Raw data were subsequently with Kraken2 (Wood et al., 2019) for taxonomic assignment using SILVA v. 138 bacterial classifier (Quast et al., 2013) and UNITE v. 9.0 for fungi (Kõljalg et al., 2020). The results were uploaded to R software (v. 4.2.2; University of Auckland, Auckland, New Zealand) and subsequently normalized (rarefaction) to 99958 reads for bacteria and 78042 for fungi. Next, Taxon IDs containing less than 10 reads or fewer in every taxonomic category were removed (Li et al., 2022a; Lu et al., 2022). Taxonomic composition graphs at the phylum and class levels were generated using the ggplot2 package (Wickham, 2016), and Shannon diversity and Berger-Parker Dominance indices were calculated with the microbiome Bioconductor package (Lahti and Shetty, 2019). Furthermore, a principal coordinate analysis (PCoA) based on the Bray–Curtis distances evaluated the beta diversity, with permutation multivariate analysis of variance (PERMANOVA) conducted via ‘adonis2’ of the Vegan package (Oksanen et al., 2024) with 999 permutations, to test the significant influences of altitude (ecosystem type) and season in microbial communities’ compositions.

To evaluate the driving factors significantly correlated with the taxonomic bacterial and fungal composition at the sampling point and season levels, partial Mantel tests using Spearman correlation were conducted with the ggcor package (Huang et al., 2020).

3 Results

3.1 Physicochemical description and variations between seasons

The Kruskal-Wallis statistical analysis did not show any significant trends in soil properties between the seasons and ecosystems (Table S2 and Table S3). However, the study revealed that certain soil parameters exhibited variations corresponding to the climatological periods (Table S3). For example, soil organic carbon was more abundant during the dry season sampling event (2021) in tropical dry forest and páramo ecosystems, while soil organic matter reached its peak in the rainy season sampling event (2022–2023) within the Andean forest and páramo ecosystems (Tables S3). Conversely, iron levels were elevated during the rainy season sampling event across all three ecosystems, while sulfur concentrations were higher in the dry season sampling event in the tropical dry forest and Andean forest ecosystems. Additionally, ten soil chemical characteristics, including pH, soil organic carbon, soil organic matter, calcium, and iron, exhibited statistically significant variations across the ecosystems during both the dry and rainy seasons events (Table S3).

3.2 Bacteria and fungi composition in ecosystems

With the normalization and the removal of low-representative taxonomic groups (<10 reads), the dataset of raw reads was kept with 11 567 095 total reads and 95 595 averaging reads per sample for bacteria, and 9 672 598 total reads for fungi, with an average of 78 004 reads per sample. The number of Taxon IDs for bacteria was 2 110, classified into 36 phyla and 92 classes, while for fungi, there were 2 071 Taxon IDs grouped into 17 phyla and 58 classes (Table S4 and Table S5).

Proteobacteria, Actinobacteriota, and Acidobacteriota characterized the bacterial community composition across the ecosystems as the predominant phyla in the tropical dry forests and Andean forests, while Acidobacteriota, Proteobacteria, and Chloroflexi dominated the páramo ecosystem (Table S4). Additionally, other abundant bacterial groups including Verrucomicrobiota, Gemmatimonadota, Firmicutes, Myxococcota, and Bacteroidota, were consistently observed across the three ecosystems (Table S5).

Regarding the differences observed between the climatic seasons, Actinobacteriota had a higher relative abundance during the rainy season event in the dry forest and Andean forest (Fig. 2A, 2B and Fig. S1). Methylomirabilota also exhibited increased abundance in the rainy season event, except for the Vínculo site in the tropical dry forest and the Yotoco and El Pailón sites in the Andean forest. Furthermore, Verrucomicrobiota displayed distinct patterns, with higher abundance specifically during the rainy season event in the tropical dry forest sites of Vínculo and Mateguadua (Fig. 2 and Fig. S1). In contrast, the taxonomic groups Gemmatimonadota, Firmicutes, Myxococcota, Chloroflexi, and Bacteroidota demonstrated consistently greater relative abundances during the dry season sampling event compared to the rainy season sampling event across all studied ecosystems. A few exceptions to this pattern were noted, including Laguna de Sonso for Gemmatimonadota, El Pailon for Firmicutes, and Chloroflexi in Duende and El

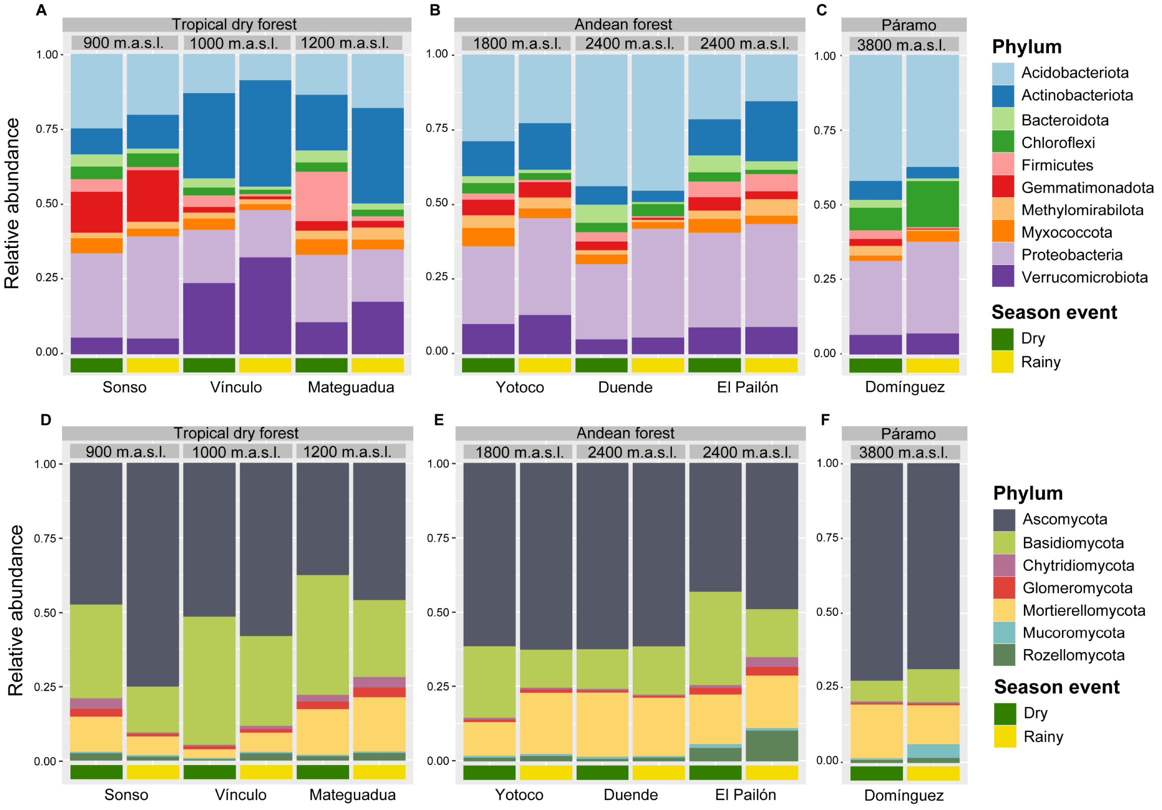

Fig. 2 Relative abundance of the most predominant phyla for soil bacteria (A–C) and fungi (D–F) associated with tropical dry forest (A, D), Andean forest (B, E), and páramo (C, F). Every sampling point shows the results for the dry season sampling event (2021) and the rainy season sampling event (2022–2023); Grey boxes denote the elevation in meters about sea level.

páramo. Specifically, in this high-altitude ecosystem, the differences in abundances between the climatic seasons were notable only for phyla that exhibited higher relative abundance during the dry period (Fig. 2C). Furthermore, Proteobacteria exhibited distinct patterns within the ecosystems, being more abundant in the dry season sampling event at Mateguadua but more prevalent during the rainy season sampling event at Yotoco and Duende (Fig. 2 and Fig. S1).

At the class level, the data revealed that Actinobacteria and Methylomirabilia, taxonomic groups within the Actinobacteriota and Methylomirabilota phyla respectively, demonstrated elevated read abundances during the rainy season sampling event. In contrast, the Verrucomicrobiae class exhibited variations in relative abundance exclusively in the Vínculo and Mateguadua sampling locations (Fig. S2). The classes Gemmatimonadetes (Gemmatimonadota), Bacilli (Firmicutes), Polyangia (Myxoccocota), and Bacteroidia (Bacteroidota) exhibited higher relative abundance during the dry season sampling event within the tropical dry forest and Andean forest ecosystems (Fig. S2 and Table S4). The Gammaproteobacteria and Alphaproteobacteria classes exhibited contrasting patterns across the studied ecosystems, with the former reporting higher read assignments during the dry season sampling event in Mateguadua, while the latter displayed increased abundances during the rainy season sampling event in Yotoco and Duende (Fig. S2 and Table S4).

For the fungal communities, the phyla Ascomycota, Basidiomycota, and Mortierellomycota were the predominant groups across the three ecosystems (Table S5). These taxa exhibited distinct differences in their abundances between the climatic seasons at the Sonso site, with Ascomycota being more abundant during the rainy season sampling event, while Basidiomycota, Mortierellomycota, and Glomeromycota were more prevalent during the dry period (Fig. 2D, 2E and Fig. S3). Consistently, Basidiomycota and Glomeromycota were also significantly more abundant during the dry seasons sampling event at the Pailón and Domínguez, respectively (Fig. 2E and Fig. S3).

At the class taxonomic level, most classes did not exhibit a consistent pattern of abundance in relation to the climatic season within the ecosystems. While certain fungal classes, such as Dothideomycetes and Sordariomycetes, were more abundant during the rainy season sampling event in specific tropical dry forest localities like Laguna de Sonso and Mateguadua, these same classes showed higher abundances during the dry season sampling event in Vinculo. Similarly, Agaricomycetes and Mortierellomycetes displayed greater abundance in the dry season sampling event at Laguna de Sonso, but were more abundant in the rainy season sampling event at El Vinculo and Mateguadua. Within the Andean forest, these two classes were more prevalent during the dry season sampling event in Duende, yet more abundant in the rainy season sampling event at El Pailón and Yotoco. Additionally, the Leotiomycetes class, the most dominant in the páramo ecosystem, exhibited its peak abundance in the dry season sampling event in this high-altitude environment, as well as in Duende and Yotoco of the Andean forest, and Laguna de Sonso of the tropical dry forest, while being more abundant in the rainy season sampling event at the other localities (Fig. S2 and Table S5).

3.3 Alpha and beta diversity analysis

The Shannon diversity index results for bacteria revealed that diversity was significantly higher during the dry seasons sampling event across all sampling sites, regardless of ecosystem type. Pailón exhibited the highest diversity values in both seasons, while Vínculo and Duende showed the most significant differences between dry and rainy periods ($p<0.0001$) (Fig. 3A). Additionally, the Berger-Parker dominance index for bacteria was close to zero, with significance observed only at Vínculo and Mateguadua concerning climatic conditions (Fig. 3B).

For fungal communities, the Shannon diversity index values were lower than those obtained for bacteria, with El Pailón being the only sampling site that exhibited significant differences between climatic seasons ($p<0.05$) (Fig. 3C). Additionally, the Berger-Parker index showed values mostly close to zero, with no significant differences between seasons, although some samples presented high values for this index (Fig. 3D).

Additionally, the beta diversity results revealed that bacterial communities, were tightly clustered within each locality, regardless of the climatic season (Fig. 3E). In contrast, the fungal communities exhibited distinct patterns with the rainy season samples from Sonso, Yotoco, and Duende being separated along the second ordination axis from the dry season samples collected at those sites (Fig. 3F). The PERMANOVA analysis further demonstrated that altitudinal had a significant impact, accounting for 20.5% of the observed variation in the bacterial communities and 7.7% in the fungal communities. Similarly, the climatic season also exhibited a significant influence, accounting for 3.7% of the variation in bacterial communities and 5.8% in fungal communities. In general, the bacterial communities exhibited greater variation, which was explained by the principal axes (68.5% for bacteria and 22.8% for fungi), suggesting that they respond with heightened sensitivity to environmental conditions compared to the fungal communities (Fig. 3E, 3F).

3.4 Factors that can forecast the soil microbial communities

The Mantel test results revealed that soil factors and

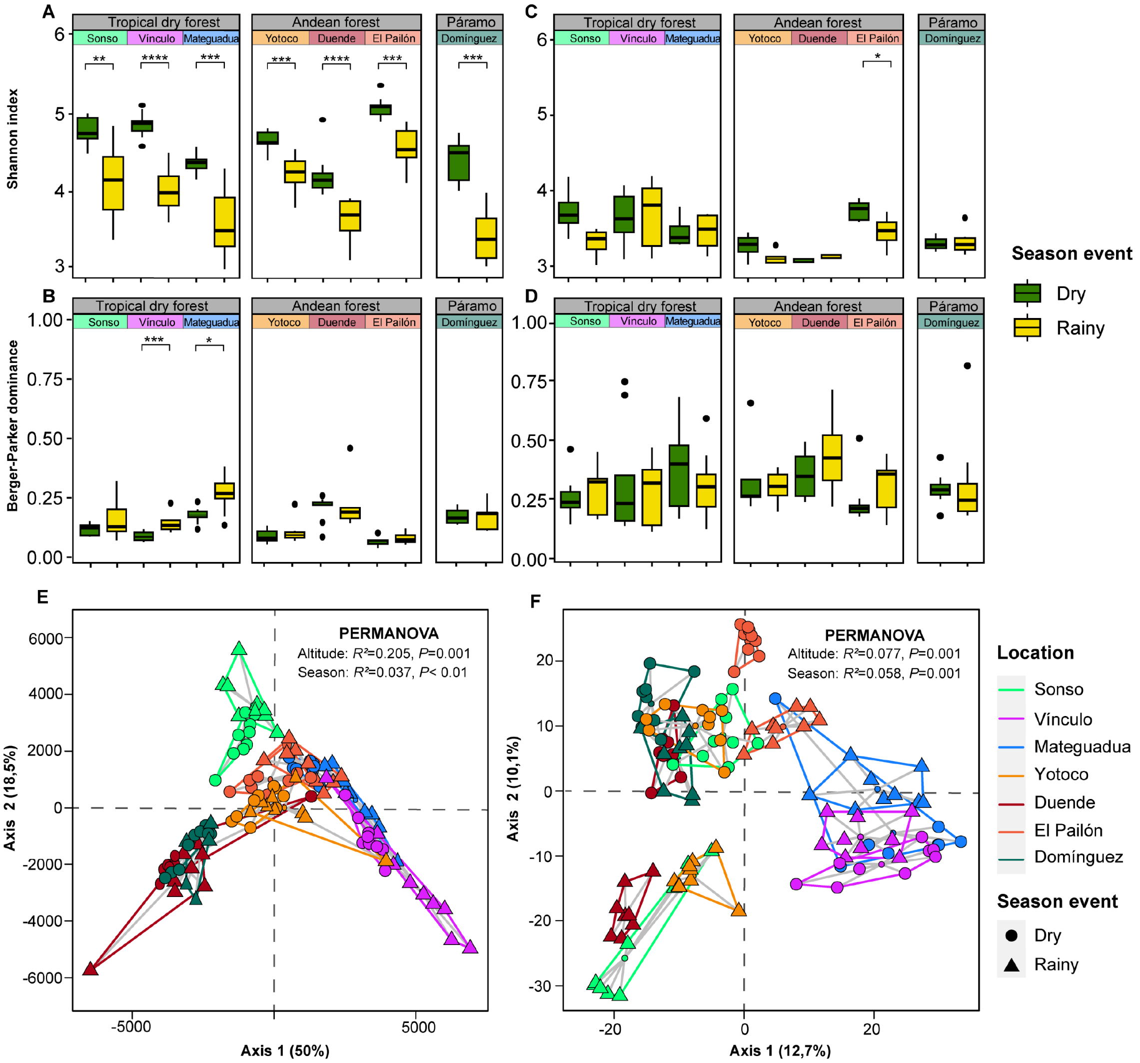

Fig. 3 The Shannon (A, C) and Berger-Parker (B, D) indexes for soil bacteria (A, B) and fungi (C, D) across three types of ecosystems in Colombia. Principal Coordinates Analysis (PCoA) showing bacterial (E), and fungal (F) communities based on the Bray-Curtis dissimilarity distance. Asterisks denote significant differences between seasons within localities: $*p < 0.05$, $**p < 0.01$, $***p < 0.001$, $****p < 0.0001$.

altitude, as environmental features associated with ecosystem type, had distinct relationships with the microbial communities during the climatic seasons (Figs. 4 and S4). For bacterial communities in the tropical dry forests during the dry season sampling event, the soil factors mainly were different across the three sampling locations (Fig. 4A). In contrast, no significant soil factors were identified for the rainy season event (Fig. 4B). In the case of the Andean forest, the dry season sampling event exhibited significance only for El Pailón, while the rainy season sampling event showed significance primarily for Yotoco (Fig. 4C, 4D).

For the fungal communities in the tropical dry forests, in contrast to the bacterial results, the rainy season sampling event exhibited the greatest number of soil factors that were significantly correlated with the microbial communities, primarily associated with Mateguadua (Fig. S4B). In opposition, the dry season sampling event results showed the strongest relationships for Vínculo (Fig. S4A). Additionally, in the Andean forest of El Pailón the fungal community during the dry season sampling event was shaped by SOC, SOM, N, and BD, while during the rainy season, were ECEC, Mg, and Na (Fig. S4C, S4D).

Lastly, the results from the páramo ecosystem Las Domínguez showed that during the dry season sampling event, ECEC was the soil factor exhibiting a correlation with the bacterial communities, while the fungal communities, ECEC, Fe, and Zn were identified as the influential soil factors (Fig. S4E). However, no significant soil variables were found to be associated with the microbial communities during the rainy season sampling event in this ecosystem (Fig. S4F).

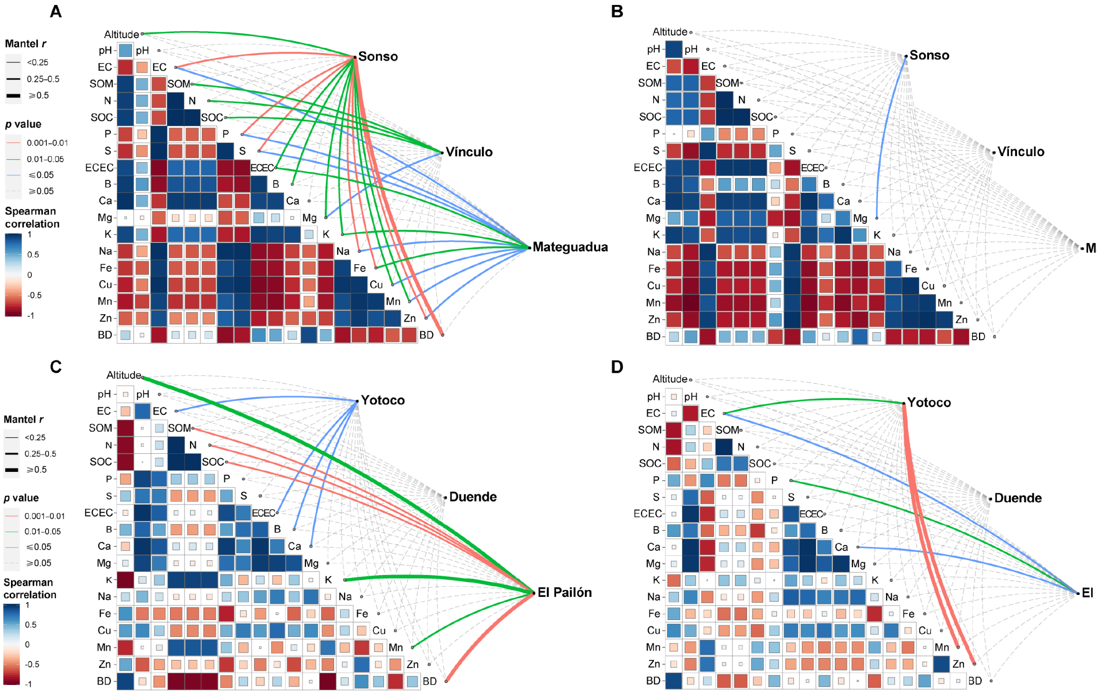

Fig. 4 Mantel test to identify the main predictor of bacterial community composition in tropical dry forest (A, B) and Andean forest (C, D) across dry (A, C) and rainy (B, D) seasons.

4 Discussion

4.1 Physicochemical description and variations between seasons

The physicochemical properties of the soil varied across seasons, although no statistically significant differences were found (Fig. 1). Despite this, a trend toward increased soil organic matter (SOM) was observed during the dry season sampling event, likely due to the accumulation of leaf litter on the soil surface (Xu et al., 2022b). Similary, although not statistically significant, higher soil organic matter values during the rainy season sampling event may have contributed to the observed increase in available phosphorus, as organic matter can reduce phosphorus absorption and enhance its release (Mabagala and Mng'ong'o, 2022). Elevated organic carbon levels during the rainy season sampling event might be linked to greater leaf area and higher photosynthesis rates, which promote carbon sequestration and increase soil organic carbon concentrations (Wright et al., 2017; Zhang et al., 2023a). Additionally, studies suggest a positive correlation between soil organic carbon and iron content, potentially explaining the higher Fe levels observed during the rainy season sampling event (Solanki et al., 2024; Sun et al., 2024). In contrast, the decrease in certain nutrients, such as sulfur and boron, during the rainy season event may be attributed to leaching processes (Lepcha and Devi, 2020; Gerhard et al., 2021; Zhuang and Tian, 2023).

4.2 Bacteria and fungi composition and diversity index in ecosystems

Our results revealed that Proteobacteria, Actinobacteriota, and Acidobacteriota were the dominant bacterial phyla across all sampling sites, consistent with previous findings in forest soils (Xu et al., 2022a). Furthermore, existing research has established that the composition of soil microbial communities can vary considerably in response to seasonal changes (Xu et al., 2018; Zhang et al., 2018). For example, bacteria showed higher abundances during the dry season sampling event across the different locations, similar to what has been reported previously (Du et al., 2018; Pan et al., 2024) (Fig. 2A–2C), this may be owing to variations in soil nutrient levels between the rainy and dry seasons sampling event. During the rainy season sampling event, increased precipitation can lead to a lower concentration of organic matter and available nutrients in the soil as they become more leached and diluted (Han et al., 2021). In contrast, the increased abundance of Methylomirabilota that we observed during the rainy season sampling event in the tropical dry forest and Andean forest aligns with the findings reported by Yashpal Bhardwaj in 2020. Their study showed that methanotrophic bacteria, to which Methylomirabilota belongs (Zhu et al., 2022), exhibit the highest abundance in the coldest seasons (Bhardwaj et al., 2020). Furthermore, Bhardwaj's research established a negative correlation between methanotrophic bacteria and soil pH. This may help explain the higher abundance of this phyla particularly at Laguna de Sonso, where the pH is lower during the rainy season event compared to the dry season event. These results are related to the Shannon diversity index, which shows higher values during the dry seasons sampling event across the different ecosystems. This may be attributed to the tendency of trees in tropical forests to exhibit deciduous behavior during dry periods, shedding their leaves to the ground (Hasnat and Hossain, 2020) and thereby increasing available resources such as organic matter that may facilitate the growth and development of a more diverse microbial community in the soil during this season (Sánchez-Galindo et al., 2021; Jin et al., 2022).

On the other hand, fungal community abundance did not show a significant difference between the two seasons (Fig. 2D–2F), this may be attributed to their capacity to link spatially separated resources through their hyphal networks, which helps the fungal community adapt to environmental changes (Jansson and Hofmockel, 2020; Li et al., 2024) However, the relative abundance of the major fungal phyla, Ascomycota and Basidiomycota, did exhibit opposite changes over the seasons, with Ascomycota increasing during the rainy period and Basidiomycota peaking in the dry season sampling event similar to trends observed in previous studies (Buscardo et al., 2021, 2024). In contrast to the bacterial community, the Shannon index in fungi (Fig. 3C) did not show a significant difference between seasons in most locations, highlighting the ability of fungal communities to be more resilient to short-term environmental changes, except in El Pailón (Andean forest) with *p* values of < 0.05. This location has a history of grazing, and in the last 7 years has undergone a restoration and conservation process, with a particular focus on the Quindio wax palm (*Ceroxylon quindiuense*). These site-specific characteristics may have influenced the results obtained. Nonetheless, this represents one of the first investigations examining the impact of seasonal variation on microbial communities within restored forest ecosystems in this region. Further research will be necessary to more thoroughly elucidate the dynamics of these microbial organisms in such restoration contexts.

Concerning beta diversity, the Principal Coordinates Analysis revealed that the compositions of the bacterial and fungal communities have different behaviors (Fig. 3E–3F). The fungal community exhibited a more distinct separation based on climatic season, with a clearer delineation of groupings according to the rainy and dry periods. In contrast, the bacterial community was more closely aligned with the specific location and ecosystem type, regardless of the seasonal conditions. Although the PERMANOVA test revealed significant results for both factors (seasons and altitude), the clustering patterns in the PCoA suggest that bacterial communities may be more influenced by characteristics related to the locations and ecosystem type, such as soil properties or altitude, rather than the fluctuations in seasonal weather patterns. This has been reported in other studies, Wei et al 2022, demonstrated that variations in bacterial communities are more strongly influenced by spatial variables than by the effect of seasonal changes, according to their beta diversity based on Bray–Curtis distance, where the sampling site explained over 30% of the bacterial variance, while season accounted for less than 3% (Wei et al., 2022). Similar results have also been found in other studies (Zhang et al., 2020; Pardo-Esté et al., 2023). In addition to this, the results presented in our 2023 and 2024 researches (Vélez-Martínez et al., 2023; Reyes-Ardila et al., 2024) provide a detailed examination of the effects of these site-specific factors, including vegetation composition, on the composition and diversity of bacterial and fungal communities within the tropical forest and páramo ecosystems of Colombia. These studies focused on a single climatic season and analyzed different subsets of sampling locations separately, offering valuable insights into how microbial communities are structured in response to vegetation and environmental variation across altitudinal gradients. In contrast, the present study integrates data from all eight sampling locations and evaluates both dry and rainy seasons, providing a broader temporal perspective on microbial dynamics. This complementary approach allows us to explore how microbial communities respond not only to spatial variation but also to short-term climatic fluctuations.

4.3 Factors that can forecast the soil microbial communities

Soil microbial communities are known to be influenced by a variety of factors, including soil properties, climate, and vegetation, despite that several studies have highlighted the importance of soil physicochemical properties as a key driver of microbial community composition (Chen et al., 2023; Pardo-Esté et al., 2023). The Mantel test and Spearman correlation coefficient values in this study indicated that the relationships between microbial communities and soil properties were generally stronger and more significant in tropical dry forest ecosystems compared to Andean forest and páramo ecosystems (Fig. 4A–4B), implying that the bacteria communities in tropical dry forests may be more vulnerable to environmental changes. For example, the observed correlation between Laguna de Sonso and phosphorus in dry season event could be attributed to the high phosphorus availability at this location (Table S2). The presence of high phosphorus levels in the soil may potentially constrain the capacity of soil microorganisms to utilize carbon, impacting the abundance, composition, and functional diversity of the microbial community (Estrada-Bonilla et al., 2017; Zhang et al., 2023b). Aside from phosphorus, the principal drivers of bacterial community abundance across tropical dry forests were EC, sulfur, sodium, iron, and zinc. The Andean forest exhibited a smaller number of key drivers influencing the microbial communities, with soil organic matter, nitrogen, and soil organic carbon being the most significant factors as reported in previous studies (Lin et al., 2023; Pan et al., 2024). However, contrary to these studies, this research did not find soil pH to be a significant driver of bacterial community composition, despite the observed range from moderately acidic to strongly acidic conditions across the sampling locations. This observation could be attributed to the indirect influence that soil pH exerts on other chemical properties of the soil (Bai et al., 2023). Our Spearman correlation analysis indicated that soil pH exhibited interactions with most of the soil parameters evaluated, suggesting that pH effects on microbial communities may be masked by the availability and dynamics of other soil elements.

In contrast to bacterial communities, fungal communities exhibited stronger associations and variations with soil factors that were more heavily influenced by climatic season (Fig. 4C–4D) as opposed to the patterns observed for bacterial communities, which showed greater dependence on specific locality or ecosystem type. During the dry season event, the main drivers for fungal communities in tropical dry forests were soil organic matter, soil organic carbon, and nitrogen. In the rainy season sampling event, the key drivers were effective cation exchange capacity, sulfur, and bulk density. These distinct seasonal patterns in the drivers of fungal community composition were maintained regardless of the specific ecosystem. These findings suggest that the structures of soil bacterial and fungal communities can be explained by distinct factors that are more closely linked to their respective ecologies. For instance, fungal communities and structures appear to be more influenced by the potential plant-fungus symbiotic relationships (Gschwend et al., 2021), which have been demonstrated to exhibit strong variations across climatic seasons (Beidler et al., 2023). Similarly, the capacity of fungi to adapt to environmental changes can be attributed to their hyphae and spore reproduction mechanisms, which allow them to adopt multiple nutritional strategies concurrently to ensure their survival (Li et al., 2024).

5 Conclusions

Seasonal variations in soil microbial communities have provided crucial insights into the complex relationships between abiotic factors, including soil physicochemical properties and climatic conditions, and the structure and function of these microbial communities. The findings suggest that while bacterial communities are more strongly influenced by soil properties, fungal communities exhibit more pronounced seasonal patterns, potentially reflecting their unique ecological adaptations. These insights offer a deeper understanding of the mechanisms driving the dynamics of soil microbial communities and their response to environmental changes, an understanding that is essential for the sustainable management of terrestrial ecosystems.

Conflicts of interest

The authors declare no conflict of interest.

Data availability statement

The sequences were deposited in the European Nucleotide Archive (ENA) under project number PRJEB61162.

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Electronic supplementary material

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