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Resistance of bacterial community in the sugarcane rhizosphere after straw burning

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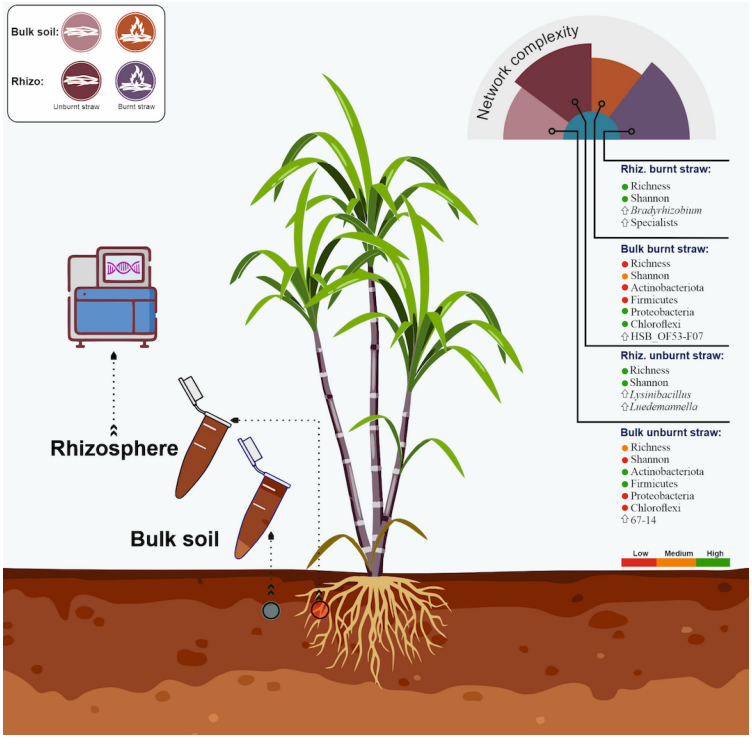
ABSTRACT

• Burning reduced Actinobacteriota and Firmicutes but increased Proteobacteria.

• Rhizosphere networks were denser, but burning reduced their overall connectivity.

• Burnt straw increased specialist and generalist taxa, especially in the rhizosphere.



Straw management significantly influences soil microbial dynamics, shaping biodiversity and resistance in agroecosystems. This study investigated how distinct straw management practices affect bacterial communities and their ecological interactions in bulk soil and the sugarcane rhizosphere. The study was conducted in an Oxisol using a split-plot design with two straw management treatments (burnt and unburnt) and two soil compartments (bulk soil and rhizosphere). Bacterial communities were characterized using 16S rRNA gene sequencing, followed by analyses of diversity, co-occurrence networks, and niche occupancy. The rhizosphere consistently exhibited higher bacterial richness and diversity, regardless of straw management. Burnt straw reduced the relative abundance of Actinobacteriota (~52%) and Firmicutes (~53%) but increased Proteobacteria (~65%) in bulk soil, whereas the rhizosphere bacterial community remained stable. Network analysis revealed higher connectivity and modularity in the rhizosphere, while burnt straw increased negative correlations and reduced microbial complexity in bulk soil. Niche occupancy analysis showed a higher proportion of specialist taxa in the rhizosphere, particularly under burnt straw. Overall, the sugarcane rhizosphere exhibited high microbial resistance to straw burning. These findings highlight the importance of sustainable straw management for preserving soil biodiversity and maintaining ecological stability in tropical cropping systems.

Keywords 16S rRNA sequencing, sugarcane straw, rhizospheric bacteriome, sustainability

1 Introduction

Modern agriculture has profoundly altered the structure and functioning of terrestrial ecosystems, particularly in tropical regions, through land-use change, intensified nutrient inputs, soil disturbance, and the simplification of biotic communities. A prominent example is the cultivation of sugarcane (*Saccharum* spp. hybrids), which occupies extensive agricultural areas and plays a key role in the global supply of sugar and ethanol (Ogura et al., 2022). However, the intensification of sugarcane production has generated serious environmental challenges that threaten the long-term sustainability of these agroecosystems (Raihan et al., 2022; Yang et al., 2024a). Among these challenges, intensive management practices such as straw burning can impair soil quality and ecosystem functioning (Pang et al., 2021; Gallo et al., 2023).

Straw burning remains a common practice in some sugarcane-producing regions, where it is used to facilitate harvesting and manage crop residues (Perillo et al., 2022). Although ash deposition can promote rapid nutrient release and temporarily stimulate ratoon regrowth (de Souza et al., 2014; Trujillo-Narcía et al., 2019), evidence suggests that straw burning disrupts soil biological activity, reduces organic carbon and nitrogen stocks, and lowers the soil C/N ratio through organic matter combustion, nutrient volatilization, and heat-induced microbial mortality (Trujillo-Narcía et al., 2019). While these impacts on soil microbial communities are increasingly well documented, most studies have focused on bulk soil responses, with limited attention to compartment-specific mechanisms that govern microbial resilience.

In contrast, straw return generally enhances soil biological integrity by improving microbial community structure and composition, particularly during the early stages following application (Suleiman et al., 2018; Xie et al., 2025). For instance, maize straw return significantly increased microbial diversity and functional potential, with the strongest effects observed after 180 days (Xie et al., 2025). Field-based evidence further indicates that straw retention and mulching regulate soil water availability, biomass allocation, straw decomposition rates, and soil organic carbon stability, whereas straw burning disrupts these linkages by accelerating carbon losses and weakening plant-soil feedbacks (Zhang et al., 2021; Wang et al., 2025). However, how these physical and biogeochemical changes translate into differential microbial responses between bulk soil and the rhizosphere under fire disturbance remains poorly understood.

Understanding how straw burning versus straw return affects microbial communities in bulk soil and the rhizosphere is therefore critical. Microorganisms drive fundamental ecosystem processes, including nutrient cycling, organic matter decomposition, and plant growth promotion (Salwan and Sharma, 2022; Bhattacharyya and Furtak, 2023). It is well established that rhizosphere microbial communities differ markedly from those in bulk soil (Yang et al., 2023a; Wei et al., 2023), as plants actively recruit and enrich beneficial microorganisms from the surrounding soil to enhance tolerance to biotic and abiotic stresses (Mendes et al., 2014; Ling et al., 2022). These interactions, largely mediated by root exudates that provide carbon sources and signaling molecules (Araujo et al., 2025), may confer a filtering or buffering capacity that stabilizes rhizosphere microbial communities under disturbance.

Here, we tested the hypothesis that straw burning induces significant shifts in bacterial community structure and composition by imposing abrupt thermal stress, accelerating organic matter loss, and altering soil physicochemical conditions, whereas straw return promotes microbial stability by maintaining soil cover, soil moisture, and carbon inputs. We further hypothesized that the rhizosphere buffers fire-induced disturbances through continuous root exudation, enhanced resource availability, and stronger plant-microbe interactions, thereby conferring greater microbial resistance than in bulk soil. By comparing bacterial communities in bulk soil and the sugarcane rhizosphere under burnt and unburnt straw conditions using 16S rRNA gene amplicon sequencing, ecological network analysis, and niche occupancy approaches, this study elucidates the mechanistic basis of rhizosphere filtering and buffering under thermal disturbance and provides insights relevant to sustainable soil management in tropical agroecosystems.

2 Materials and methods

2.1 Study site

The study was conducted during the 2023 and 2024 growing season in a sugarcane field located at Sítio Cabeceiras, Palmeira do Piauí, Brazil (8°67′74″ S, 44°25′34″ W). The regional climate is classified as tropical savanna (Aw) according to the Köppen–Geiger system, with a mean annual rainfall of approximately 900 mm and an average temperature of 30 °C. The soil was classified as a Yellow Latosol (Oxisol) according to the Brazilian Soil Classification System (SiBCS) and USDA Soil Taxonomy. The sugarcane cultivar RB036066 was grown in an area adjacent to a wetland, characterized by high soil moisture and favorable conditions for crop development.

2.2 Experimental design and treatments

The study was conducted using a randomized complete

block design arranged in a split-plot scheme with three replicates. The main plots consisted of two straw management systems applied after plant cane harvest: (i) straw retention without burning and (ii) straw removal by burning. Within each main plot, subplots were defined according to the soil microbial compartments evaluated, namely the rhizosphere and bulk soil. For both straw management systems, samples were collected from each compartment. The experimental area comprised 12 plots, with six plots under straw retention without burning and six under straw burning. In the no-burning treatment, crop residues were retained on the soil surface at a rate of 15 t ha^{-1} immediately after plant cane harvest, which occurred four months before sampling. In contrast, in the burning treatment, straw was removed by burning shortly after harvest. Each plot covered a total area of 84 m^2, consisting of six rows 10 m in length and spaced 1.4 m apart, with an effective sampling area of 56 m^2. Ratoon fertilization was performed in accordance with technical recommendations for sugarcane cultivation (Quaggio et al., 2022).

2.3 Straw burning

Straw burning is a traditional management practice historically employed in the study area across successive cropping cycles to reduce the accumulation of plant residues on the soil surface and to facilitate ratoon emergence and establishment. In the present study, straw burning was applied as a single, non-recurrent event during the experimental period. The procedure was carried out during the early morning, when relative air humidity was higher, and the ambient temperature was approximately 16 °C. These conditions allowed greater control of the burning process and minimized potential thermal impacts on adjacent experimental plots. Burn intensity was qualitatively classified as low to moderate, characterized by predominant surface straw consumption, ash deposition, and the absence of visible damage to ratoon regrowth.

2.4 Soil sampling

Soil sampling was conducted in two treatment areas: (i) unburnt and (ii) burnt. Sampling was performed approximately 120 days after the burning event, corresponding to the late tillering stage and the onset of stalk elongation in sugarcane. This period was selected because it represents a critical phase of crop development, characterized by increased root activity and intensified rhizosphere interactions (Liu et al., 2023).

Within each plot, rhizospheric soil adhering to the roots of three randomly selected plants was collected and pooled to form a composite sample. Non-rhizospheric (bulk) soil samples were collected at a depth of 0–10 cm, approximately 20 cm away from the plant roots. Sterile tools disinfected with 70% ethanol were used to prevent cross-contamination. All samples were transported in cooled containers and stored at −18 °C until analysis at the Sugarcane Breeding Program Laboratory, Federal University of Piauí (UFPI).

2.5 DNA extraction, amplification, and sequencing

Microbial DNA was extracted from 0.5 g of rhizosphere and bulk soil using the PowerLyzer® PowerSoil® DNA Isolation Kit (MoBio, Carlsbad, CA, USA), following the manufacturer's protocol. DNA extractions were performed in triplicate. DNA quality and concentration were assessed using a NanoDrop 2000 spectrophotometer (Thermo Scientific). The V4 hypervariable region of the 16S rRNA gene was amplified using primers 515F and 806R (Caporaso et al., 2011). Negative controls (no-template controls) were included in all PCR runs to monitor contamination, and amplification specificity was confirmed by agarose gel electrophoresis based on the expected amplicon size. Each PCR reaction (25 µL) contained 12.25 µL of nuclease-free water (Certified Nuclease-Free, Promega, Madison, WI, USA), 5.0 µL of 5× reaction buffer (2 mM $MgCl_2$), 0.75 µL of dNTP mix (10 mM), 0.75 µL of each primer (515F at 40 µM and 806R at 10 µM), 0.5 µL (1 U) of Platinum® Taq High Fidelity DNA Polymerase (Invitrogen, Carlsbad, CA, USA), and 2.0 µL of template DNA. A negative control (no DNA template) was included using nuclease-free water.

PCR amplification was performed with an initial denaturation at 95 °C for 3 min, followed by 35 cycles of 98 °C for 20 s (denaturation), 55 °C for 20 s (annealing), and 72 °C for 30 s (extension), with a final extension at 72 °C for 3 min. PCR products were purified using Agencourt AMPure XP beads (Beckman Coulter, Brea, CA, USA) following the manufacturer's instructions. DNA concentrations were measured with a Qubit 2.0 fluorometer (Invitrogen, Carlsbad, CA, USA) using the dsDNA BR Assay Kit (Invitrogen). Equimolar amounts of each sample were pooled, and the pooled library was diluted to 2 nM, denatured, and further diluted to a final concentration of 8.0 pM with a 20% PhiX spike-in (Illumina, San Diego, CA, USA) for sequencing on the Illumina MiSeq platform.

Raw sequence data were processed using QIIME 2 (version 2023.7.0). Sequences were demultiplexed, and quality filtering was performed with DADA2 (Callahan et al., 2017) using the consensus method to remove chimeric and low-quality reads. After filtering, approximately 1 395 000 high-quality sequences were retained, averaging ~70 000 sequences per sample. Singletons and doubletons were removed, and samples were rarefied to 47 800 reads, corresponding to the lowest sequencing depth among samples. Taxonomic assignment was performed at 97% similarity using the SILVA reference database (version 138) (Quast

et al., 2013). The resulting ASV matrix was used for downstream statistical analyses. All raw sequences have been deposited in the NCBI Sequence Read Archive under BioProject ID PRJNA1250553.

2.6 Bioinformatic and statistical analysis

The ASV table was used to calculate alpha diversity indices, including richness and the Shannon index. The data were previously evaluated for compliance with the assumptions of residual normality and homogeneity of variances, which were adequately met. Differences between unburnt and burnt straw treatments were assessed using Duncan's multiple range test at a significance level of $p < 0.05$. Relative abundances were analyzed at both the phylum and genus levels. To identify taxa differentially enriched between treatments, including potential plant growth-promoting bacteria (PGPB), Linear Discriminant Analysis Effect Size (LEfSe) was applied (Segata et al., 2011).

Community interaction complexity was evaluated using co-occurrence network analysis implemented with the WGCNA package (Langfelder and Horvath, 2008). Spearman correlation coefficients were calculated, and significant associations were retained based on thresholds of $\rho > 0.7$ (positive) or $\rho < -0.7$ (negative) and $p < 0.01$. Networks were visualized using Gephi (Bastian et al., 2009), focusing on topological properties such as the number of nodes, edges, and the proportion of positive and negative correlations. In addition, summary networks were generated using pooled data from all samples to illustrate modular structure and connection patterns at the phylum level.

Niche occupancy was assessed using the multinomial species classification test (CLAM) (Chazdon et al., 2011), which classifies taxa as generalists, specialists, or rare based on their distribution across two habitats. The analysis was performed using the clamtest function in the vegan R package, applying the supermajority rule (K = 2/3, $p < 0.005$). All diversity analyses, network calculations, and CLAM tests were conducted in R version 4.3.0 (R Core Team, 2023).

3 Results

Bacterial richness and diversity differed between bulk soil and the rhizosphere (Fig. 1A, 1B). The sugarcane rhizosphere under unburnt straw was clearly distinct from the bulk soil. Bulk soil under burnt straw exhibited the lowest bacterial richness. However, when each soil compartment was analyzed separately, no significant differences were detected between burnt and unburnt straw treatments (rhizosphere vs. rhizosphere; bulk soil vs. bulk soil). Consistently, the Shannon diversity index indicated higher bacterial diversity in the sugarcane rhizosphere compared to in bulk soil (p-value 0.007 09), regardless of straw treatment.

Actinobacteriota, Firmicutes, Proteobacteria, and Chloroflexi were the dominant phyla in both soil compartments (Fig. 2A). Straw burning reduced the relative abundance of Actinobacteriota in bulk soil but had no significant effect in the rhizosphere, where its abundance remained comparable to that under unburnt straw. Burning also decreased the relative abundance of Firmicutes in both compartments, while increasing the relative abundance of Proteobacteria and Chloroflexi. In contrast, the relative abundance of Acidobacteriota increased in bulk soil following burning but declined in the rhizosphere.

At the genus level, *Bacillus* was the most abundant taxon, followed by JG30-KF-AS9 and *IMCC26256*, with distinct distribution patterns between treatments (Fig. 2B). Overall, straw burning increased the relative abundance of *JG30-KF-AS9* (Ktedonobacterales), *IMCC26256* (Actinomycetes), and *Acidothermus* in bulk soil, while reducing the abundance of *67-14* (Solirubrobacterales) and *KD4-96* (Ktedonobacterales). Under unburnt straw retention, bulk soil was enriched in *67-14* and *Ammoniphilus*, whereas the rhizosphere was enriched in *Lysinobacillus* and *Luedemannella*

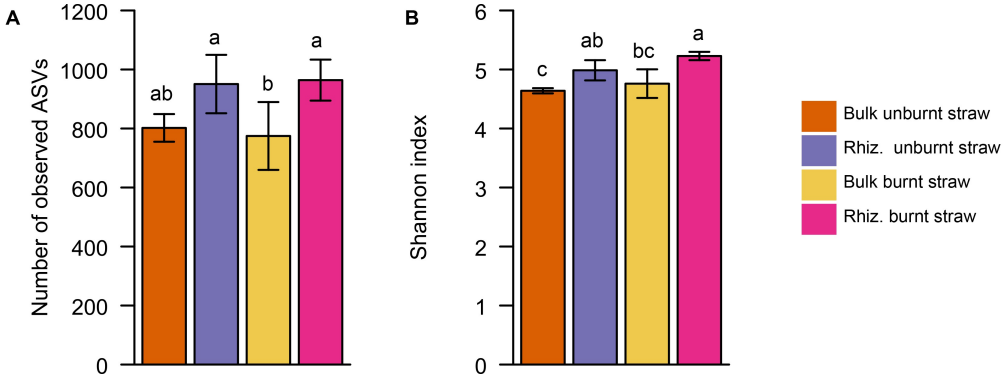


Fig. 1 Alpha diversity of prokaryotic communities in bulk soil and the sugarcane rhizosphere under unburnt straw retention and burnt straw. (A) Richness and (B) Shannon diversity of prokaryotic communities. Different lowercase letters indicate statistically significant differences according to Duncan's test ($p < 0.05$).

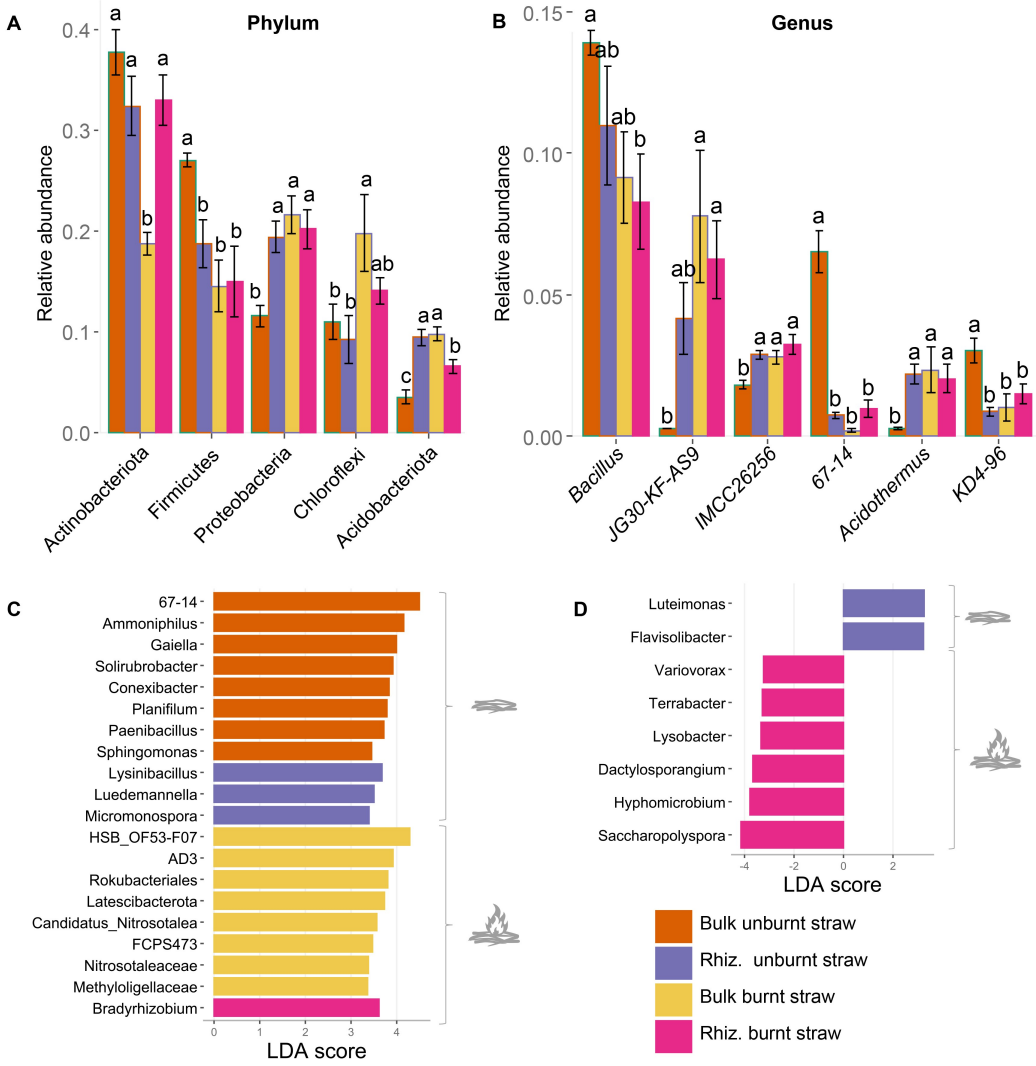


Fig. 2 Composition and differential abundance of dominant taxa in sugarcane under unburnt straw retention and burnt straw. Relative abundance at the phylum (A) and genus (B) levels. Linear Discriminant Analysis Effect Size (LEfSe) (C) of the main prokaryotic taxa enriched in bulk soil and rhizosphere, and (D) major plant growth-promoting bacteria enriched in the rhizosphere.

(Fig. 2C). Under burnt straw conditions, *HSB_OF53_F07* (Ktedonobacterales) was enriched in bulk soil, while *Bradyrhizobium* predominated in the rhizosphere. When comparing rhizospheric communities between treatments, *Luteimonas* and *Flavisolibacter* were enriched under straw retention, whereas *Saccharopolyspora* and *Hyphomicrobium* were more abundant under burnt straw (Fig. 2D).

Co-occurrence network analysis revealed that the rhizosphere harbored a higher number of nodes and connections (edges) than bulk soil (Fig. 3A; Table S1). Under burnt straw conditions, both soil compartments exhibited an increased number of nodes but a lower average degree (i.e., fewer connections per node), indicating reduced network complexity compared with unburnt straw. In addition, the bulk soil network under burnt straw displayed a higher proportion of negative correlations and a larger network diameter, together with decreases in average degree and clustering coefficient. Modularity analysis identified 52 distinct modules of varying sizes and compositions (Fig. 3B), with modules M1 and M2 being the most representative, accounting for 12.71% and 12.43% of the network, respectively. At the phylum level (Fig. 3C), major bacterial groups such as Actinobacteriota (~250 connections), Proteobacteria (~140), Firmicutes (~120), and Chloroflexi (~90) exhibited the highest connectivity, highlighting their central positions within the microbial interaction network.

Niche occupancy analysis using the CLAM model revealed contrasting patterns between treatments in both soil compartments (Fig. 4). The rhizosphere exhibited a higher proportion of specialist taxa than bulk soil, particularly under burnt straw conditions (Fig. 4A, 4B). In both compartments, straw burning increased the proportion of generalist taxa relative to unburnt straw. In bulk soil, burning also increased the proportion of specialist taxa compared with

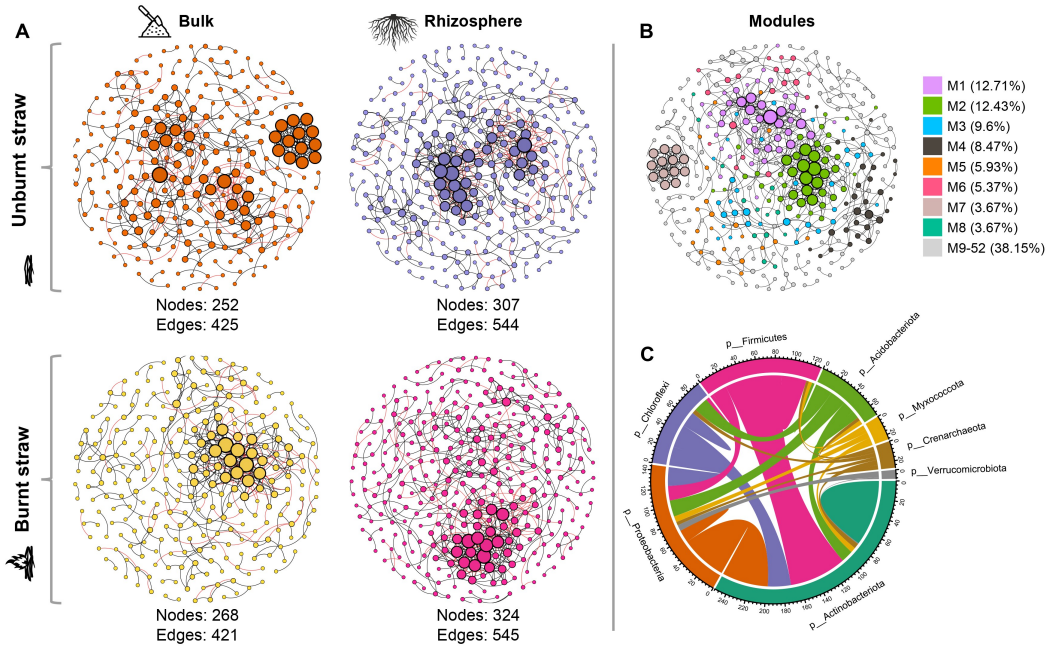


Fig. 3 Co-occurrence network analysis of the prokaryotic community in sugarcane soil under unburnt straw retention and burnt straw. (A) Networks of bulk soil and rhizosphere, with node size representing the number of connections and edges indicating positive (black) and negative (red) correlations; (B) Overall network showing modules differentiated by color and their respective connectivity; (C) Number of connections at the phylum level.

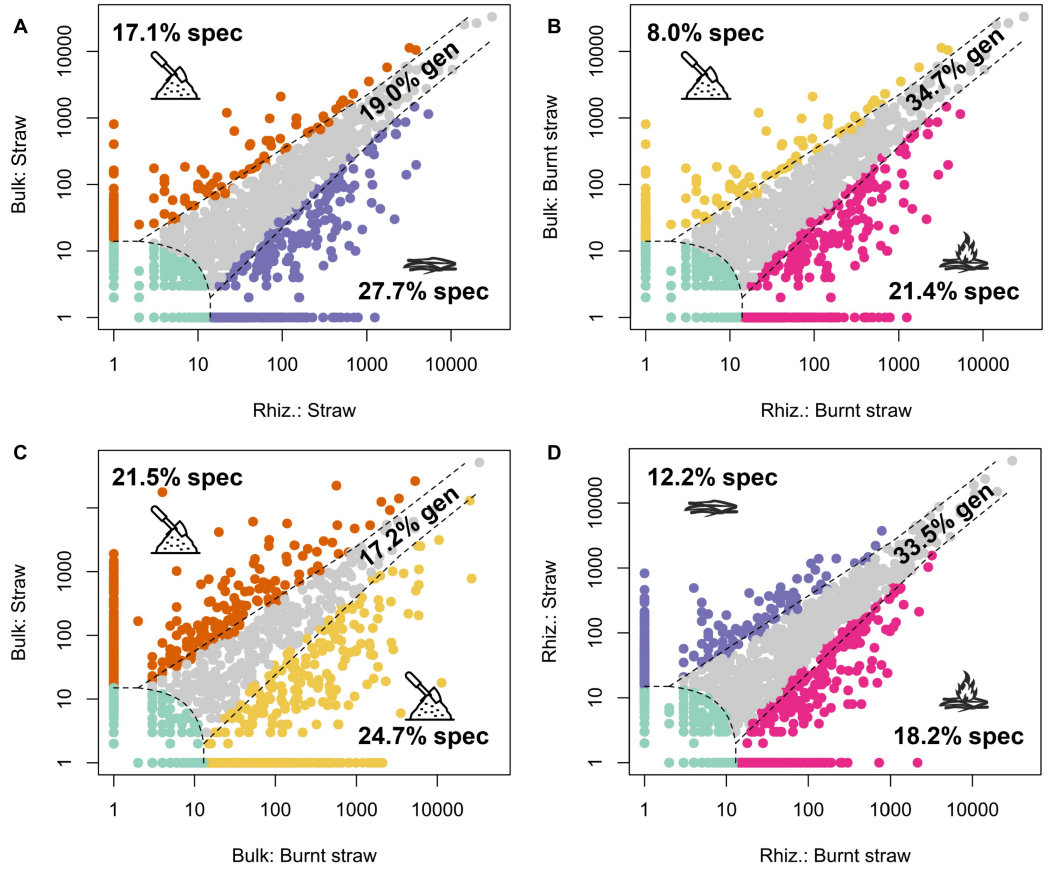


Fig. 4 Niche occupancy of the prokaryotic community in sugarcane soil under unburnt straw retention and burnt straw. (A) Comparison between bulk soil and rhizosphere under unburnt straw; (B) Comparison between bulk soil and rhizosphere under burnt straw; (C) Comparison between unburnt and burnt straw in bulk soil; (D) Comparison between unburnt and burnt straw in the rhizosphere.

straw retention (Fig. 4C). Similarly, within the rhizosphere, burnt straw enhanced the proportion of specialists, although both rhizospheric communities maintained a high representation of generalist taxa (Fig. 4D).

4 Discussion

This study examined how straw burning versus straw retention influences the composition, diversity, and ecological interactions of bacterial communities in the sugarcane rhizosphere and bulk soil. By integrating 16S rRNA gene sequencing with ecological network and niche occupancy analyses, we evaluated the extent of microbial resistance (stability) and explored the mechanisms underlying community stability under contrasting straw management practices.

Our findings indicate that the sugarcane rhizosphere maintained microbial stability at a single sampling time point despite the disturbance imposed by straw burning. Although straw burning substantially altered the structure and composition of bacterial communities in bulk soil, the rhizosphere remained comparatively stable. This pattern supports the hypothesis that straw management exerts distinct effects on bulk soil and the rhizosphere. The relative stability of rhizosphere bacterial communities suggests that this compartment, characterized by intense root-microbe interactions and continuous root exudation, functions as a biological buffer against environmental disturbance, maintaining a more stable microbial assemblage (Mendes et al., 2018; Ling et al., 2022; Marschmann et al., 2024). This buffering capacity is consistent with concepts of rhizosphere habitat filtering and ecological insurance, whereby plants selectively enrich adapted taxa and promote community stability under stress (Araujo et al., 2025). Beyond altering organic matter inputs, straw management also modifies soil physical conditions that regulate microbial responses to disturbance. For example, straw incorporation improves soil structure, nutrient availability, moisture retention and moderates soil temperature, thereby creating a more stable hydrothermal environment for plants and soil biota (Suleiman et al., 2018; Indoshi et al., 2025). Such physical buffering likely contributes to the greater microbial resistance observed in rhizosphere communities, where root activity further stabilizes microhabitats. In contrast, straw burning removes this protective layer, exposing bulk soil to greater thermal and moisture fluctuations and amplifying microbial community reorganization. Accordingly, the greater sensitivity of bulk soil communities to burning reinforces our second hypothesis that the rhizosphere microbiome exhibits higher resistance (stability) to disturbance.

When soil compartments were analyzed separately, straw management did not significantly affect bacterial richness or diversity, in agreement with previous studies (Zheng et al., 2018; Liu et al., 2021; Wang et al., 2023). Nevertheless, burnt straw was associated with lower richness and diversity in bulk soil relative to the rhizosphere, underscoring the stabilizing role of plant–microbe interactions and the dynamic physicochemical gradients characteristic of the rhizosphere (Gao et al., 2024).

Both straw-burning and straw-return practices induced pronounced shifts in microbial composition and relative abundance. Actinobacteriota, Firmicutes, Proteobacteria, and Chloroflexi dominated across treatments, consistent with their well-established roles in organic matter decomposition, phytohormone production, and nutrient cycling (Aguilar-Paredes et al., 2023). Straw burning reduced the relative abundance of Actinobacteriota in bulk soil, likely reflecting changes in soil physicochemical conditions such as increased pH, electrical conductivity, and nutrient availability following combustion (Arunrat et al., 2023). These conditions tend to favor copiotrophic and stress-tolerant groups, including Proteobacteria and Chloroflexi.

Although Firmicutes include many thermotolerant taxa, their relative abundance also declined after burning, in agreement with previous studies showing that Firmicutes often increase immediately after fire events but decrease over short timescales as post-fire conditions evolve (Bukar et al., 2019; Arunrat et al., 2024). Collectively, these patterns suggest a transient microbial response to burning, characterized by the initial proliferation of fire-tolerant taxa followed by rapid community reorganization as soil conditions stabilize. Although soil physicochemical properties were not directly measured in this study, fire-induced changes in temperature, nutrient availability, and soil chemistry likely contributed to the observed taxonomic shifts.

Under straw retention, the rhizosphere was enriched in *Luteimonas* and *Flavisolibacter*, genera that have been associated with plant-beneficial functions, including phytohormone production (*Luteimonas*) and biological nitrogen fixation (*Flavisolibacter*) (Domínguez-Castillo et al., 2021; Bender et al., 2022). In contrast, straw burning favored stress-adapted taxa such as *Saccharopolyspora* and *Hyphomicrobium* in the rhizosphere. *Saccharopolyspora* is known to thrive in extreme or post-fire environments and to produce antimicrobial secondary metabolites, whereas *Hyphomicrobium* plays key roles in nitrogen cycling and methanol degradation (Shivlata and Satyanarayana, 2015; Bertrand et al., 2023; Wang et al., 2024).

Similarly, bulk soil under burnt straw was enriched in *JG30-KF-AS9*, *IMCC26256*, and *Acidothermus*, suggesting tolerance to thermal stress and the capacity to exploit resources released following combustion (Arunrat et al., 2023; Tomazelli et al., 2023; Yang et al., 2023b; Leite et al., 2024; Orth et al., 2025; Zhang et al., 2025).

Co-occurrence network analyses revealed clear differences in microbial interaction patterns between the rhizosphere

and bulk soil, reinforcing the role of root activity in shaping microbial network complexity. In this context, lower network complexity refers to a reduction in connectivity-related metrics, particularly a lower average degree, indicating fewer interactions per taxon. Although straw burning increased the number of nodes in bulk soil networks, the reduced average degree suggests that a greater number of taxa were connected through fewer edges, resulting in sparser and more fragmented networks with diminished interaction density and functional integration (Papatheodorou et al., 2023). Modularity analysis further showed the presence of 52 distinct modules, reflecting high modularity and network compartmentalization. While increased modularity is often associated with enhanced resilience to disturbance, it also implies reduced cross-module connectivity and limited information or resource flow across the network (Guo et al., 2022; Yang et al., 2024b; Idbella et al., 2025). At the phylum level, Proteobacteria, Actinobacteriota, and Firmicutes accounted for most interactions, highlighting their high node degree and centrality and underscoring their key roles in maintaining network cohesion and nutrient cycling (Wongkiew et al., 2022; Yang et al., 2024b).

Niche occupancy analysis further highlighted contrasting ecological responses of microbial communities to straw burning (Fig. 4). The rhizosphere consistently harbored a higher proportion of specialist taxa, particularly under burnt straw conditions, likely reflecting the stability of rhizosphere microhabitats and the continuous supply of resources mediated by root exudation (Du et al., 2025; Liu et al., 2025). Straw burning also increased the proportion of generalist taxa across both soil compartments, suggesting that fire-induced disturbance generates novel or transient niches that can be exploited by microorganisms with broad ecological tolerances (Papatheodorou et al., 2023).

In bulk soil, burnt straw increased the proportion of specialist taxa relative to straw retention, whereas in the rhizosphere, the proportion of specialists also increased, but generalists remained dominant. Together, these patterns indicate a reorganizing system in which rhizosphere stability favors the persistence of specialist taxa, while disturbance promotes opportunistic colonizers with broader niche breadths. This dynamic supports the concept of a microbial buffering effect mediated by root activity (Papatheodorou et al., 2023; Du et al., 2025).

These results demonstrate that straw burning alters bacterial community structure, niche organization, and diversity patterns in sugarcane soils. In contrast, the rhizosphere functions as a critical ecological buffer, sustaining highly connected and taxonomically important taxa that remain comparatively stable under disturbance at the time of sampling. Together, these findings reinforce the pivotal role of root-associated microbiomes in maintaining soil health and underscore the importance of minimizing fire disturbance through sustainable straw management. Such practices may enhance microbial stability and contribute to the long-term resilience and productivity of tropical agroecosystems.

As a limitation, this study assessed the bacterial community at a single time point, which allows inference on community resistance or stability but does not permit evaluation of true resilience. In addition, soil physicochemical properties were not directly measured, limiting our ability to mechanistically link fire-induced changes in temperature, moisture, pH, nutrient availability, or electrical conductivity to the observed shifts in bacterial community structure. The analysis also focused exclusively on bacteria using 16S rRNA gene sequencing and therefore did not capture potential responses of fungi or archaea, which play key roles in organic matter decomposition, nutrient cycling, and post-fire soil recovery. Furthermore, straw burning was treated as a management practice but was not characterized in detail in terms of fire intensity, duration, or spatial heterogeneity, factors known to strongly influence microbial mortality and recolonization dynamics.

To address these limitations, future studies should adopt time-series sampling designs to explicitly quantify microbial resilience and recovery trajectories following straw burning and straw retention. Integrating ITS sequencing for fungi and archaeal markers would provide a more comprehensive view of soil microbiome responses to fire-related disturbances. Moreover, metagenomic approaches or enzyme-based functional assays would enable direct assessment of functional potential and activity, overcoming the constraints of taxonomic inference based solely on 16S rRNA data. Finally, validating these patterns across multiple soil types, climatic regions, sugarcane cultivars, and management histories will be essential to assess the generality of rhizosphere buffering mechanisms and to inform sustainable straw management strategies in tropical agroecosystems.

5 Conclusion

This study provides clear evidence that the sugarcane rhizosphere exhibits high microbial resistance (stability) to straw burning. Despite pronounced structural and compositional shifts in bulk soil, the rhizosphere maintained stable bacterial diversity, community composition, and network connectivity. In contrast, straw burning disrupted bulk soil communities, resulting in less cohesive and more competitive network structures dominated by stress-tolerant taxa. The rhizosphere, therefore, functioned as an ecological buffer, preserving microbial stability and maintaining modular organization. Overall, these findings demonstrate that straw management practices differentially influence bacterial community structure and stability in bulk soil and the rhizosphere.

Electronic supplementary material

Supplementary material is available in the online version of this article at https://doi.org/10.1007/s42832-026-0436-1 and is accessible for authorized users.

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Conflicts of interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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