

Growth stage as the main drive over genotype and plant growth-promoting bacteria on bacterial communities in the rhizosphere of prickly-pear cactus

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ABSTRACT

Despite its strategic importance for food security in semiarid regions, no studies have assessed the rhizosphere microbiome of the prickly-pear cactus (*Nopalea cochenillifera*) and how its growth stage, bacterial inoculation, and genotypes may shape the rhizosphere. Thus, the aim of this study was to assess diversity, composition, and enrichment of bacterial communities in the rhizosphere of the prickly-pear cactus genotypes 'Baiana' and 'Doce', both with and without inoculation with *Bacillus subtilis* and *Paenibacillus* sp., at 90 and 270 days of growth. In this study we cultivated samples rhizospheric soil, extracted DNA, and assessed the bacterial communities by 16S rRNA amplicon sequencing by Illumina platform. The bacterial communities in the rhizosphere were significantly driven by plant growth stage and showed high diversity, while both inoculation and genotype showed lower effects. Key bacterial phyla typical of semiarid regions were predominant, including Actinobacteriota, Proteobacteria, and Firmicutes. Enrichment patterns of bacterial genera shifted with plant growth, with *Streptomyces* and *Bradyrhizobium* predominating at 90 days, and *Bacillus* and *Gaiella* at 270 days. PGPB inoculation further shaped specific taxa, while non-inoculated plants showed distinct enrichment over time. This study showed that the bacterial communities in the rhizosphere of *N. cochenillifera* was primarily shaped by plant growth stage, with key bacterial groups potentially associated to stress tolerance which provide important insights into soil microbial ecology in semiarid regions.

1. Introduction

In semi-arid regions, cactus cultivation represents a valuable strategy for supporting animal production during drought periods. This plant species presents high adaptability to semi-arid regions and contains high nutritional value, which is important to support animal production (Araújo Júnior et al., 2023). Particularly, the prickly-pear cactus (*Nopalea cochenillifera*) has been used as forage in semiarid regions,

mainly due to its nutritional value compared to other prickly-pear species (Dubeux Jr et al., 2021). On the other hand, the productivity of *N. cochenillifera* can vary significantly across genotypes, reflecting both genetic potential and adaptive traits (Alves et al., 2016). In addition, each genotype has specific morphological traits, such as root growth, which may influence microbial communities associated with the rhizosphere (Xie et al., 2023).

The rhizosphere is the narrow soil zone surrounding plant roots,

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where root traits drive microbial communities (Yang et al., 2024). Thus, assessing the rhizosphere microbiome of cactus is essential to understand how plant traits interact with soil microorganisms and shape beneficial associations. Previous studies have already assessed the microbial communities associated with different cactus species, such as *Opuntia cholla* (Manríquez-Rivera et al., 2025), *Echinocactus platyacanthus* (Estrada-González et al., 2023), *Pereskia aculeata* (Vega et al., 2020), *Cereus jamacaru* (Kavamura et al., 2018), *Myrtillocactus geometrizans*, *Opuntia robusta* (Fonseca-García et al., 2016), and *Opuntia ficus-indica* (Lyra et al., 2021). These studies showed the ecological importance of the rhizosphere microbiome and its potential role in stress adaptation, nutrient acquisition, and plant performance.

However, the rhizosphere microbiome of *N. cochenillifera* remains poorly understood, particularly when comparing genotypes and growth periods. It is known that rhizosphere–microbes interaction is strongly shaped by host-related factors, including genotype and growth stage (Han et al., 2025). These differences in growth stage and genotypes have been shown to influence root exudation patterns which play a central role in selecting and recruiting rhizosphere microorganisms (Araújo et al., 2025). For instance, Han et al. (2025) found that distinct soybean genotypes shaped rhizosphere microbial communities, with shifts across developmental stages. Beyond these factors, the inoculation of plant growth-promoting bacteria (PGPB) can modulate rhizosphere communities (Vuolo et al., 2022; Cheng and Ma, 2025). For instance, Cheng and Ma (2025) inoculated PGPB in maize and found that inoculation enhanced beneficial bacteria and microbial interactions in the rhizosphere. These PGPB directly promote plant growth, while indirectly altering microbial assembly through competition with native taxa and enrichment of beneficial microorganisms (Kampouris et al., 2025).

In this context, we propose two hypotheses for this study: a) the bacterial communities in the rhizosphere of *N. cochenillifera* differs significantly comparing genotypes and growth period; and b) the inoculation of PGPB shapes the composition and interactions of the bacterial

communities in the rhizosphere of *N. cochenillifera*. Therefore, the aim of this study was to investigate the bacterial communities in the rhizosphere of *N. cochenillifera* (genotypes ‘Baiana’ and ‘Doce’) under inoculation with *Bacillus subtilis* and *Paenibacillus* sp. The rhizosphere was evaluated at two growth stages, i.e., early (90 days) and late (270 days) stages, to assess how microbial diversity, community composition, and enrichment patterns are influenced by genotype, plant growth stage, and PGPB inoculation.

2. Materials and methods

2.1. Study area

This field-study with prickly-pear cactus was conducted at the Campus Prof. Cinobelina Elvas from Federal University of Piauí, located in Bom Jesus, Piauí State (9° 4′ 30″ S, 44° 21′ 26″ W). The predominant soil is classified as Oxisol (USDA Soil Taxonomy; Soil Survey Staff, 2022) which presents 17 % clay, 5 % silt, and 78 % sand. Soil chemical properties were assessed by Teixeira et al. (2017) at the beginning of the study (Table S1). During the study, the climatic conditions were recorded (Fig. 1).

2.2. Experimental design and planting

The experiment followed a completely randomized design in a split-split plot arrangement (2 × 3 × 2), with three replications. The main plot factor was the growth stage of the prickly-pear cactus, evaluated at 90 and 270 days after planting. The subplot factor corresponded to PGPB inoculation treatments, which included non-inoculated control, inoculation with *Bacillus subtilis* (strain IPA-CC29), and inoculation with *Paenibacillus* sp. (strain IPA-CC38). The sub-subplot factor consisted of two cactus genotypes, *Nopalea cochenillifera* ‘Baiana’ and ‘Doce’. These strains were used in previous experiments (Aquino et al., 2019), and

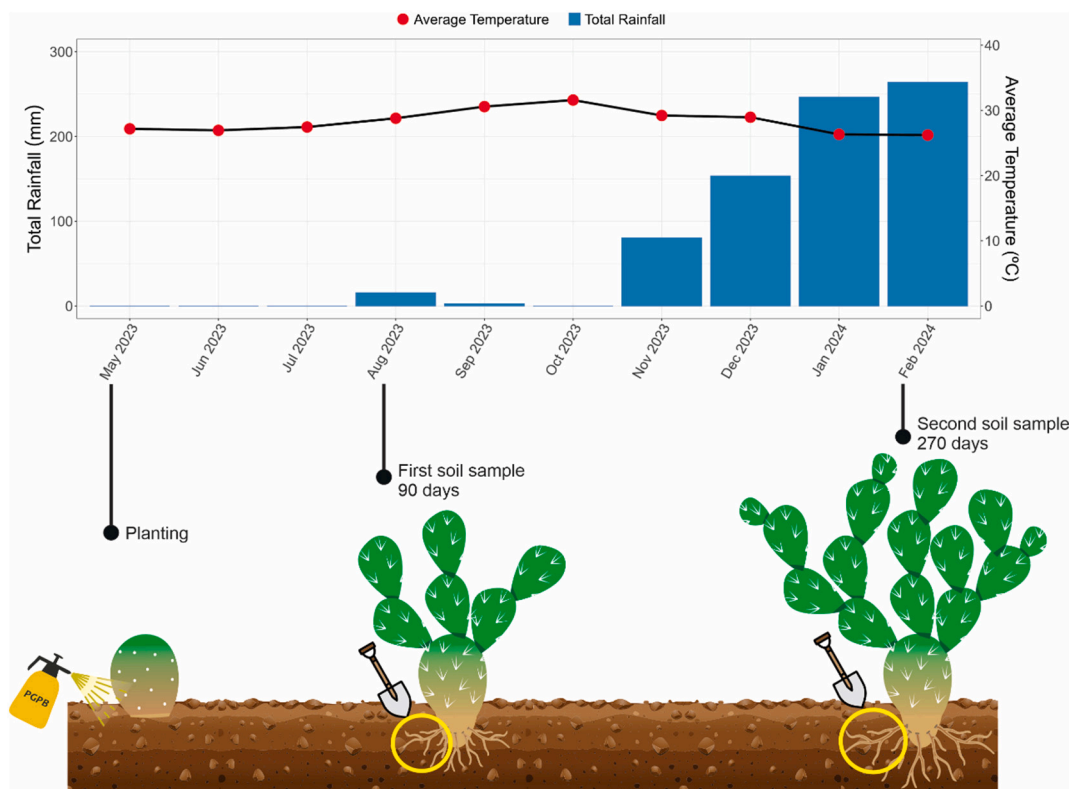


Fig. 1. Climatic conditions during rhizosphere soil sampling of prickly-pear cactus genotypes ‘Baiana’ and ‘Doce’, both non-inoculated and inoculated with *Bacillus subtilis* and *Paenibacillus* sp., at 90 and 270 days of growth.

their growth-promoting characteristics include the production of indole-3-acetic acid (IPA-CC29: 1.41 mg L⁻¹; IPA-CC38: 1.13 mg L⁻¹) and acetylene-reducing activity (IPA-CC29: 5.03 nmol C₂H₄ h⁻¹; IPA-CC38: 7.10 nmol C₂H₄ h⁻¹).

To obtain the PGPB inoculants, *B. subtilis* and *Paenibacillus* sp were grown in Erlenmeyer flasks containing 50 mL of liquid medium (Tryptone Soy Broth) and incubated in a rotatory shaker (200 rpm; 31 °C) for 72 h. Bacterial growth was assessed by measuring optical density (OD) at a wavelength of 540 nm using a spectrophotometer. An OD₅₄₀ of approximately 0.8–1.0 corresponded to a bacterial density of about 10⁸ CFU mL⁻¹ (Cappuccino and Sherman, 2014). The planting was done using one cladode per hole, with a spacing of 0.75 × 0.50 m. After planting, the inoculation of *B. subtilis* and *Paenibacillus* sp was performed by spraying the liquid inoculant diluted in water at a 5:1 ratio directly in the root area (Fig. 1).

2.3. Soil sampling, DNA extraction and sequencing

The sampling was conducted in the same prickly-pear cactus cultivation area at two different stages, at 90 and 270 days of plant development. A total of 36 samples were collected and rhizospheric soil samples were obtained by using a spade to remove the roots from the soil and collected with a stainless-steel spatula, while preserving the plant structure as much as possible. All equipment used for sampling was previously sterilized with 70 % alcohol. Bulk soil samples were also collected from the interplot corridor at depths of 0–10 cm.

After the collection of rhizospheric soil samples, all samples were stored at –20 °C in a freezer and subsequently sent to the Soil Microbiology Laboratory of the Sugarcane Breeding Program at the Federal University of Piauí (PMGCA-UFPI/RIDESA), where microbial DNA was extracted.

Microbial DNA was extracted from rhizosphere and bulk soil samples using 0.5 g of each sample with the PowerLyzer PowerSoil DNA Isolation Kit (MoBio Laboratories, Carlsbad, CA, USA), following the manufacturer's protocol. DNA quality and concentration were assessed using a NanoDrop 2000 spectrophotometer (Thermo Scientific, Waltham, MA, USA). The V4 hypervariable region of the 16S rRNA gene was amplified using region-specific primers 515F and 806R (Caporaso et al., 2011). Each 25 µL PCR reaction contained 12.25 µL of nuclease-free water (Certified Nuclease-Free, Promega, Madison, WI, USA), 5.0 µL of 5× reaction buffer (MgCl₂ 2 mM), 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 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 conditions consisted of an initial denaturation at 95 °C for 3 min, followed by 35 cycles of denaturation at 98 °C for 20 s, annealing at 55 °C for 20 s, and extension at 72 °C for 30 s. A final extension step was carried out at 72 °C for 3 min. Following amplification, PCR products were purified using Agencourt AMPure XP beads (Beckman Coulter, Brea, CA, USA) as per the manufacturer's instructions. DNA concentrations were quantified with the 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.

2.4. Statistical analysis

The sequences were submitted to the NCBI Sequence Read Archive under the identification PRJNA1367571. Raw sequence data were processed using QIIME 2 version 2023.7.0. Sequences were demultiplexed, and quality filtering was performed with DADA2 (Callahan and McMurdie, 2017), using the consensus method to remove chimeric and low-quality reads. Taxonomic assignment was performed at 100 %

similarity against the SILVA reference database (version 138) (Quast et al., 2013), resulting in an ASV table. The generated table contained 10,855,758 (ten million, eight hundred fifty-five thousand, seven hundred fifty-eight) sequences; however, after rarefaction (based on the lowest sample size), the total number of sequences was reduced to 4,173,156 (four million, one hundred seventy-three thousand, one hundred fifty-six).

The generated table was loaded into the Microeco package (version 1.13.0) of the RStudio software, version 4.4.1 (R Core Team, 2021), after which beta diversity, alpha diversity, microbial community composition, enrichment, and hierarchical abundance were analyzed. Figures were also generated in RStudio using the ggplot package (version 3.5.1; Wickham, 2016).

Beta diversity was assessed through the structure of the microbial community, examined using Principal Component Analysis (PCA). Additionally, PerMANOVA was conducted to evaluate differences among the factors. Alpha diversity was assessed using observed ASV values and the Shannon diversity index. Means were compared using the Wilcoxon test with a significance level of 0.05. To illustrate the microbial community composition at the phylum level, a Venn diagram was generated, and mean values were compared using analysis of variance (ANOVA) followed by Duncan's test, with a significance level of 0.05. Enrichment was evaluated using Linear Discriminant Analysis Effect Size (LEfSe) to identify differentially abundant taxa at the genus level that characterize and distinguish microbial communities across the studied factors (Segata et al., 2011). Hierarchical taxonomic abundance analysis was performed to determine which taxa at the class level predominated within each phylum in the community for each studied factor.

3. Results

PCA analysis showed that the two sampling periods (90 and 270 days) clustered into distinct bacterial groups (PERMANOVA <0.05) (Fig. 2A). At 90 days, neither PGPB nor genotype significantly affected the bacterial communities (PERMANOVA *p* > 0.05), although bulk soil clustered separately from rhizosphere samples (Fig. 2B). At 270 days, only PGPB inoculation had a significant effect (PERMANOVA *p* < 0.05), but group separation in the PCA was partial (*R*² = 25 %) (Fig. 2C). Bacterial richness and diversity were significantly higher at 90 days than at 270 days (*p* < 0.001; Fig. 3). Within each period, no significant differences were observed for genotype (*p* > 0.05).

The five dominant bacterial phyla in the rhizosphere were *Actinobacteriota*, *Proteobacteria*, *Firmicutes*, *Chloroflexi*, and *Acidobacteriota* (Fig. 4; Fig. S1). Period-dependent differences were detected (*p* < 0.05): *Proteobacteria*, *Acidobacteriota*, *Planctomycetota*, *Crenarchaeota*, *Mycococota*, *Verrucomicrobiota*, and *Gemmatimonadota* were more abundant at 90 days, while *Actinobacteriota* and *Chloroflexi* predominated at 270 days. *Firmicutes* showed no significant change. PGPB inoculation and genotype did not significantly influence phylum-level composition within periods (*p* > 0.05).

At the genus level, enrichment patterns also varied over time (Fig. 5A). At 90 days, *Streptomyces*, *Sphingomonas*, *Mycobacterium*, *Microvirga*, and *Bradyrhizobium* predominated; at 270 days, the most enriched genera were 67–14, *Bacillus*, *Gaiella*, *Glitter-GS-136*, and *Ammoniphilus*. PGPB inoculation influenced specific taxa (Fig. 5B and C). In *B. subtilis*-inoculated plants, *Nitrososphaeraceae*, *Candidatus Udaeobacter*, *SC-I-84*, *C0119*, and *WD2101_soil_group* were enriched at 90 days, while only *Mycobacterium* was enriched at 270 days. In *Paenibacillus* sp.-inoculated plants, enrichment occurred for *Chloroplast* at 90 days and for *JG30-KF-CM66*, *Iamia*, *Rubellimicrobium*, *OLB14*, and *Ellin6067* at 270 days. In non-inoculated plants, *Hyphomicrobium* was enriched at 90 days, whereas *Sinomonas*, *Burkholderia-Caballeronia-Paraburkholderia*, and *WWH38* predominated at 270 days.

Genotype-specific enrichment was observed (Fig. 5D and E). In the 'Baiana' genotype, the genera *Gemmatimonas*, *Fimbrioglobus*, *mle1-27*, *Clostridium_sensu_stricto_13*, and *Kineococcus* were enriched at 90 days,

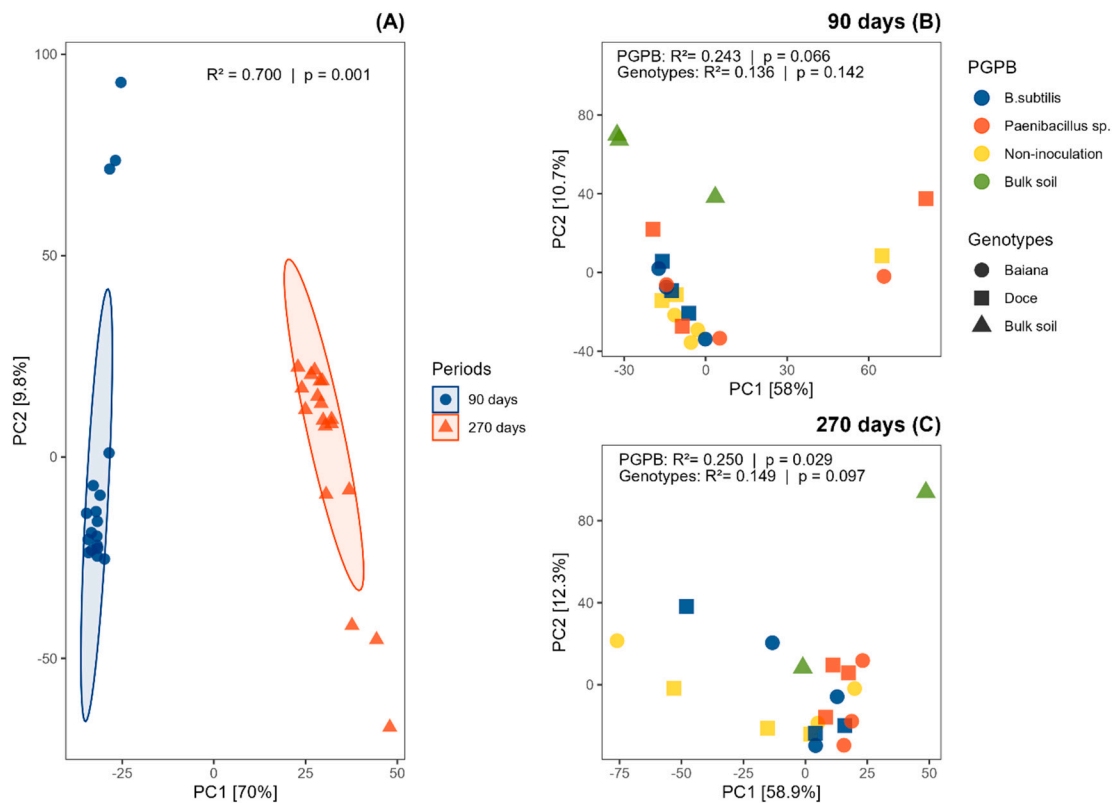


Fig. 2. Beta diversity of rhizosphere microbial communities of prickly-pear cactus genotypes ‘Baiana’ and ‘Doce’, both non-inoculated and inoculated with *Bacillus subtilis* and *Paenibacillus* sp., at 90 and 270 days of growth.

whereas *Sumerlaea*, *Roseateles*, *Dyadobacter*, and *Clostridium_sensu_stricto_13* were enriched at 270 days. In the ‘Doce’ genotype, *Dyella* was the most enriched genus at 90 days and *Tumebacillus*, *Azospirillum* and *Myxococcus* at 270 days.

Class-level hierarchical analysis showed the most abundant taxa within the dominant phyla (Fig. 6). *Alphaproteobacteria* and *Gammaproteobacteria* dominated *Proteobacteria*, with *Alphaproteobacteria* more abundant. *Actinobacteriota* was primarily composed of *Acidimicrobiia* and *Actinobacteria*, with the latter predominating. *Bacilli* dominated *Firmicutes*; *Acidobacteriae* dominated *Acidobacteriota*, and *Chloroflexia* was most abundant in *Chloroflexi*.

4. Discussion

4.1. Growth stage prevails over genotype and inoculation in shaping the bacterial communities in the rhizosphere of *N. cochenillifera*

This is the first study assessing the bacterial communities in the rhizosphere of two prickly-pear cactus genotypes belonging to *N. cochenillifera*, which were inoculated with PGPBs and assessed at early (90 days) and late (270 days) stages of plant growth under field conditions in the semi-arid region. Our results partly confirm the proposed hypotheses showing that the bacterial communities in the rhizosphere of *N. cochenillifera* were not significantly shaped by genotype at the community level, although specific genera were genotype-enriched, indicating a limited genotypic effect. In contrast, PGPB inoculation influenced bacterial composition only at 270 days, supporting a stage-dependent effect on certain taxa. Thus, we observed a temporal effect on microbiome structure, while genotype and inoculation drove specific microbial groups. However, it is important to note that precipitation differed between the two sampling periods (Fig. 1), which may have influenced soil moisture and consequently affected microbial activity and community composition. Therefore, this environmental variation

should be considered as a potential confounding factor when interpreting the effect of growth stage.

The results showed that the growth period significantly drives the rhizosphere microbiome in prickly-pear cactus. This means that the rhizosphere environment changes as the plant develops with changes in microbial colonization. Thus, in early stages of plant growth, the root exudation is more diverse and abundant (Liu et al., 2024), providing a variety of carbon sources that favor specific microbial groups. For instance, young roots release high concentrations of sugars, amino acids, and organic acids (e.g., malate, citrate), which selectively enrich copiotrophic bacteria such as *Pseudomonas*, *Bacillus*, and *Rhizobium* (Upadhyay et al., 2022a, b). On the other hand, during later plant stages, i.e., mature plants, the root exudation is more stable, as roots become more lignified (Hafner et al., 2025), which favor other specific microbial groups. At the later stage, the release of more complex compounds such as phenolics, terpenoids, and lignin-derived aromatics tends to increase, supporting oligotrophic and decomposer taxa including *Actinobacteria* and *Chloroflexi* (Chaparro et al., 2013). These results confirm that plant growth stage is a dominant driver of microbiome structure (Pantigoso et al., 2020; Lopes et al., 2023).

Previous studies with *N. cochenillifera* genotypes (‘Doce’ and ‘Baiana’) reported different levels of primary and secondary metabolites in cladodes, which varied according to seasonality and phenological stage (Alves et al., 2017; Pessoa et al., 2024). Such variation extends to root exudates, as metabolic allocation patterns shift across development, influencing the type and concentration of compounds secreted below-ground. These variations may influence root deposition, which accounts for approximately 5–21 % of photosynthetic products (Upadhyay et al., 2022a, b), potentially explaining the differences in the bacterial communities in the rhizosphere observed in our study. Indeed, in cacti (*Cereus jamacaru*), Kavamura et al. (2013, 2018) found distinct microbiome structures when comparing two different growth periods, attributing part of this shift to stage-dependent changes in root

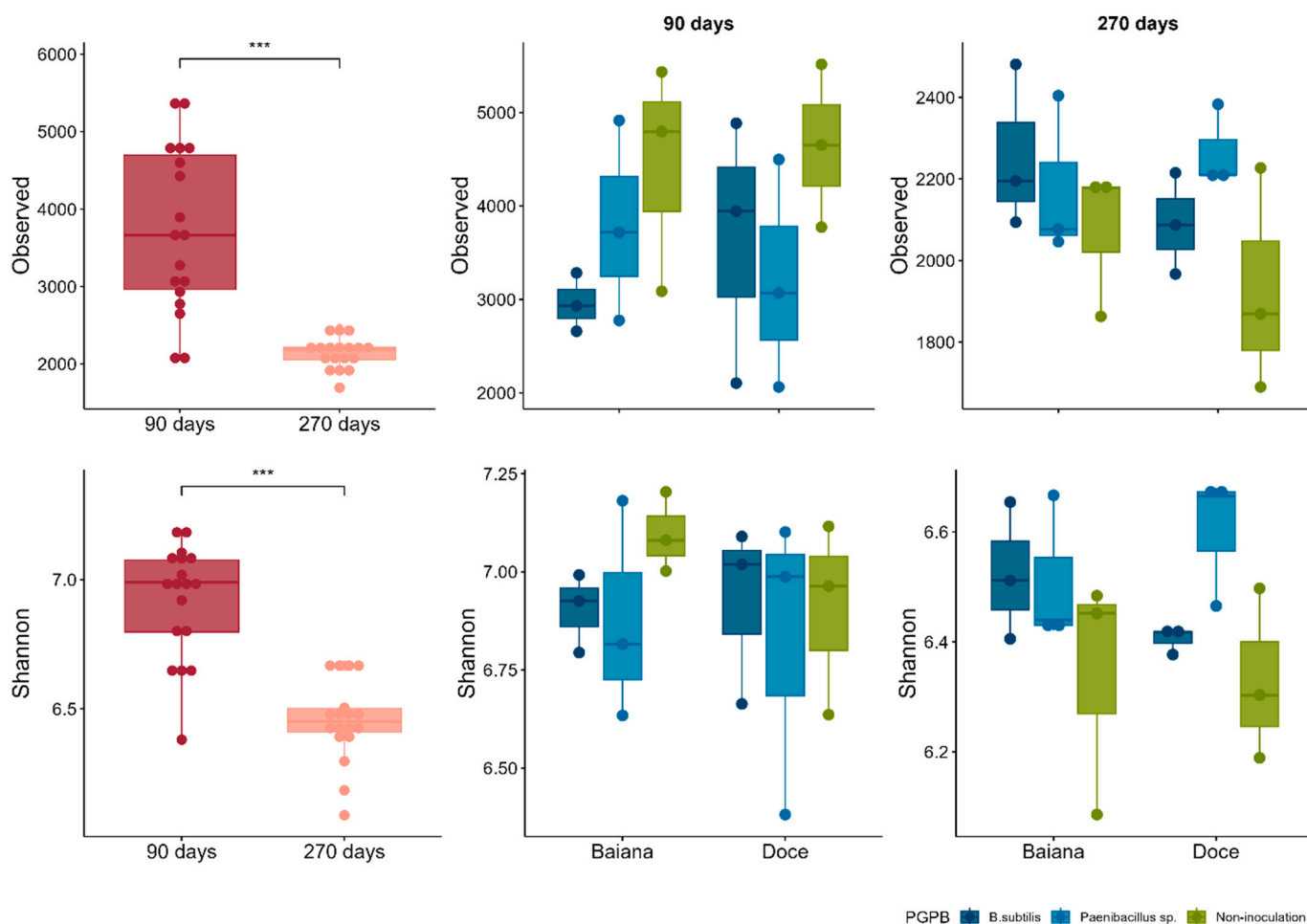


Fig. 3. Alpha diversity of rhizosphere microbial communities of prickly-pear cactus genotypes ‘Baiana’ and ‘Doce’, both non-inoculated and inoculated with *Bacillus subtilis* and *Paenibacillus* sp., at 90 and 270 days of growth.

exudation profiles under semi-arid stress conditions.

Regarding the inoculation of PGPB and *N. cochenillifera* genotypes, our results showed only subtle effects on bacterial community structure, with no changes in richness, diversity, or composition, indicating that the native soil microbiome studied can be resistant and resilient. This means that when an external organism is introduced, soils which harbor a well-established native microbiome may compete with and suppress the introduced organism, thereby maintaining community function and structure (resistance), or it may adapt and reorganize to establish a new stable state (resilience) (Kost et al., 2024). Indeed, cactus species cultivated in semi-arid regions generally share a core group of adapted rhizosphere-associated microorganisms (Fonseca-García et al., 2016; Zineb et al., 2024). Nevertheless, we acknowledge that the observed differences in precipitation between sampling times may have partially contributed to the temporal variations detected, and this should be considered a limitation of the present study.

4.2. Recruitment of stress-mitigating bacterial groups in cactus rhizospheres

The analysis of the bacterial composition in the rhizosphere of *Nopalea cochenillifera* showed the predominance of phyla typically associated with semi-arid soils, such as Actinobacteriota, Proteobacteria, Firmicutes, Chloroflexi, and Acidobacteriota (Zhu et al., 2024), which varied across plant growth stages. These results are consistent with previous studies conducted in semi-arid soils (Pan et al., 2024; Liu et al., 2025) and in cactus rhizospheres (De La Torre-Hernández et al., 2020; Zineb et al., 2024). For instance, Karray et al. (2020) reported

similar enrichment of Actinobacteria, Alphaproteobacteria, Firmicutes, and Chloroflexi in *Opuntia ficus-indica* under varying aridity gradients.

The relative abundance of Actinobacteriota increased during the wetter period (270 days), differing from patterns commonly reported for arid environments where this phylum predominates under dry conditions (Leal et al., 2024; Rodríguez et al., 2024). Although the mechanisms underlying this pattern remain uncertain, precipitation may have indirectly influenced microbial composition, possibly through effects on soil nutrient availability and organic matter turnover (Zhang et al., 2019; Zhang et al., 2024a, b). This suggests further studies incorporating soil chemical parameters to confirm this hypothesis.

Temporal variation in the composition of bacterial genera suggests ecological succession within the rhizosphere of *N. cochenillifera*. The early dominance of genera, such as *Streptomyces* and *Sphingomonas* may reflect their ability to rapidly colonize and exploit labile root exudates (Worsley et al., 2021), while the later enrichment of taxa, such as *Bacillus*, *Gaiella*, and *Ammoniphilus* could indicate a shift toward communities adapted to more stable or nutrient-limited conditions (Zhang et al., 2024a, b). Such temporal turnover points to dynamic microbial assembly processes, potentially driven by plant developmental stage and seasonal moisture fluctuations, which together shape the ecological balance of the cactus rhizosphere.

Several genera with previously described plant growth-promoting potential were detected among the dominant taxa at different growth stages and across genotypes, including *Streptomyces*, *Sphingomonas*, *Microvirga*, *Bradyrhizobium*, *Bacillus*, *Burkholderia*–*Caballeronia*–*Paraburkholderia*, and *Azospirillum*. These taxa have been associated in other studies with functions such as nitrogen fixation, hormone production, or

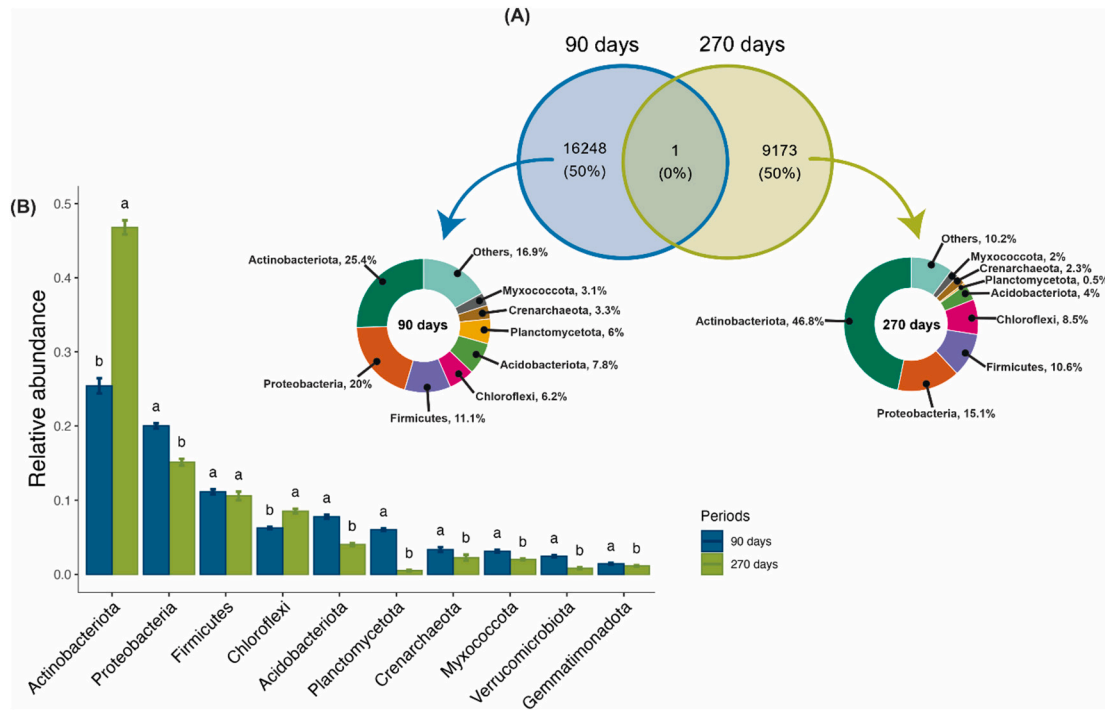


Fig. 4. Composition of the rhizosphere microbial community of prickly-pear cactus at 90 and 270 days of growth and comparison among the predominant phyla using Duncan's test ($p < 0.05$).

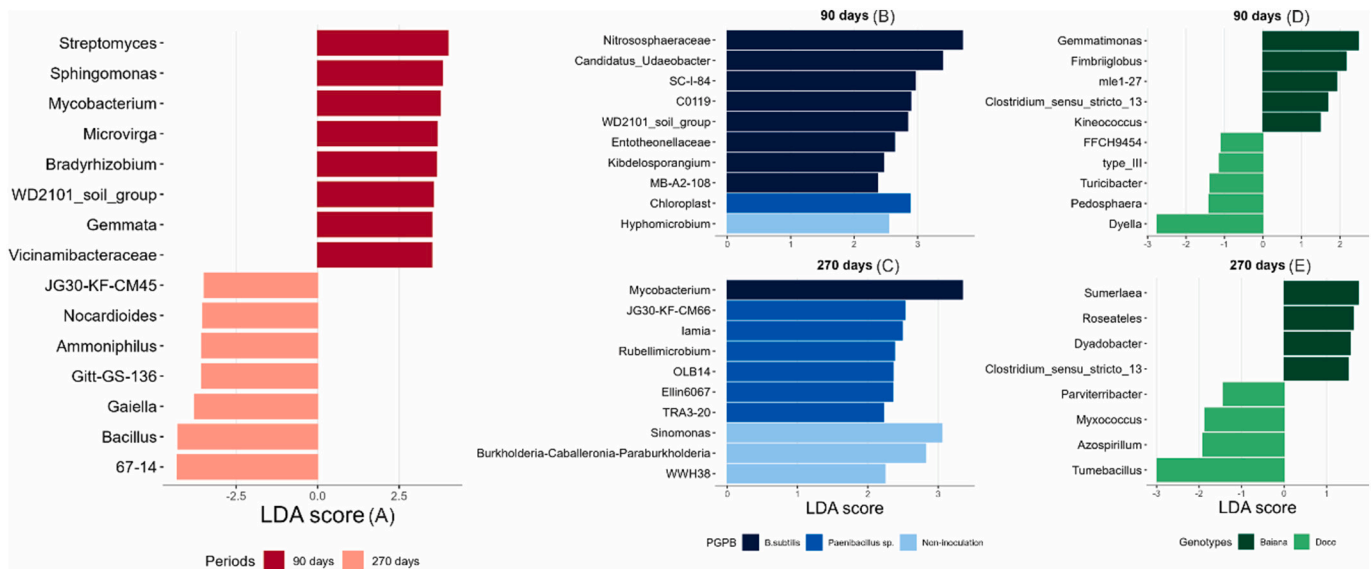


Fig. 5. Genus-level enrichment of bacteria in the rhizosphere of prickly-pear cactus genotypes 'Baiana' and 'Doce', both non-inoculated and inoculated with *Bacillus subtilis* and *Paenibacillus* sp., at 90 and 270 days of growth.

organic compound degradation (Bonatelli et al., 2021; Wilhelm et al., 2021; Sharma et al., 2025; Pelagio-Flores et al., 2025).

4.3. Insights, limitations, and practical implications for assessing cactus rhizosphere

The findings of this study provide valuable insights into the bacterial communities inhabiting the rhizosphere of *Nopalea cochenillifera* cultivated in a semiarid environment. Our results showed that plant growth stage promoted a strong influence on bacterial community structure, which was composed of taxa typically associated with semiarid soils.

These shifts suggest that rhizosphere microbial composition is dynamic over time and may respond to environmental fluctuations and plant developmental changes.

Despite the significance of these findings, our study presents several limitations. These include the scarcity of recent data on PGPB inoculation and root exudation in cacti, as well as the challenge of obtaining responses across different growth stages due to the long cultivation cycle of prickly-pear cactus (approximately two years). In addition, our approach was based solely on taxonomic inference, and functional validation (e.g., metagenomics) is needed to verify the ecological and agronomic relevance of the observed taxa.

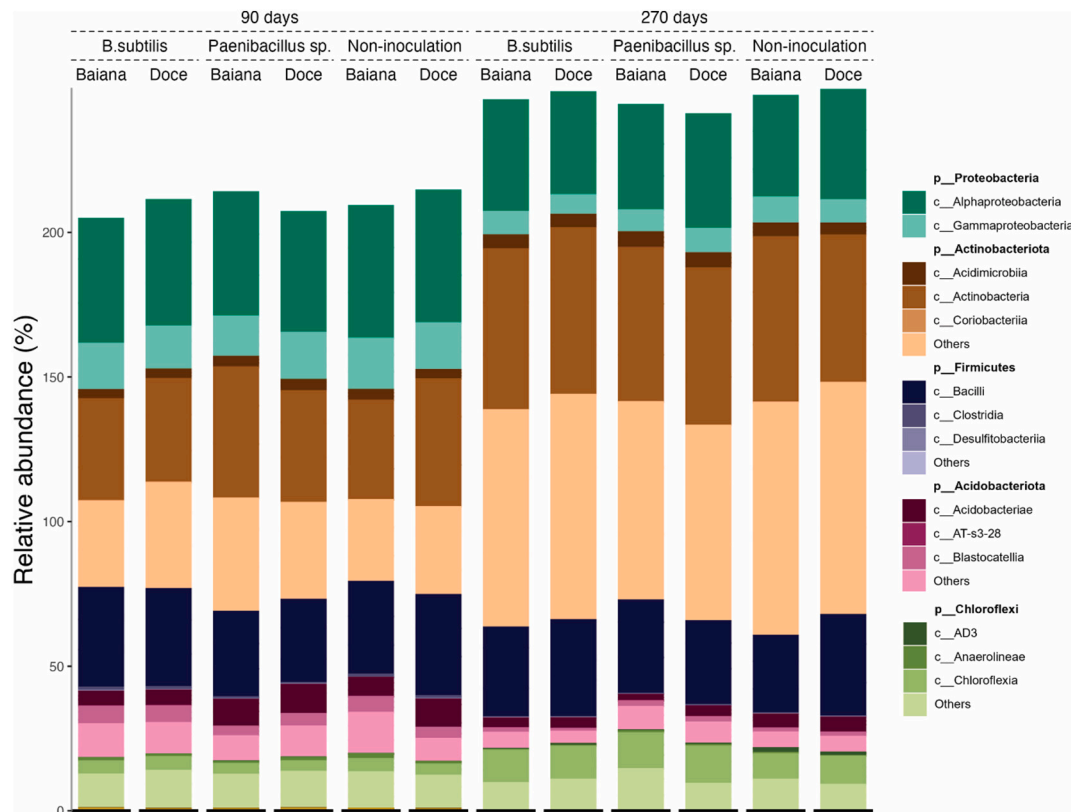


Fig. 6. Hierarchical abundance at the phylum and class levels in the rhizosphere of prickly-pear cactus genotypes 'Baiana' and 'Doce', both non-inoculated and inoculated with *Bacillus subtilis* and *Paenibacillus* sp., at 90 and 270 days of growth.

While our data did not indicate major microbiome disturbances following inoculation, this observation should be interpreted cautiously, as plant performance and functional parameters were not measured. Nonetheless, the persistence of core microbial taxa across treatments suggests a degree of community stability under semiarid conditions. Future studies integrating functional assays and plant growth responses are needed to confirm whether these bacterial groups contribute to beneficial plant–microbe interactions. Moreover, the presence of taxa commonly described as PGPBs highlights the potential of semiarid soils as reservoirs of stress-adapted microbial diversity, although their biotechnological use as inoculants requires further experimental validation.

5. Conclusions

The bacterial communities in the rhizosphere of the prickly-pear cactus genotypes 'Doce' and 'Baiana', both non-inoculated and inoculated with *B. subtilis* and *Paenibacillus* sp., was significantly shaped by plant growth stage. Key bacterial taxa associated with semiarid regions were predominant in the rhizosphere, many of which are known to contribute to abiotic stress tolerance and plant growth promotion. These findings provide fundamental insights into the microbial ecology of *Nopalea cochenillifera* and highlight the importance of studying the microbiome of cacti cultivated in semiarid regions. Nevertheless, further studies are required to better understand ecological interactions in the rhizosphere through network analysis, to identify functional groups and the composition of root exudates in cacti, and to determine how these factors correlate with the recruitment of specific taxa.

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.apsoil.2025.106661>.

CRediT authorship contribution statement

Rhaiana Oliveira de Aviz: Writing – original draft, Methodology, Investigation. **Janaira Rocha Campos:** Writing – original draft, Investigation. **Davila Esmelinda Oliveira Silva:** Writing – original draft, Investigation. **Mayanna Karlla Lima Costa:** Writing – original draft, Methodology, Investigation. **Marcos Renan Lima Leite:** Writing – original draft, Investigation. **Sandra Mara Barbosa Rocha:** Writing – original draft, Investigation. **Pâmalla Graziely Carvalho Moraes:** Writing – original draft, Investigation. **Gonçalves Albino Dauala:** Writing – original draft, Investigation. **Maria Helena Ferreira Duarte:** Writing – original draft, Visualization. **Cacio Luiz Boechat:** Writing – original draft, Visualization. **Rafael de Souza Miranda:** Writing – original draft, Visualization. **Elaine Martins da Costa:** Writing – original draft, Visualization. **Arthur Prudêncio de Araujo Pereira:** Writing – review & editing, Writing – original draft, Formal analysis. **Erika Valente de Medeiros:** Writing – review & editing, Writing – original draft. **Lucas William Mendes:** Writing – review & editing, Writing – original draft, Formal analysis. **Ademir Sergio Ferreira Araujo:** Writing – review & editing, Writing – original draft, Supervision.

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Declaration of competing 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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Data availability

Data will be made available on request.

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