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Diversity and Community Structure of Endophytic Bacteria in the Bark and Stem of *Cryptocarya massoy* Revealed by 16S rRNA Amplicon Sequencing

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ABSTRACT

The masoi tree (*Cryptocarya massoy*), endemic to Papua, is valued for its essential oils rich in massoia lactone. However, conventional extraction methods raise sustainability concerns, highlighting the need for alternative sources of bioactive compounds. This study investigated the diversity and community structure of endophytic bacteria in different tissues of *C. massoy* using 16S rRNA amplicon sequencing. Bark (KBP), inner stem (BP), and twig bark (KRC) samples were collected and surface-sterilized before genomic DNA extraction. The full-length 16S rRNA gene was amplified and sequenced using the Oxford Nanopore Technologies (ONT) platform. Sequencing reads were quality-filtered, taxonomically classified against the NCBI database, and analyzed to characterize bacterial diversity and community composition. Agarose gel electrophoresis confirmed successful amplification of the approximately 1,500 bp target gene. BP yielded the highest sequencing output (192 Mbp), whereas KRC showed the highest proportion of reads with quality scores above Q15 (69.8%). Alpha diversity analysis indicated that BP harbored the richest and most diverse bacterial community, followed by KRC and KBP. Taxonomic profiling revealed that *Pantoea* dominated all three samples, particularly KRC. In contrast, BP exhibited a more diverse community, with notable contributions from *Pseudomonas, Paraflimonas, Erwinia,* and *Paraburkholderia*. These findings demonstrate tissue-associated variation in endophytic bacterial community composition, with the inner stem harboring greater bacterial diversity. This study provides information on the endophytic bacterial diversity of *C. massoy* and offers their possible roles in the biotransformation of plant derived compounds.

1. Introduction

The masoi tree (*Cryptocarya massoy*) is an endemic species of Papua with high economic value that has long been utilized in traditional medicine and essential oil production. The bark of *C. massoy* contains massoia lactone as the main component of its essential oil (Hastanti *et al.* 2018). This compound is widely used in the fragrance, food, and cosmetic industries, and essential oils derived from the bark and stem of masoia contain high concentrations of massoia lactone, making them valuable commodities in the global market (Rali *et al.* 2007). Although massoia lactone has significant economic potential, its traditional extraction raises sustainability concerns (Ningsih & Hamzah 2022). Large-scale logging and limited cultivation threaten the conservation of this plant, while the high extraction cost further constrains production (Gatot *et al.* 2007). These challenges highlight the need to explore endophytic bacteria associated with *C. massoy*, which may produce secondary metabolites with similar characteristics.

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Endophytic bacteria are microorganisms that live within healthy plant tissues without causing disease or adverse effects to the host. Their symbiotic interactions with plants contribute to the biosynthesis of bioactive compounds and enhance plant tolerance to environmental stress and pathogens (Long *et al.* 2004). Studies of endophytic bacteria face challenges, as only about 1% of microbial species can be cultured, while the remaining 99% remain unculturable under standard laboratory conditions (Sekiguchi 2006). Metagenomic approaches are therefore required to investigate microbial diversity without prior cultivation (Chen & Pachter 2005). One widely applied method is amplicon sequencing, which involves analyzing DNA fragments amplified with specific primers targeting marker genes. Third-generation sequencing (TGS) technologies enable rapid and accurate metataxonomic profiling. The most common marker for bacterial identification is the 16S rRNA gene, a conserved region of ribosomal RNA (Nilsson *et al.* 2019). Amplified fragments are sequenced, analyzed, and compared with reference databases such as GenBank, allowing phylogenetic resolution down to the species level (Schoch *et al.* 2012).

This study examined the diversity of endophytic bacterial communities associated with the masoi tree (*C. massoy*) by analyzing microbial populations across different plant tissues. Third-generation sequencing (TGS) technology using Oxford Nanopore Technologies (ONT) was applied to profile bacterial communities without cultivation, allowing a broader characterization of microbial diversity compared to conventional culture-based approaches. Given the economic importance of massoia lactone and the environmental issues associated with its conventional extraction, understanding the diversity of endophytic bacteria in *C. massoy* is essential for exploring more sustainable approaches.

2. Materials and Methods

2.1. Sample Collection and Preparation from Stem and Bark of *Cryptocarya massoy*

Samples were collected from Wurkendik Village, West Fakfak District, Fakfak Regency, West Papua (GPS: 2°42’40,44148” S 132°10’6,14069” E; 76 mdpl) (Figure 1).

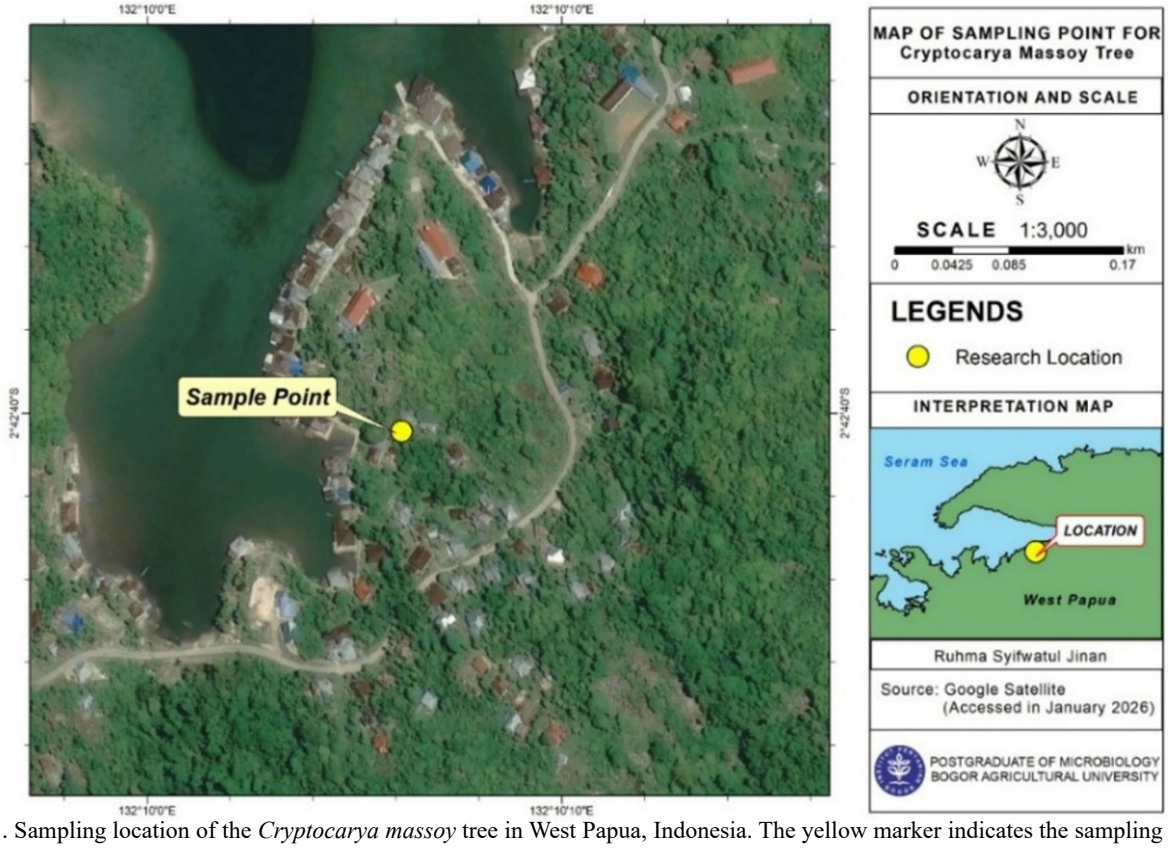


Figure 1. Sampling location of the *Cryptocarya massoy* tree in West Papua, Indonesia. The yellow marker indicates the sampling point of plant tissues used in this study. The map includes geographic orientation, scale, and regional context within West Papua

Plant material consisted of bark and quaternary stems from masoi trees that had not yet flowered or fruited, with an approximate age of 4–5 years. Samples were collected from three tissue compartments: bark of the main stem (KBP), inner stem tissue (BP), and bark of twigs/branches (KRC). The selected tissue types were intended to represent different internal microhabitats within the tree. Surface sterilization was performed following the method of Coombs and Franco (2003). Samples were washed, cut into 2 cm fragments, and immersed in 70% ethanol for 1 min, followed by immersion in 1% NaOCl for 3 min, and 70% ethanol for 1 min. Lastly, samples were rinsed with sterile water for 3 sec. To confirm sterilization success, 0.1 mL of the final rinse was inoculated onto TSA medium.

2.2. DNA Extraction and Quantification

Genomic DNA from masoi bark and stem tissues was extracted using the ZymoBIOMICS™ DNA Miniprep Kit following the manufacturer's instructions with slight procedural detailing. Briefly, a ZR BashingBead™ lysis tube was prepared and supplemented with 750 µL of ZymoBIOMICS™ lysis solution. Subsequently, 250 µL of the sample was added, followed by vortexing for 20 minutes and centrifugation at 10,000 × g for 1 minute.

Approximately 400 µL of the resulting supernatant was transferred to a Zymo Spin III-F filter placed in a collection tube and centrifuged at 8,000 × g for 1 minute. The filtrate was then combined with 1,200 µL of ZymoBIOMICS™ DNA Binding Buffer. From this mixture, 800 µL was loaded onto a Zymo Spin II-CR column and centrifuged at 10,000 × g for 1 minute, after which the collection tube was discarded. The column was washed by adding 400 µL of ZymoBIOMICS™ DNA Wash Buffer 1, followed by centrifugation and filtrate removal. The column was then transferred to a new collection tube, supplemented with 700 µL of ZymoBIOMICS™ DNA Wash Buffer 2, and centrifuged at 10,000 × g for 1 minute. For DNA elution, the Zymo Spin II-CR column was placed into a sterile 1.5 mL microtube, and 50 µL of ZymoBIOMICS™ DNase/RNase-free water was added prior to centrifugation at 10,000 × g for 1 minute. To further purify the DNA, the Zymo Spin III-HRC filter was pre-centrifuged at 8,000 × g for 3 minutes. Next, 600 µL of ZymoBIOMICS™ HRC Prep Solution was added to a fresh collection tube. The eluted DNA was then applied onto the Zymo Spin III-HRC filter and centrifuged at 16,000 × g for 3 minutes to obtain the final purified genomic DNA.

2.3. Metabarcoding Analysis of the Bacterial Community

DNA concentration was measured using NanoDrop spectrophotometers and a Qubit fluorometer. DNA was amplified with the 16S primer (27F-1492R) (Polz & Cavanaugh 1998) using KOD Multi & Epi (Toyobo, KME-101). Library preparation was performed using the Nanopore Ligation sequencing amplicons - Native Barcoding Kit 96 V14 (SQK-NBD114.96), and the final library was sequenced using the Nanopore GridION platform. Nanopore sequencing was operated using MinKNOW software version 25.03.7. Basecalling was performed using Dorado version 7.8.3 with the high-accuracy model.

2.4. Metagenomic Data Analysis

For bioinformatic analysis, adapters and primers were trimmed using Dorado version 7.8.3, and reads were filtered based on quality and length using NanoFilt and visualized with NanoPlot. Reads were clustered at 97% with the Proname workflow and classified using Blastn against the NCBI nt database. Blast results were filtered based on the highest percent identity, bitscore, and a length ≥1,000 bp. Classifications with a percent identity below 95% were discarded. The taxonomic level was adjusted to genus level if the percent identity was ≥95.0% and to species level if the percent identity was ≥97.5%. If multiple classifications remained, the taxonomic level was adjusted to the lowest common ancestor. Downstream analyses and visualizations were performed using Pavian, Krona Tools, and RStudio with R version 4.3.

Alpha diversity indices, including Observed OTUs, Chao1, ACE, Shannon, Simpson, Inverse Simpson, and Fisher's alpha, were calculated based on the OTU table generated at a 97% similarity threshold. Diversity analysis was performed in R (version 4.3.0) using the vegan package. Sequencing depth across samples was comparable (134,096–135,099 reads per sample); therefore, rarefaction was not performed prior to diversity analysis. Heatmap visualization was generated using log10-transformed relative abundance data with the addition of a pseudo-count to avoid zero values.

3. Results

3.1. The Amplified Fragments of the Bacterial 16S rRNA Gene from stem and bark of *Cryptocarya massoy* DNA samples

Qualitative analysis was conducted using 1% agarose gel electrophoresis. The results revealed clear DNA fragments with amplicon sizes ranging from 1,500 to 1,600 bp, corresponding to the V1-V9 regions, based on the DNA ladder. These findings are consistent with the target gene region (V1-V9) of the bacterial universal primers. This result demonstrates that the PCR was successful, with the expected amplicon size in the samples and no contamination in the control. The visualization of the PCR products through 1% agarose gel electrophoresis is shown in Figure 2.

3.2. General Information on Metagenome Dataset

The DNA sequencing results of the KBP, BP, and KRC samples revealed variations in sequencing output and read quality among samples. BP generated the largest amount of sequencing data, with a total of 192,189,631 bases and an average read length of 1,422.6 bp. The mean read quality across all samples was 15.3, and the N50 read length ranged from 1,409 to 1,410 bp. KRC showed the highest proportion of reads with quality scores above Q15 (69.8%), followed by BP (67.5%) and KBP (68.1%). BP exhibited the highest basecall quality score (26.8) and greater variation in read length. Overall, differences in sequencing output and quality were observed among the three samples (Table 1).

The sequencing quality analysis was performed as part of was performed as part of sequencing

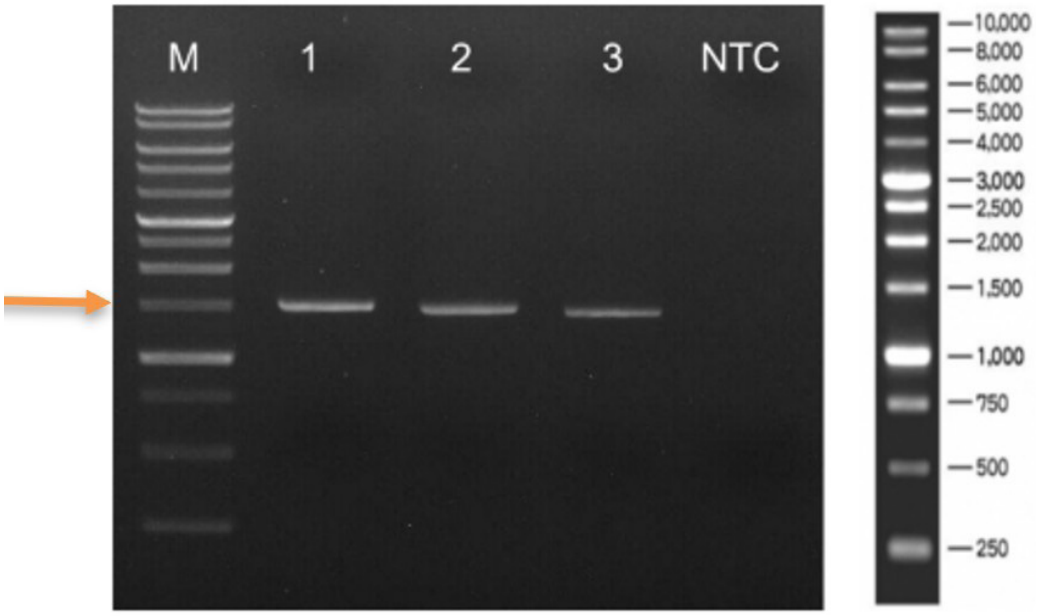


Figure 2. Gel electrophoregram of 16S rRNA gene amplification using primers 27F and 1492R. M: DNA ladder 1 kb; 1: KBP; 2: BP; 3: KRC; NTC: negative control. A single band of approximately 1,450 bp was observed in all samples

Table 1. Summary of sequencing output and read quality metrics for KBP, BP, and KRC samples. Parameters include total bases, mean read length, mean read quality, number of reads, N50 read length, standard deviation of read length, and quality filtration thresholds (>Q10 and >Q15). KRC showed the highest proportion of reads with quality scores >Q15, whereas BP produced the largest amount of sequencing data

Parameter	KBP	BP	KRC
Total Base (bp)	190,105,868.0	192,189,631.0	190,105,868.0
Mean read length (bp)	1,417.7	1,422.6	1,417.7
Mean read quality	15.3	15.3	15.3
Number of reads (n)	134,096.0	135,099.0	134,096.0
Read length N50 (bp)	1,409.0	1,410.0	1,409.0
STDEV read length (bp)	31.7	34.8	31.7
Quality of filtration			
>Q10	100%	100%	100%
>Q15	68.1%	67.5%	69.8%
Score quality basecall	25.9	26.8	26.7

*Samples were collected from three tissue compartments: bark of the main stem (KBP), inner stem tissue (BP), and bark of twigs/branches (KRC)

quality control to ensure that the generated reads were of sufficient length and quality for reliable downstream taxonomic classification and diversity analyses. The distribution of read lengths across the three samples ranged from approximately 1,300 to 1,600 bp, with the majority of reads concentrated between 1,400 and 1,500 bp (Figure 3). This size range corresponds to the expected full-length 16S rRNA amplicon generated using primers 27F–1492R, indicating successful amplification of the target region. The average read quality scores (Q-scores) were predominantly distributed between Q10 and Q20, with the highest density observed at Q15–Q18. Samples A (KBP), B (BP), and C (KRC) exhibited comparable read length distributions and overall sequencing quality profiles. Although minor variations in quality scores were observed among samples, the majority of reads demonstrated moderate to high quality.

3.3. Bacterial Diversity

Metabarcoding analysis revealed differences in bacterial diversity and richness among BP, KBP, and KRC samples based on multiple alpha diversity indices,

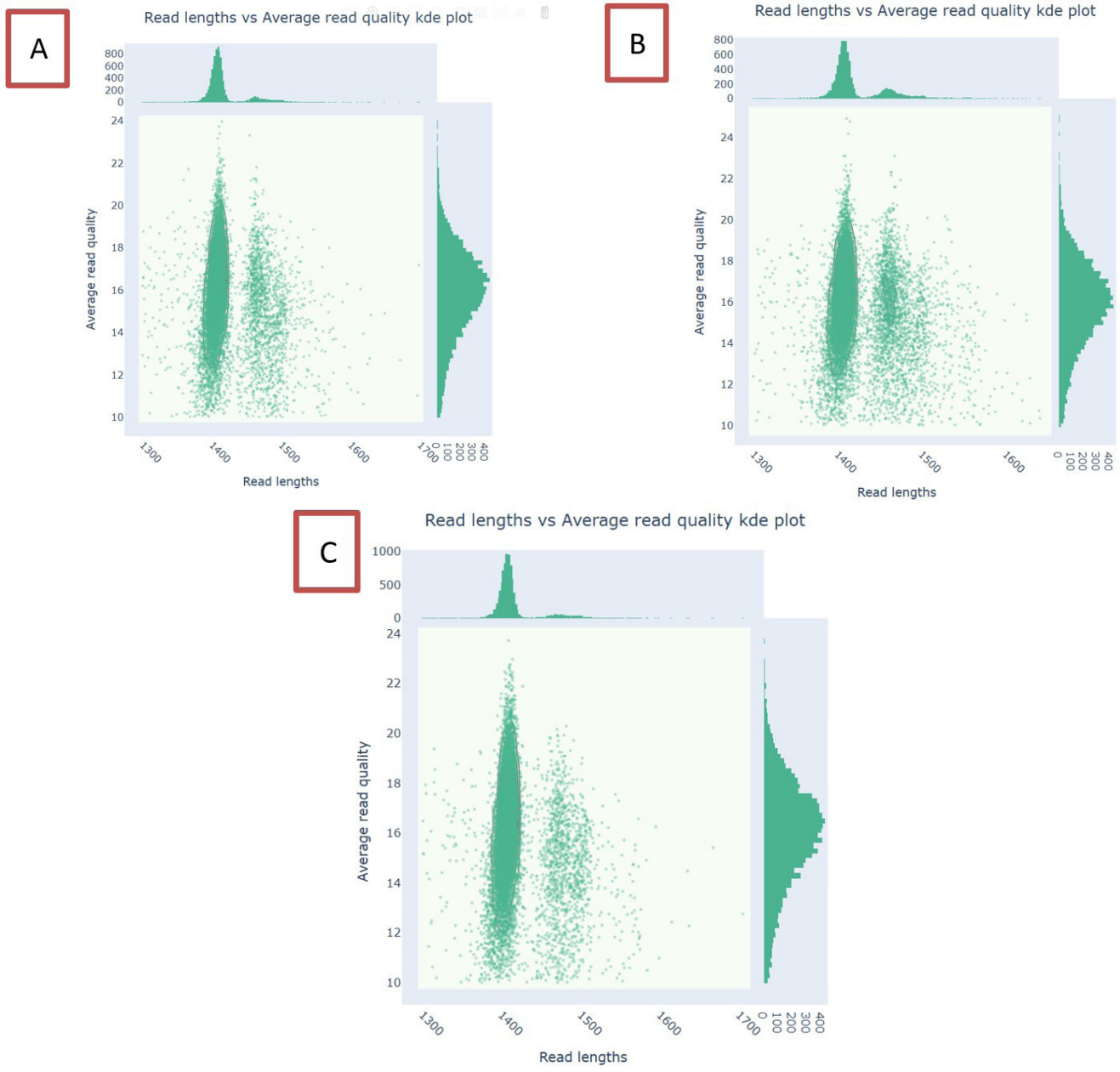


Figure 3. Graph of the relationship between read length and average read quality for (A) KBP samples, (B) BP samples, and (C) KRC samples

including Observed OTUs, Chao1, ACE, Shannon, Simpson, Inverse Simpson, and Fisher indices (Figure 4). The Observed OTUs values revealed clear differences in species richness among samples. Sample BP exhibited the highest number of observed OTUs, with 296 OTUs, followed by KRC with 54 OTUs and

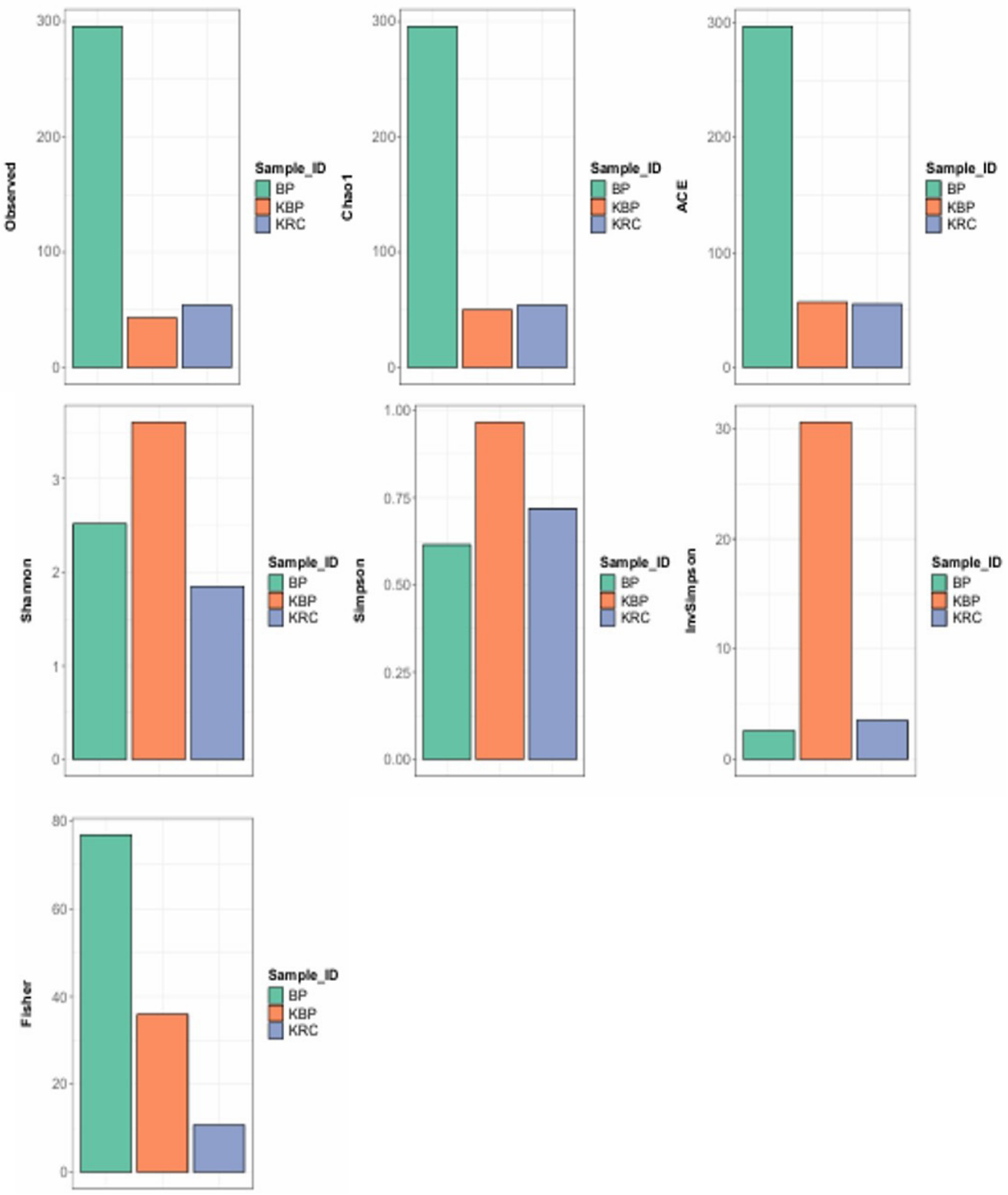


Figure 4. Alpha diversity of endophytic bacterial communities across different tissues of *Cryptocarya massoy*. Diversity indices include Observed OTUs, Chao1, ACE, Shannon, Simpson, Inverse Simpson, and Fisher. Differences among samples indicate variation in microbial richness and diversity across plant tissues

KBP with 43 OTUs. The estimated richness indices, Chao1 and ACE, were also highest in BP (296.02 and 297.09, respectively), compared to KRC (54.11 and 55.23) and KBP (49.80 and 56.82). The Fisher index further supported this pattern, showing the highest value in BP (76.85), indicating a greater number of bacterial taxa in this sample. In contrast to the richness pattern, sample KBP showed the highest diversity index values, with Shannon and Simpson indices of 3.61 and 0.97, respectively, as well as the highest Inverse Simpson value (30.62). Sample BP exhibited lower diversity index values (Shannon = 2.52; Simpson = 0.62), whereas KRC showed the lowest Shannon index (1.85) and an intermediate Simpson value (0.72).

Overall, these results indicate that BP tends to exhibit higher bacterial richness, whereas KBP shows a higher level of microbial diversity and community evenness, while KRC displays an intermediate pattern among the three samples. The distribution of OTUs among samples was further evaluated using a Venn diagram (Figure 5). Sample BP exhibited the highest number of unique OTUs (131), followed by KRC (43) and KBP (5). Only one OTU was shared among all three samples, whereas three OTUs were shared between BP and KRC, two OTUs between KRC and KBP, and five OTUs between BP and KBP. This pattern indicates that the bacterial community composition in each sample is highly distinct and tends to be tissue-specific.

3.4. Endophytic Bacterial Communities in Bark and Stem Tissues

Abundance analysis revealed distinct patterns of bacterial community composition among the analyzed tissues of *Cryptocarya massoy.*

Abundance analysis showed that Gammaproteobacteria was the dominant class in all samples, with relative abundances of 81.02% in BP, 13.25% in KBP, and 98.66% in KRC (Figure 6). Other classes, such as Alphaproteobacteria and Betaproteobacteria, were detected mainly in BP, but at much lower proportions. At the family level, Erwiniaceae was the dominant family, particularly in KRC, with a relative abundance of 97.81% in KRC, followed by 11.47% in BP and 4.82% in KBP. Meanwhile, Pseudomonadaceae was detected in BP (5.85%) and KBP (3.61%), whereas Sphingomonadaceae was present at lower abundances in BP (0.62%) and KBP (1.20%). At the genus level, *Pantoea* was the dominant genus across all samples, especially in KRC, where it accounted for almost the entire bacterial community. Other genera, including *Pseudomonas* and *Sphingomonas*,

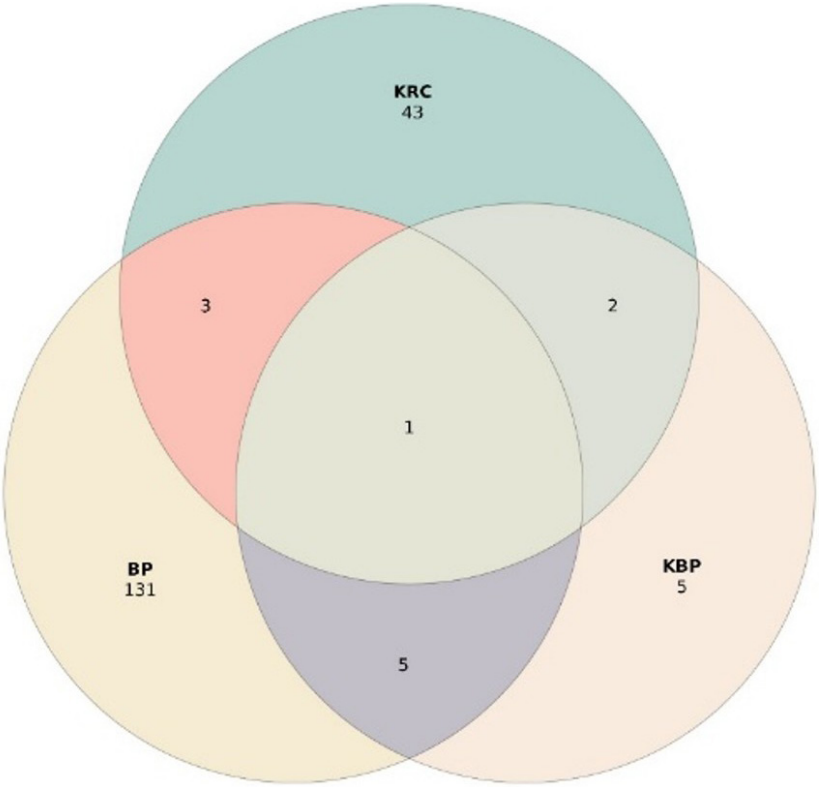


Figure 5. Venn diagram illustrating the distribution of bacterial operational taxonomic units (OTUs) among KBP, BP, and KRC samples

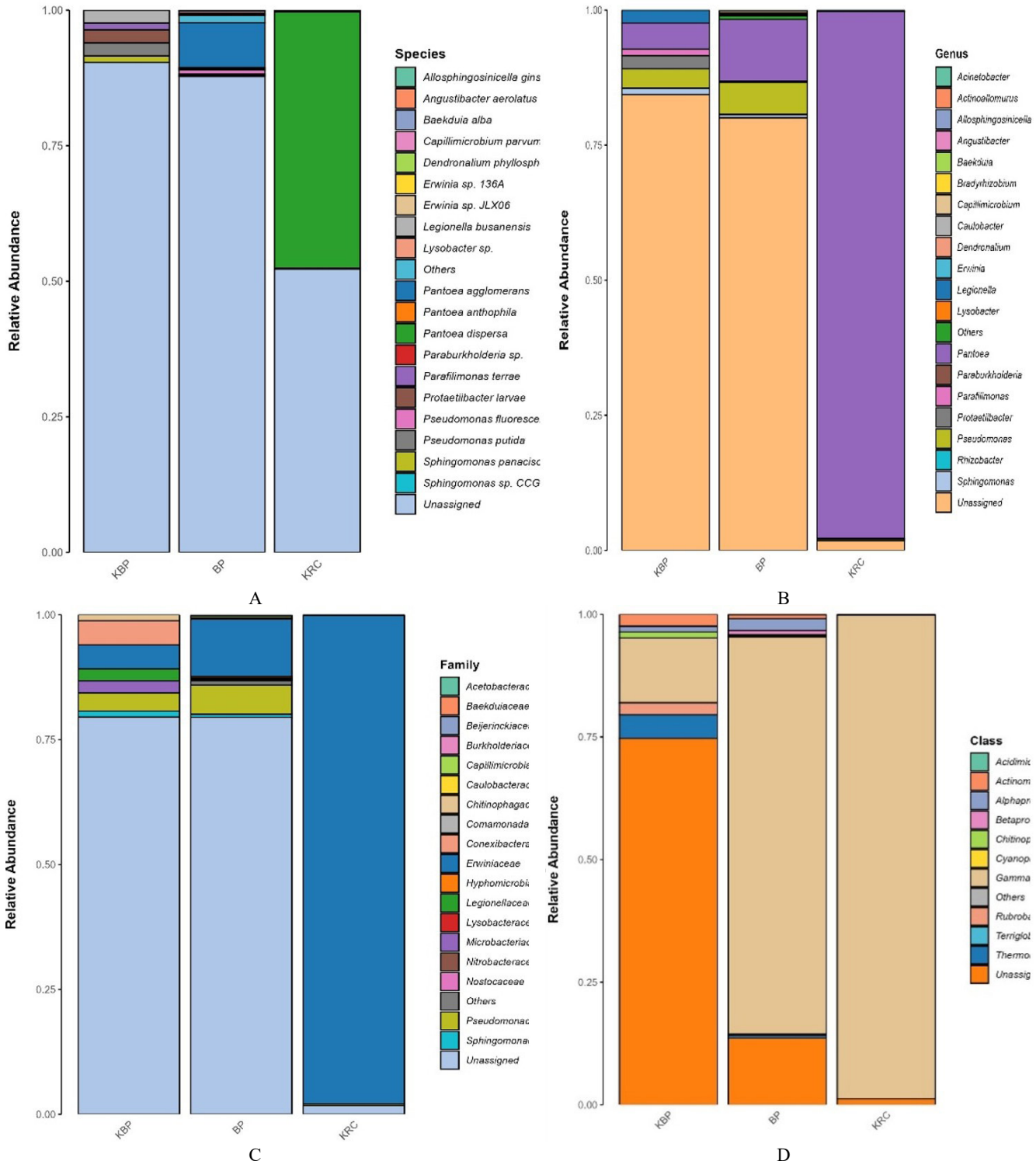


Figure 6. Taxonomic composition of endophytic bacterial communities in KBP, BP, and KRC samples at different taxonomic levels: (A) species, (B) genus, (C) family, and (D) class. Relative abundances are shown as stacked bar plots, highlighting differences in community structure among tissues

were more prevalent in BP and KBP but contributed only minor proportions to the overall community structure. At the species level, *Pantoea dispersa* was identified as the dominant species in KRC, followed by BP and KBP. In contrast, BP and KBP exhibited a more complex species composition, with several taxa contributing to the community structure at lower relative abundances.

The taxonomic composition of bacterial communities at the genus level (Figure 7) shows clear differences in abundance patterns among the three sample groups (KBP, BP, and KRC). The color scale reflects the log10 relative abundance, with red and yellow indicating dominant taxa and dark blue representing very low abundance. Consistently, the genus *Pantoea* emerged as the most dominant taxon in all samples, with the highest abundance in KRC. *Pseudomonas* was also detected with relatively high abundance in KBP and BP, but lower than *Pantoea*. In contrast, several other genera such as *Parafilimonas*, *Erwinia*, and *Paraburkholderia* showed higher abundance in BP compared to KBP and KRC, indicating that BP has a more diverse and even bacterial community. For other genera at the bottom of the heatmap (*Capillimicrobium, Microlunatus, Ramlibacter, Acinetobacter, Lysobacter,* and *Baekduia*), the relative abundance is generally low, but still more detectable in KBP and especially BP compared to KRC. Qualitatively, this pattern suggests that BP is the location with the highest bacterial community diversity and complexity, KBP is intermediate, while KRC has the simplest community, heavily dominated by *Pantoea*.

4. Discussion

Metabarcoding analysis of different tissues from a single *Cryptocarya massoy* individual revealed variations in the diversity and abundance of bacterial communities in the stem (BP), bark (KBP), and twigs/branches (KRC). Bacterial taxonomic diversity was higher in BP compared to KBP and KRC, as indicated by the number of observed OTUs and the distribution of unique and shared taxa in the Venn diagram (Figure 5). Meanwhile, the abundance

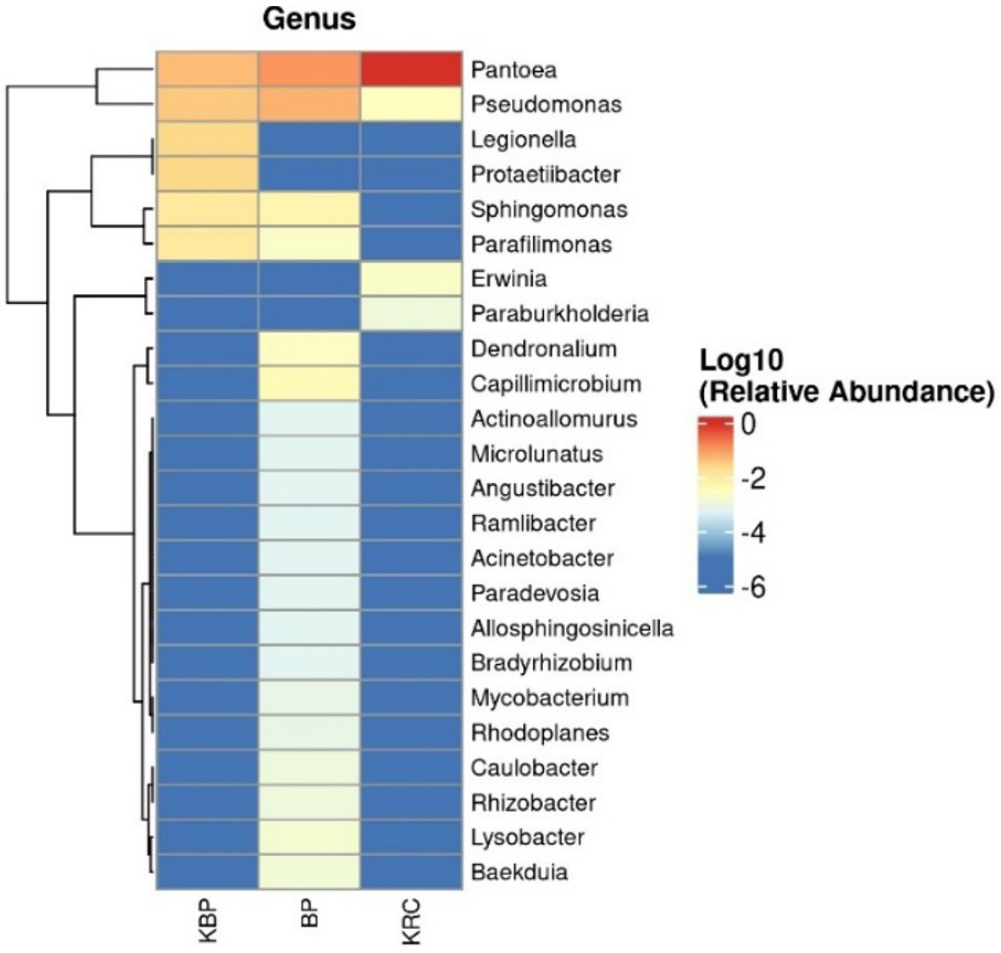


Figure 7. Heatmap of bacterial genus abundance across different sample groups (KBP, BP, KRC). Red to yellow shades represent higher bacterial abundance (Log10 scale), while blue indicates lower abundance

and evenness of bacterial communities in KBP and KRC were categorized as moderate and low, respectively, based on the Shannon and Simpson indices (Figure 4). The BP sample exhibited the highest richness and evenness values, indicating that stem tissues potentially provide a more stable microhabitat for endophytic bacteria. In contrast, the KRC sample showed strong dominance by a single taxon, which correlated with lower diversity index values, whereas KBP displayed an intermediate community structure.

These results indicate that the distribution of endophytic bacterial communities in *C. massoy* is tissue-specific. If one or two dominate a community, the diversity is considered low, even though the total number of individuals in the ecosystem is large. It is also known that the dominance value has an inverse relationship with the level of diversity; the higher the level of dominance, the lower the level of diversity (Haq *et al.* 2021). Shannon measures the abundance and evenness among species; the higher the Shannon value, the more diverse and balanced the community (Willis 2019). The Shannon value will be low if a dominant species is found (Almeida *et al.* 2023). The plant microbiome is shaped not only by environmental factors but also by the host's physiological traits and biological functions, resulting in tissue-specific microbial communities (Vandenkoornhuyse 2015). For example, studies on *Orchids* have shown that microbial communities differ significantly between roots, stems, leaves, and reproductive organs, and that plant organs consistently influence microbiota composition and structure (Haruna *et al.* 2018; Alibrandi *et al.* 2026). This pattern is consistent with the concept that internal trunk tissues provide a more stable and heterogeneous habitat for endophytes, with access to xylem flow that connects the roots and aerial organs, thus becoming a corridor for the colonization of many endophytic taxa (Hardoim *et al.* 2008). Furthermore, comprehensive reviews on endophytic bacteria show that endophytic communities are often greatly influenced by microhabitat conditions, host tissue structure, and microbial adaptation and colonization abilities — such as motility, adhesion capacity, and tolerance to internal plant tissue conditions (Ali *et al.* 2021). Since tree trunks provide stable vascular tissues, intercellular spaces, and internal nutrient supply, they tend to be a safe and stable habitat for endophytic microbes to live and develop, explaining why BP has the highest diversity (Compant *et al.* 2019). Conversely, the low diversity in KBP reflects that the bark is a more extreme microhabitat (temperature fluctuations, drought, UV radiation), so only a subset of taxa can survive. This finding aligns with organ-specific studies on three Acer species, where the organ explained >50% of bacterial community variation, and twig/trunk tends to have lower diversity compared to other habitats due to more limiting physical conditions (Guo *et al.* 2025).

All samples originated from the same individual tree; nevertheless, the structure of the bacterial communities differed among tissues. These bacteria belonged to the dominant class identified in each sample. Gammaproteobacteria was the predominant bacterial class across all samples, with relative abundances of 81.02% in BP, 13.25% in KBP, and 98.66% in KRC. Twigs primarily function as structural supports for trees and may also provide microhabitats with physicochemical conditions that favor the proliferation of Proteobacteria. This may partly explain the high dominance of Gammaproteobacteria in KRC. These findings are consistent with previous studies reporting the enrichment of Proteobacteria in woody tissues (Bulgarelli *et al.* 2013; Ren *et al.* 2018). Studies on Lauraceae species, including *Cryptocarya*, have shown that Proteobacteria constitute a major proportion of plant-associated bacterial communities (57.17% of total sequences) (Wu *et al.* 2023). Similarly, Proteobacteria have been reported as the dominant phylum in *Cinnamomum camphora*, ranging from 35.15% to 89.72% of the bacterial population (Elmaghzob *et al.* 2019). The dominance of certain genera in more exposed parts; in our case, branches (KRC) dominated by *Pantoea*, is also consistent with patterns described in studies of endophytic communities in woody plants. For example, a study on poplar trees found that the endophytic community in various parts of the tree (including wood) encompassed many taxa of *Proteobacteria, Firmicutes*, and *Actinobacteria*, with the internal community showing a different composition from epiphytic or outer parts (Ulrich *et al.* 2008). This dominance of *Pantoea* is interesting because many phyllosphere studies report other genera such as *Sphingomonas* and *Methylobacterium* as dominant taxa on leaf surfaces, for example in tea (Tan & Zou 2001) and various other plant species (Vorholt 2012; Bashir *et al.* 2022). Genera such as *Pseudomonas, Bacillus, Acinetobacter*, and *Sphingomonas* are commonly found as endophytes in various plant tissues, suggesting that there is a core group of plant endophytes that are adaptable to internal conditions (Trivedi *et al.* 2019). Apart from the dominance of *Pantoea*, several other genera, including *Pseudomonas, Sphingomonas, Parafilimonas, Erwinia,* and *Paraburkholderia*, were relatively more abundant in BP than in KBP and KRC. Many of these taxa have been described as Plant Growth-Promoting Bacteria

(PGPB) with functions such as phosphate solubilization, siderophore production, and systemic resistance induction (Hardoim *et al.* 2008; Compant *et al.* 2019; Trivedi *et al.* 2020). These findings support the interpretation that the main trunk is not just a passive transport pathway, but also a hotspot for functional endophytic diversity. The presence of *Erwinia* and *Paraburkholderia* at intermediate abundance is also consistent with reports that these two genera are often part of endophytic communities in woody plants and alpine plants, with some strains enhancing cold stress tolerance or supporting plant growth (Hardoim *et al.* 2008; Marian *et al.* 2025). In terms of function, diverse and stable endophytic communities (such as in BP) are likely to support the host through various mechanisms: production of secondary metabolites, phytohormones, siderophores, nutrient-solubilizing enzymes, or even bioprotection against pathogens, as outlined in reviews on the diversity and role of endophytic bacteria (Khan *et al.* 2020). This provides scientific evidence that the tree trunk could be a reservoir of endophytic microbes that have ecological and agronomic benefits for plants.

There are several limitations to this interpretation. Most of the available literature still relies on culture-dependent or PCR-based approaches, primarily focusing on roots, leaves, or stems of cultivated plants. Specific studies comparing internal tree compartments such as trunks, bark, and branches remain relatively limited. Studies on endophytes in woody trees have reported the presence of microbial communities within wood and internal tissues; however, the available data are often limited and do not consistently describe specific microhabitats in detail. Although the present results are consistent with existing theories and previous findings, the interpretation should be approached with caution. More comprehensive investigations, including shotgun metagenomics, functional analyses, and microhabitat-level environmental assessments, are required to better elucidate the mechanisms underlying the observed community patterns.

The results of this study indicate that tissue structure and spatial position are important determinants of endophytic community assembly. Internal tissues such as the trunk appear to provide a more supportive microhabitat for endophytic diversity and stability than more exposed tissues such as branches or bark. These findings provide empirical support for plant–microbe ecological interaction theory and suggest potential avenues for exploring the functional and biotechnological applications of endophytic communities. Future studies should focus on the functional characterization of selected culturable endophytic isolates through metabolomic analysis, detection of lactone-related compounds (e.g., GC–MS/LC–MS), and genome-based screening of fatty acid and polyketide biosynthetic genes. These approaches would facilitate the identification of endophytic bacteria capable of producing bioactive compounds analogous to massoia lactone for sustainable biotechnological applications.

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