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RESEARCH ARTICLE
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# Exploration of Secondary Metabolites from Mangroves and their Simbionts on the Merauke Coast for Innovations in Medicine and Cosmetics

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## ABSTRACT

The mangrove ecosystem holds significant potential as a source of bioactive secondary metabolites produced by both mangrove plants and their symbiotic microorganisms. This study aims to identify mangrove species along the Merauke coastal area, isolate and characterize secondary metabolites from the plants and their symbionts, and evaluate their antibacterial, enzymatic, and antioxidant activities, including GC–MS-based analysis of bioactive compounds as a foundation for innovations in natural pharmaceuticals and cosmetics. The methodology includes morphological identification of mangrove plants, phytochemical screening, isolation of microbial symbionts, molecular identification based on the 16S rRNA gene, antibacterial assays against *Pseudomonas aeruginosa* and *Escherichia coli*, enzymatic activity tests (protease, lipase, amylase), and chemical profiling using GC–MS. The results revealed five dominant mangrove species: *Acanthus ilicifolius, Hibiscus tiliaceus, Avicennia alba, Pyrenaria microcarpa*, and Ceriops tagal. Phytochemical tests confirmed the presence of alkaloids, saponins, steroids, tannins, and flavonoids, with the highest antioxidant activity observed in *A. ilicifolius* and *H. tiliaceus*. Molecular identification of microbial symbionts yielded three species: *Pseudoalteromonas maricolaris* strain NCIMB 2033, *Pseudoalteromonas piscicida* strain 80953-1, and Photobacterium ganghwense. Antibacterial and enzymatic assays demonstrated variable activity levels, while GC–MS analysis identified major compounds such as oleic acid, methyl oleate, linoleic acid, and methyl palmitate. In conclusion, mangrove plants and their symbionts from the Merauke coast represent promising sources of secondary metabolites with bioactive properties that support the development of natural marine biotechnology–based pharmaceuticals and cosmetic innovations.

**Keywords:** Mangroves, Microbial symbionts, Secondary metabolite, GC–MS, Natural pharmaceuticals.

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## INTRODUCTION

Mangrove ecosystems are highly productive coastal habitats that play a crucial role in maintaining ecological stability, supporting biodiversity, and sustaining coastal resilience in tropical and subtropical regions.

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These ecosystems function as natural barriers against coastal erosion, serve as nurseries for marine organisms, and contribute significantly to global carbon sequestration and nutrient cycling (Ariyanto & Pringgenies, 2024a). Due to their strategic ecological functions, mangroves have long been recognized as keystone ecosystems in coastal environments (Ariyanto et al., 2019). In recent years, however, mangroves have gained increasing attention not only for their ecological importance but also for their immense potential as sources of bioactive secondary metabolites with applications in medicine and cosmetic industries.

The mangrove areas along the Merauke Coast, Papua, Indonesia, represent a unique and relatively pristine coastal ecosystem characterized by high habitat heterogeneity and limited anthropogenic pressure (Zou et al., 2024). This region forms a complex ecological mosaic composed of diverse mangrove plant species and dynamic microbial communities inhabiting leaves, roots, sediments, and surrounding waters. Despite this ecological richness, mangroves from eastern Indonesia, including the Merauke Coast, remain scientifically underexplored compared to mangrove ecosystems in western and central regions of the country. This uneven research focus has resulted in significant knowledge gaps, particularly concerning the chemical diversity and biotechnological potential of mangrove-derived secondary metabolites and their associated symbiotic microorganisms (Ariyanto & Pringgenies, 2024b).

Mangrove plants are known to produce a wide range of secondary metabolites, such as flavonoids, alkaloids, terpenoids, tannins, phenolic acids, and saponins. These compounds are not directly involved in primary metabolic processes but play essential roles in plant defense, stress adaptation, and ecological interactions. The extreme and fluctuating environmental conditions experienced by mangroves including salinity stress, tidal inundation, hypoxia, and intense solar radiation act as strong selective pressures that drive the evolution of unique metabolic pathways. As a result, mangrove-derived metabolites often exhibit distinctive chemical structures and potent biological activities, making them attractive candidates for pharmaceutical and cosmetic development (Sulaiman et al., 2022).

Numerous studies have reported that secondary metabolites isolated from mangrove plants possess a broad spectrum of bioactivities, including antibacterial, antioxidant, anti-inflammatory, antifungal, anticancer, and wound-healing properties (Zou et al., 2024). These activities are highly relevant to the development of natural therapeutic agents and cosmeceutical products, particularly in response to increasing concerns over synthetic chemical ingredients and antimicrobial resistance. In cosmetic science, mangrove-derived compounds have shown promising potential as natural antioxidants, UV-protective agents, skin-soothing ingredients, and preservatives, aligning with the global trend toward sustainable and plant-based cosmetic formulations (Pringgenies & Setyati, 2021).

In addition to plant derived metabolites, microbial symbionts associated with mangrove ecosystems have emerged as prolific and often underappreciated sources of novel bioactive compounds. Mangrove-associated microorganisms—including endophytic and rhizospheric bacteria and fungi live in close association with their host plants and are exposed to intense ecological competition (Samsudin et al., 2019). These conditions stimulate the production of chemically diverse secondary metabolites that support microbial survival and mediate interactions with the host plant and surrounding environment. Importantly, many metabolites produced by microbial symbionts are structurally distinct from those synthesized by the host plants, thereby expanding the chemical diversity accessible through mangrove bioprospecting (Yu et al., 2024).

Recent research has demonstrated that mangrove-associated microorganisms produce secondary metabolites with remarkable biological activities, such as antibacterial, antioxidant, anti-inflammatory, cytotoxic, and enzyme-inhibitory effects. Compared to terrestrial microorganisms, mangrove-derived microbes often exhibit higher novelty rates in metabolite structures, reflecting the unique selective pressures of coastal and intertidal environments. Fungi and actinobacteria isolated from mangrove ecosystems, in particular, have been reported to yield compounds with strong pharmaceutical potential, including anticancer agents and antibiotic leads effective against drug-resistant pathogens (Han et al., 2025). These findings highlight mangrove microbial symbionts as promising yet underutilized resources for drug discovery and cosmetic innovation.

The resilience of mangrove ecosystems to extreme environmental stressors is closely linked to their chemical ecology. Secondary metabolites function as adaptive tools that enhance tolerance to salinity fluctuations, oxidative stress, and microbial invasion. From a biotechnological perspective, these adaptive compounds are highly valuable, as environmental stress-driven metabolites often possess enhanced stability and multifunctional bioactivities. Moreover, the interaction between mangrove plants and their microbial symbionts can influence metabolite production through co-evolutionary mechanisms, suggesting that integrated plant–microbe studies may reveal bioactive compounds that are absent when organisms are studied in isolation (Samsudin et al., 2019).

Despite growing global interest in marine and coastal bioprospecting, studies integrating mangrove plants and their symbiotic microorganisms within a single analytical framework remain limited. Many investigations focus solely on plant extracts or isolated microbial strains, without considering the ecological and biochemical interactions that shape metabolite diversity (Pringgenies & Setyati, 2021). This fragmented approach may overlook synergistic effects and obscure the full biotechnological potential of mangrove ecosystems. Furthermore, few studies have applied comprehensive analytical techniques, such as combined phytochemical screening, bioactivity assays, molecular identification, and gas chromatography–mass spectrometry (GC–MS), to systematically characterize secondary metabolites from mangroves and their symbionts, particularly in relatively undisturbed regions like the Merauke Coast (Yu et al., 2024).

In the context of sustainable development, mangrove bioprospecting aligns closely with the principles of green chemistry, biodiversity conservation, and circular bioeconomy. The exploration of natural bioactive compounds from mangrove ecosystems offers opportunities to develop environmentally friendly pharmaceuticals and cosmetic ingredients while promoting the sustainable use of local biological resources. For Indonesia, which hosts one of the largest mangrove areas in the world, responsible exploration of mangrove-derived metabolites represents a strategic pathway to strengthen marine biotechnology and natural product-based industries (Pringgenies & Setyati, 2021).

Therefore, this study aims to explore mangrove species along the Merauke Coast and to characterize secondary metabolites derived from both mangrove plants and their associated microbial symbionts using an integrated bioprospecting approach. The research combines phytochemical screening, bioactivity assays, molecular identification of microbial symbionts, and chemical profiling using GC–MS analysis. By linking ecological context with chemical and biological characterization, this study seeks to identify key secondary metabolites with potential applications in medicine and cosmetics. The findings are expected to contribute to the discovery of novel bioactive compounds, enrich current knowledge on mangrove chemical ecology, and reinforce the importance of conserving mangrove ecosystems as invaluable sources of future biotechnological innovation.

## MATERIALS & METHODS

### Sampling and Identification of Mangrove Species

Sampling was conducted in the mangrove ecosystem along the Merauke Coast, Papua, Indonesia, an intertidal environment characterized by fluctuating salinity, strong tidal gradients, and heterogeneous substrate conditions. This study was designed as an exploratory bioprospecting investigation rather than a quantitative ecological survey. Therefore, mangrove species were purposively selected based on their local dominance, accessibility, and apparent healthy condition, with the primary objective of exploring potential secondary metabolites rather than assessing species distribution or abundance.

Fresh plant materials, including leaves, bark, and roots, were collected from selected mangrove individuals using sterile gloves and sterile polyethylene bags to minimize contamination. Sampling was conducted during a single field campaign, and all samples were transported under cooled conditions and stored at 4°C prior to laboratory analysis, following standard procedures for natural product exploration (Alongi, 2020). Given the exploratory nature of the study, no plot-based or transect-based replication was applied, and the sampling strategy was not intended to support statistical comparisons among species or sites.

Mangrove species identification was performed based on morphological characteristics, following standard taxonomic keys and descriptions provided by Tihurua et al. (2020). Diagnostic traits, including leaf shape and venation patterns, bark texture, fruit morphology, and root structures, were examined and documented through high-resolution photographic records. Species identification was further supported by visual comparison with published herbarium references and regional mangrove identification guides.

Voucher specimens were not deposited in a registered herbarium, and molecular identification was not conducted in this study. Consequently, species identification should be regarded as morphological-based identification**,** suitable for exploratory bioprospecting purposes but not intended for taxonomic revision or phylogenetic analysis. This limitation is acknowledged, and future studies are recommended to incorporate voucher deposition and molecular confirmation to enhance taxonomic verifiability.

### Preparation of Extracts and Phytochemical Screening

Plant materials were washed with distilled water, air-dried at room temperature, and ground into powder. The samples were macerated using analytical-grade methanol at a ratio of 1:10 (w/v) for 72h at room temperature. The extracts were filtered and concentrated under reduced pressure using a rotary evaporator at 45°C, then stored in amber vials at 4°C until analysis.

Qualitative phytochemical screening was performed to detect the presence of major secondary metabolite classes, including alkaloids, flavonoids, saponins, terpenoids, tannins, and phenolics, following standard colorimetric and precipitation-based assays. The screening was conducted as a presence/absence assessment, without semi-quantitative scoring or extract yield determination. Accordingly, the results were interpreted as indicative of metabolite class diversity rather than relative abundance among species.

### Antioxidant Activity Assay

Antioxidant activity was evaluated using the DPPH radical scavenging assay following Sedjati et al. (2020). Crude extracts at several concentrations were mixed with 0.1mM DPPH solution and incubated for 30 min in the dark. Absorbance was measured at 517nm, and percentage inhibition was calculated relative to the DPPH control. $IC_{50}$ values were estimated from concentration–inhibition curves as an indicator of antioxidant potential.

This assay was conducted as a preliminary screening, and no positive control, regression parameters (equation or $R^2$), or measures of variability were included. Therefore, $IC_{50}$ values are interpreted descriptively to indicate relative antioxidant activity rather than for rigorous quantitative comparison. Antioxidant strength was categorized as very strong (<50ppm), strong (50–100ppm), moderate (100–150ppm), weak (150–200ppm), or very weak (>200ppm).

### Antibacterial Activity of Mangrove Extracts

Antibacterial activity was evaluated using the agar well diffusion method as a preliminary screening assay, following established procedures with minor modifications (Balouiri et al., 2016). Test bacteria included *Staphylococcus aureus, Escherichia coli*, and *Pseudomonas—aeruginosa*. Crude extracts were prepared at a concentration of 100mg/mL in 1% DMSO, and 50µL of each extract was

loaded into 6mm diameter wells on inoculated agar plates.

Plates were incubated at 37°C for 24 h, after which inhibition zones were measured using a digital caliper. Ciprofloxacin (10µg/mL) and 1% DMSO were used as positive and negative controls, respectively. This assay was intended to provide qualitative indications of antibacterial activity, and no minimum inhibitory concentration (MIC) or minimum bactericidal concentration (MBC) values were determined. Accordingly, inhibition zones were interpreted descriptively and were not used for quantitative comparison between crude extracts and the standard antibiotic.

**Isolation and Bioactivity Screening of Symbiotic Bacteria**

Leaves and roots were processed for bacterial isolation following surface sterilization procedures adapted from established protocols. Plant materials were rinsed sequentially in sterile seawater, 70% ethanol for 1 min, 2% sodium hypochlorite for 3 min, and finally rinsed three times in sterile seawater prior to plating onto Marine Agar. Plates were incubated at 28°C for 3–5 days, and morphologically distinct colonies were selected for purification. Pure isolates were preserved in 20% glycerol at –20°C for subsequent analyses.

This study did not include imprint or rinse controls to validate complete surface sterilization, and colony-forming unit (CFU) counts or isolation frequencies were not recorded; therefore, results are reported as exploratory isolations of culturable bacteria rather than definitive quantifications of endophytic populations.

Primary antibacterial activity of purified isolates was screened using the cross-streak method. Promising isolates exhibiting inhibition in cross-streak were further evaluated by agar well diffusion assays following Setyati et al. (2023). Enzymatic potentials (amylase, protease, and lipase) were assessed qualitatively on appropriate indicator media (starch hydrolysis for amylase, skim milk agar for protease, tributyrin agar for lipase, and carboxymethyl cellulose (CMC) agar for cellulase), with halo formation indicating positive activity as described by Zainuddin et al. (2021).

**Molecular Identification of Symbionts**

Genomic DNA was extracted from selected bacterial isolates using a commercial Qiagen DNA extraction kit according to the manufacturer's instructions. The 16S rRNA gene was amplified using universal bacterial primers 27F (5′-AGAGTTTGATCMTGGCTCAG-3′) and 1492R (5′-TACGGYTACCTTGTTACGACTT-3′). PCR amplification products were visualized on 1% agarose gel electrophoresis, purified, and subjected to Sanger sequencing.

Obtained sequences were analyzed using the BLASTn algorithm against the NCBI GenBank database to determine closest phylogenetic affiliations. Taxonomic assignment was performed at the genus level, as sequence similarity values ranged below the generally accepted threshold for confident species-level identification (≥98.7–99%). Phylogenetic relationships were inferred using MEGA X software through multiple sequence alignment and tree construction based on neighbor-joining methods with bootstrap analysis (Kumar et al., 2018).

The 16S rRNA sequences generated in this study were used for comparative and phylogenetic analysis but were not deposited in GenBank; therefore, molecular identification is presented as tentative and descriptive**,** intended to support bioactivity screening rather than formal taxonomic designation.

**GC–MS Analysis**

Chemical profiling of selected bioactive extracts was performed using an Agilent 7890B gas chromatograph coupled with a 5977A mass selective detector**,** equipped with a DB-5MS capillary column (30m × 0.25mm i.d., 0.25µm film thickness). The injector temperature was maintained at 250°C, and the oven temperature was programmed from 60°C to 300°C at a ramp of 10°C/min. Helium was used as the carrier gas at a constant flow rate.

Samples were analyzed without chemical derivatization; therefore, the GC–MS analysis was intended for qualitative profiling of volatile and semi-volatile constituents only. Compound identification was carried out by comparing mass fragmentation patterns with those in the NIST 14 mass spectral library, and results were reported as tentative identifications. No internal standards, retention indices, or absolute quantification procedures were applied. Relative abundance was estimated based on peak area normalization, and detected compounds were grouped according to general chemical classes to support comparative interpretation of extract composition.

**Statistical Analysis**

All experimental results, including inhibition zone diameters, enzymatic activity indices, and GC–MS chemical profiles, were obtained from technical triplicate measurements within the same experimental run to ensure analytical consistency. Given the exploratory nature of the study and the absence of independent biological replication, no inferential statistical analyses were performed. Data are therefore presented descriptively as mean values and comparative patterns, supported by tables and figures, to highlight relative trends among extracts and isolates rather than to infer statistical significance with Analysis of Variance - Tukey HSD used Rstudio 4.3.2 software.

## RESULTS

**Identification of Mangrove Plants**

Vegetation assessment along the Merauke Coast identified five dominant mangrove and mangrove-associated species: *Acanthus ilicifolius*, *Avicennia alba*, *Ceriops tagal*, *Hibiscus tiliaceus*, dan *Pyrenaria microcarpa* (Fig. 1). Species such as *H. tiliaceus* and *P. microcarpa* were primarily located in the land–mangrove transition zone, reflecting the heterogeneous structure of the southern Papua coastline. The presence of both true mangroves and associated species indicates a dynamic habitat capable of supporting diverse microbial assemblages.

**Phytochemical Screening**

Phytochemical profiling revealed that all five mangrove species contained major classes of secondary metabolites, alkaloids, saponins, steroids, and tannins, with varying distribution patterns. These results confirm that Merauke mangroves harbour rich chemical diversity with potential applications for pharmaceutical and cosmetic development derived from coastal natural products.

**Antioxidant Activity of Mangrove Extracts**

The DPPH assay indicated that extracts of *Acanthus ilicifolius* and *Hibiscus tiliaceus* exhibited notable radical-scavenging activity within the concentration range tested. Variations in antioxidant responses were observed among the mangrove extracts; however, given the exploratory nature of the study and the absence of independent biological replication, the results are presented descriptively to highlight relative activity patterns rather than statistically significant differences. These findings suggest the potential of selected mangrove species from the Merauke Coast as sources of antioxidant compounds for further investigation.

**Antibacterial Activity of Leaf and Root Symbionts Against *Staphylococcus aureus*, *Escherichia coli, Pseudomonas aeruginosa* (Fig. 1)**

Antibacterial activity varied substantially between leaf- and root-associated symbionts. Most leaf isolates produced no inhibitory zones (0mm), but several demonstrated measurable activity: D.AA.4.1.I (12.05±0.05mm), D.PM.4.2.H (5.675±0.225 mm) and D.CT.4.2.G (6.6±0.1mm) at 24 h.

Root-associated isolates showed notably stronger activity. Six of the 22 isolates tested produced inhibition zones between 9.6 and 29.3mm. Isolate A.HT.2.1.A exhibited the highest activity, increasing from 20.78±0.23mm (24 h) to 29.3±0.5mm (72 h), nearly matching the positive control (23.3± 0.3mm). These findings indicate that mangrove roots serve as a key microhabitat for microorganisms capable of producing potent antibacterial metabolites. Similar to the results observed against *Staphylococcus aureus*, most symbiotic isolates exhibited no detectable inhibitory activity against *Escherichia coli* under the assay conditions. A limited number of leaf-associated isolates produced measurable inhibition zones, including D.AA.4.1.I (12.7±0.9mm at 24 h), D.CT.4.2.G (8.03±0.33mm), and D.PM.4.2.H (6.58±0.23mm). Among root-associated isolates, A.HT.2.1.A showed the largest inhibition zone (11.63±0.13 mm at 24 h), followed by A.PM.2.1.D and A.LR.2.1.B, which produced inhibition zones in the range of 9-10mm.

Given the exploratory nature of this screening and the absence of standardized potency thresholds for crude symbiotic extracts, inhibition zones are reported descriptively without classification into activity strength categories. Several isolates showed reduced inhibition zone diameters at 72 h compared to 24 h; however, no chemical analyses were conducted to determine the underlying cause, and this observation is therefore reported descriptively without mechanistic interpretation. Overall, the results indicate that only a small subset of symbiotic isolates exhibited detectable antibacterial activity against *E. coli* under the conditions tested.

Moderate inhibition of *P. aeruginosa* was observed primarily in leaf-derived symbionts. Isolates D.AA.4.1.I, D.CT.4.2.G, and D.PM.4.2.H produced inhibition zones of 8.7±0.5mm, 6.775±0.325mm, and 5.275±0.225mm, respectively, during 48-72 h. Declining inhibition after 72h suggests reduced stability of the metabolites produced.

**Enzymatic Activity**

Hydrolytic enzyme assays showed variation among isolates (Table 1). Leaf-derived isolates D.CT.4.2.G, D.CT.2.1E, and D.CT.4.1E exhibited proteolytic indices ranging from 3.84 to 4.68 at 48 h. These observations reflect differences in hydrolytic potential among the Merauke mangrove symbionts, based on halo formation on indicator media

All isolates of hydrolysis exhibited larger zones than their growing zones (Fig. 3). Lipase and amylase enzyme showed significant differences ($P<0.05$), but protease enzyme has no significant.

Fig. 4 illustrates that the enzyme on leaf lipase and protease have no significant ($P>0.05$) differences, and the amylase enzyme showed significant differences ($P<0.05$). Protease activity was not significantly different between growth and hydrolysis zones in both roots and leaves.

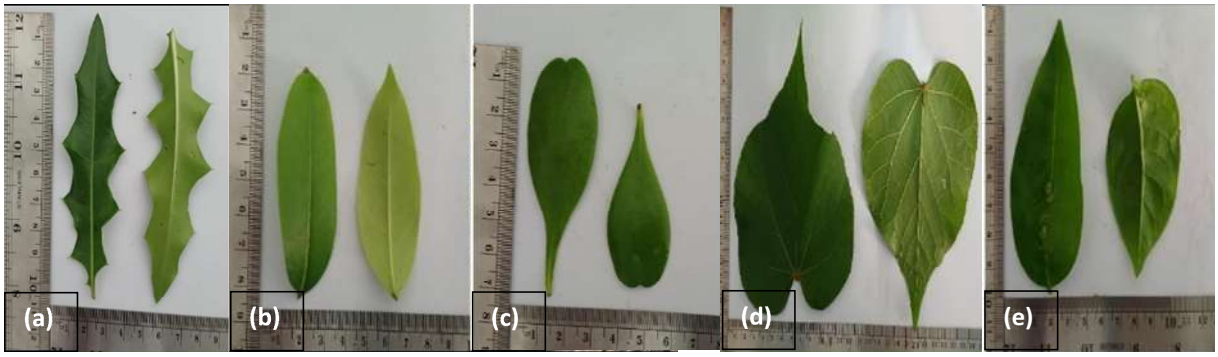


**Fig. 1:** *A. ilicifolius* (a), *A. alba* (b), *C. tagal* (c), *H. tiliaceus* (d), and *P. microcarpa* (e).

**Table 1:** Lipolytic, Proteolytic and Amylase activity of mangrove leaf and root symbionts

| Source | Isolate Code | Lipolytic Index (IL) |
|---|---|---|
| Leaf Symbionts | D.CT.2.1E | 1.38±0.13 |
| | D.CT.4.2G | 1.34±0.01 |
| | D.PM.4.2H | 1.33±0.06 |
| | D.AI.4.2F | 1.10±0.10 |
| | D.AVI.2.1A | 0.46±0.01 |
| Root Symbionts | A.AA.4.2H | 1.18±0.09 |
| | A.AA.4.2J | 1.06±0.01 |
| | A.AVI.2.1D | 1.13±0.23 |
| | A.BC.4.2I | 1.22±0.07 |
| | A.LR.2.1B | 0.67±0.18 |
| Source | Isolate Code | Proteolytic Index (IP, 48 h) |
| Leaf Symbionts | D.CT.4.2G | 4.68±0.15 |
| | D.CT.2.1E | 4.23±0.07 |
| | D.CT.4.1E | 3.84±0.18 |
| | D.AA.2.1A | 2.18±0.18 |
| | D.AI.4.2F | 1.88±0.12 |

## Molecular Identification of Leaf and Root Symbionts

BLAST analysis of 16S rRNA sequences (Table 2) showed that most isolates belonged to the genera *Pseudoalteromonas* and *Photobacterium*. Leaf isolate D.PM.4.2H exhibited 97.28% similarity to *Pseudoalteromonas maricolaris* (NR_025126.1), a species reported to produce antibacterial and enzymatic metabolites. Root isolate A.PM.2.2F showed 98.87% similarity to *Photobacterium ganghwense* (NR_043295.1), a genus known for enzyme production and diverse secondary metabolites. Leaf isolate D.CT.4.2.G aligned with *Pseudoalteromonas* sp. (95.51%), supporting the dominance of metabolite-producing marine bacteria within Merauke mangrove tissues. Species-level assignment is reported only for sequences with ≥98.7% identity; others are limited to genus level.

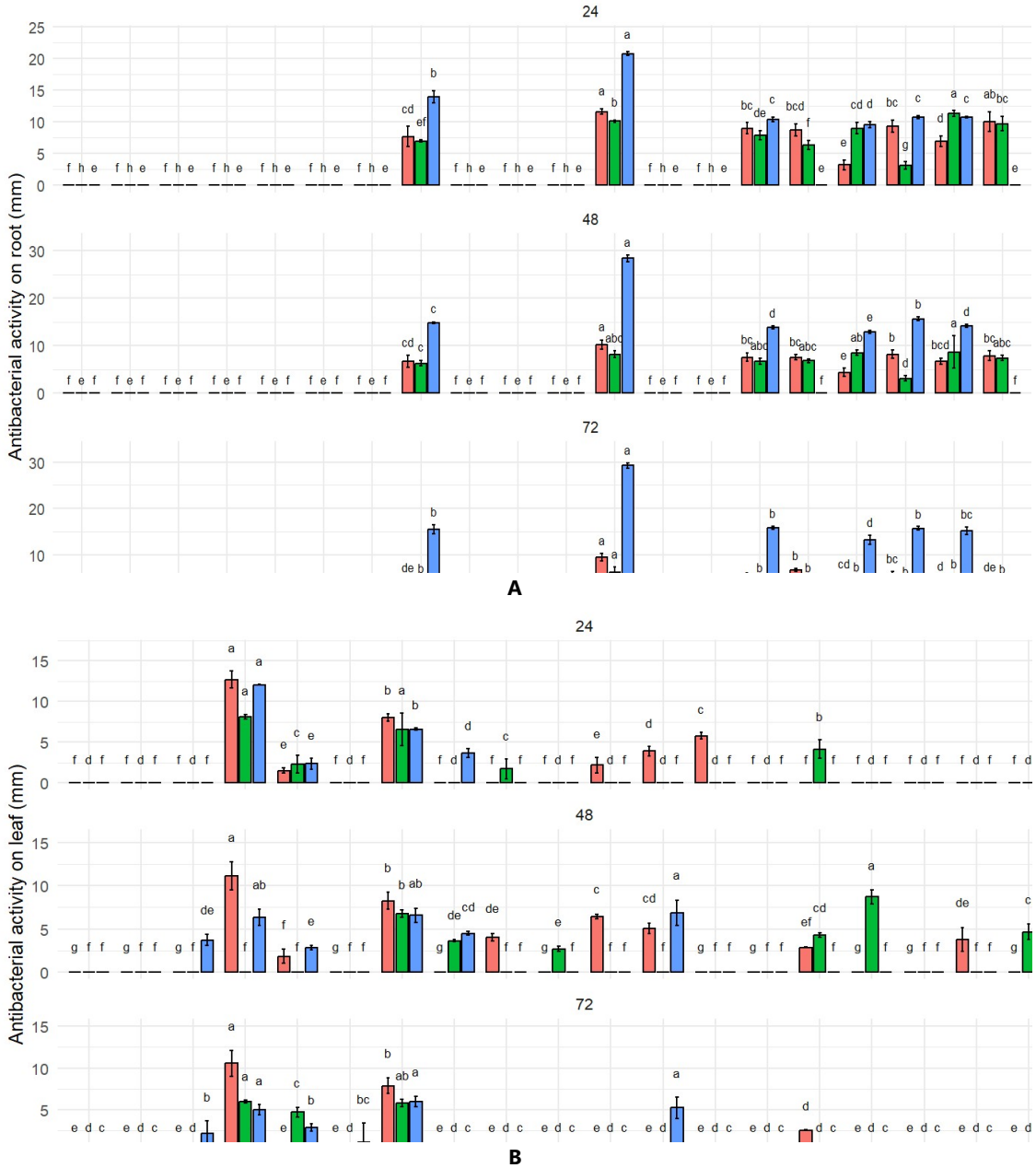


**Fig. 2:** Antibacterial activity of leaf and root symbionts against *Staphylococcus aureus, Escherichia coli, Pseudomonas aeruginosa* a) on root b) on leaf.

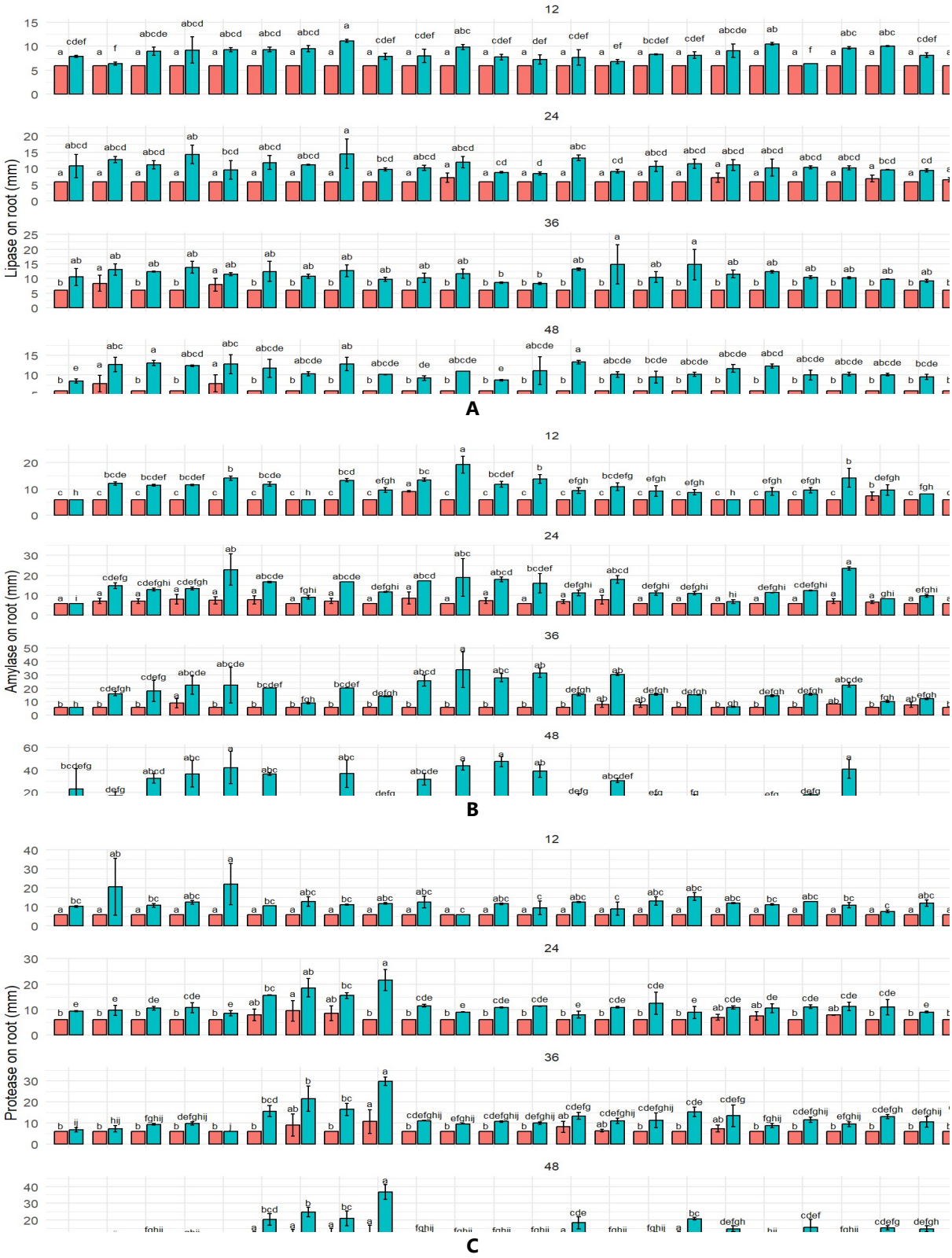


**Fig. 3:** Enzyme on root (a) lipase, (b) amylase, and (c) protease).

**Table 2:** Molecular Identification of Selected Leaf and Root Symbionts

| Isolate | Host Tissue | Closest Genus (NCBI BLAST) | % Identity | Sequence Length (bp) | Accession Number | Notes |
|---|---|---|---|---|---|---|
| D.PM.4.2H | Leaf | *Pseudoalteromonas* | 97.28 | 1483 | NR_025126.1 | Antibacterial, enzymatic |
| D.CT.4.2.G | Leaf | *Pseudoalteromonas* | 95.51 | 1475 | PX362271.1 | Moderate activity |
| A.PM.2.2F | Root | *Photobacterium ganghwense* | 98.87 | 1462 | NR_043295.1 | Bioactive metabolites |


**Fig. 4:** Enzyme on leaf (a) amylase, (b) lipase, and (c) protease.

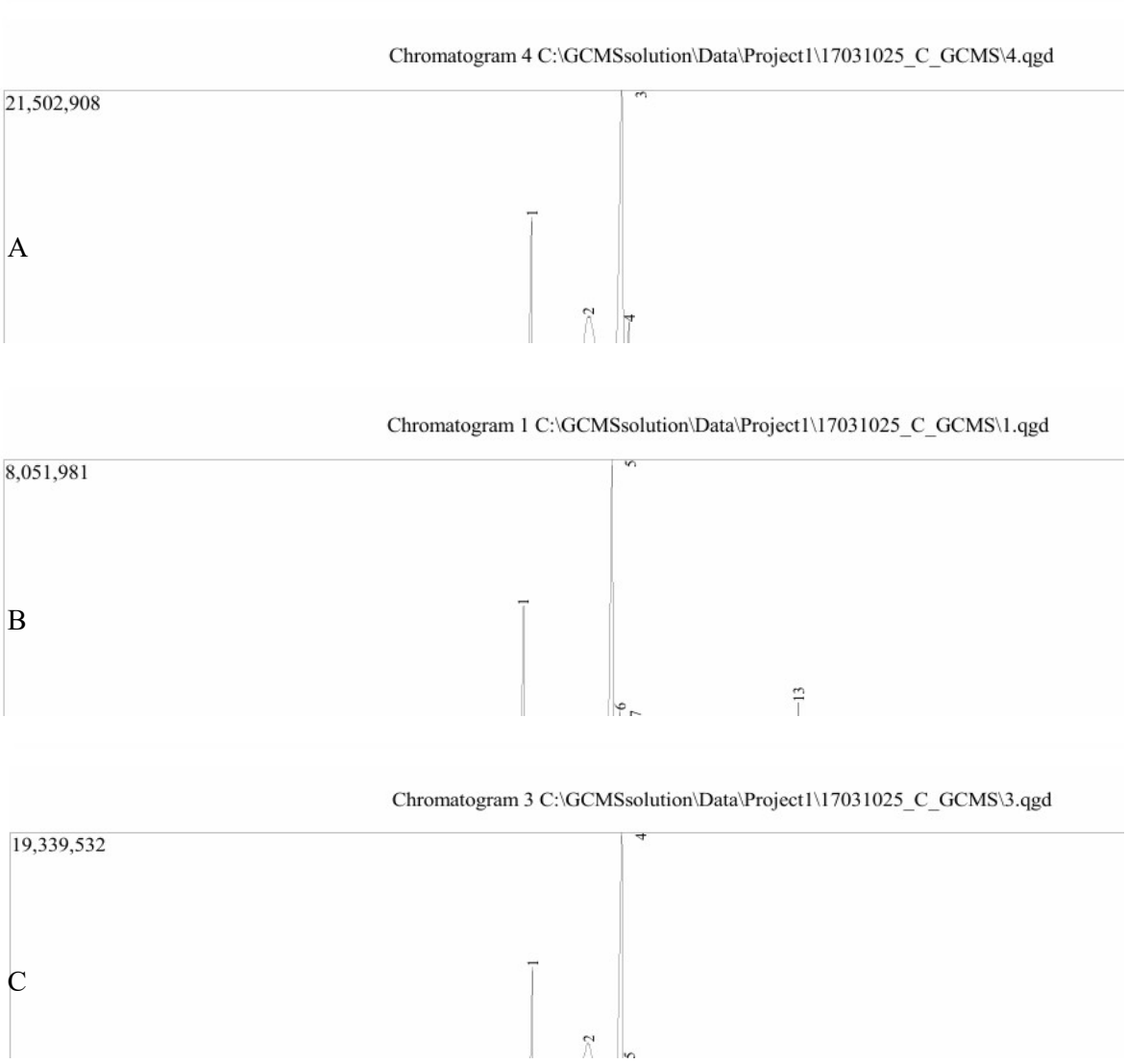


**Fig. 5:** GC–MS Profiles of Mangrove Symbionts: Leaf of *Pyrenaria microcarpa* (a), Leaf of *Ceriops tagal* (b), and Root of *Pyrenaria microcarpa* (c).

**GC–MS Analysis of Symbiont Extracts**

GC-MS profiling revealed a consistent dominance of fatty acids and derivatives across leaf and root symbionts. *P. microcarpa* (leaf) (Fig. 5a) shows major components were oleic acid (28.23%), methyl oleate (23.89%), methyl palmitate (9.12%) and linoleic acid (8.07%). Minor compounds included methyl stearate and cis-9-octadecenal. *C. tagal* (leaf) (Fig. 5b) shows dominant constituents, including oleic acid (26.12%), methyl oleate (24.87%) and oleic acid isomers (17.25%). Additional compounds such as cis-9-octadecen-1-ol and muscalure indicated chemical complexity. *P. microcarpa* (root) (Fig. 5c) shows root symbionts displayed the highest lipidic metabolite dominance, with oleic acid (30.12%), methyl oleate (21.52%) and oleic acid isomers (18.88%). Minor compounds included methyl palmitate, methyl stearate and several oxygenated derivatives. Overall, GC–MS results demonstrate that mangrove-associated microbes synthesize bioactive lipid compounds with strong potential for pharmaceutical and cosmetic innovation.

## DISCUSSION

The identification of *Acanthus ilicifolius*, *Avicennia alba*, *Ceriops tagal*, *Hibiscus tiliaceus*, and *Pyrenaria microcarpa* as seen in Fig. 1, along the Merauke Coast reflects a structurally diverse mangrove ecosystem with high ecological and biotechnological value. As a pioneer species, *A. ilicifolius* contributes to sediment stabilization and provides microhabitats, consistent with reports from other regions (Kathiresan & Bingham, 2001; Alongi, 2020). *A. alba*, characterized by its pneumatophores, supports gas exchange and coastal protection, aligning with prior findings in Southeast Asian mangroves (Alongi, 2020). *C. tagal*, known for salinity tolerance, serves as a reliable ecological indicator for estuarine quality, corroborating studies in tropical mangrove estuaries (Serosero et al., 2020; Ayyaz et al., 2023). Collectively, these species confirm the high biotechnological potential of Merauke mangroves as sources of bioactive metabolites (Sedjati et al., 2020; Pringgenies et al., 2024).

Phytochemical screening revealed the presence of major secondary metabolites including tannins, steroids, alkaloids, and saponins. *A. ilicifolius* contained tannins, known for antioxidant and antimicrobial activity (Gong et al., 2019; Wu et al., 2023). *H. tiliaceus* displayed steroids and tannins, supporting previously reported anti-inflammatory potential (Awal et al., 2016). *A. alba* and *P. microcarpa* contained saponins and tannins, consistent with defensive chemistry observed in Avicennia species elsewhere (Alongi, 2020). *C. tagal* exhibited the most chemically diverse profile, reinforcing its reported pharmacological versatility (Gupta & Gupta, 2020; Nengsih et al., 2021). While direct antibacterial activity was limited in crude extracts, the metabolite diversity aligns with prior studies suggesting the need for fractionation to reveal specific bioactivities (Sedjati et al., 2020; Duryat et al., 2024).

Antioxidant assays indicated that *A. ilicifolius* and *H. tiliaceus* exhibited the highest radical-scavenging activity, likely driven by phenolics such as flavonoids and tannins. This pattern corresponds with previous reports of strong antioxidant potential in *A. ilicifolius* from other regions (Sedjati et al., 2020; Zhang et al., 2022). Moderate activity observed in *A. alba*, *P. microcarpa*, and *C. tagal* reflects the presence of saponins and alkaloids, which generally exhibit weaker radical-scavenging effects (Nengsih et al., 2021; Zhu et al., 2024). Such interspecies variation highlights biochemical specialization and adaptive strategies to the local environment (Duryat et al., 2024).

Root-derived symbiotic bacteria demonstrated higher antibacterial activity than leaf-derived isolates, with several isolates showing moderate inhibition against *Pseudomonas aeruginosa* (e.g., A.PM.2.1.B) as see in Fig. 2. This trend agrees with prior studies reporting that mangrove roots harbor more metabolically active symbionts due to nutrient-rich and anaerobic sediment conditions (Pringgenies et al., 2021; Sulaiman et al., 2022). Lower activity against *P. aeruginosa* compared to *E. coli* aligns with known Gram-negative resistance mechanisms, particularly efflux pumps (Sedjati et al., 2020). Previous studies have similarly observed that root-associated microbes typically display stronger antimicrobial potential than leaf isolates, supporting the idea that mangrove sediments select for bioactive metabolite producers (Zhang et al., 2022; Putri et al., 2025).

Enzymatic assays revealed hydrolytic activity among leaf- and root-derived isolates (Fig. 3) Root microbiota such as A.AVI.2.2G exhibited notable proteolytic, lipolytic, and amylolytic activity, reflecting adaptation to nutrient-rich, anaerobic sediments (Table 1). These results correspond with reports that marine microorganisms are significant sources of industrially relevant enzymes, including alkaline proteases and lipases (Barzkar, 2020; Putri et al., 2025). Such enzymatic potential suggests applicability in cosmetic and pharmaceutical formulations, particularly for enzymatic exfoliation or peptide-based active ingredients (Fig. 4).

Molecular identification (Table 1) confirmed the dominance of *Pseudoalteromonas* and *Photobacterium* among symbionts, genera widely recognized for producing antimicrobial, antioxidant, and anti-inflammatory metabolites (Paulsen et al., 2019; Martinez-garcia et al., 2024). The GC–MS analysis of plant-symbiont extracts revealed compounds such as oleic acid, methyl oleate, linoleic acid, muscalure, and allyl octadecanoate, which are associated with anti-inflammatory, antimicrobial, emollient, and aromatic properties (Pringgenies et al., 2023; Wang et al., 2025; Kusuma & Rahmawat, 2025). These findings are consistent with prior reports demonstrating that mangrove-associated bacteria contribute to bioactive fatty acid production (Zubair et al., 2021; Nisha et al., 2025)

Environmental conditions along the Merauke Coast, including fluctuating salinity, tidal gradients, and nutrient availability, appear to shape the metabolite profiles of mangrove symbionts. Similar observations in other mangrove ecosystems suggest that local environmental pressures can have a stronger influence on microbial community composition than geographic distance alone (Sulaiman et al., 2022). This reinforces the potential of Merauke's mangrove ecosystem as a rich source of natural products for pharmaceutical, cosmetic, and biotechnological applications.

Despite revealing the bioactive potential of Merauke mangroves and their symbionts, this study has several limitations. Sampling was limited to a few dominant species and specific sites, which may not capture the full chemical and microbial diversity of the region. Enzymatic and antibacterial activities were assessed qualitatively or descriptively, without quantitative enzyme units or MIC/MBC determinations, limiting direct comparisons with other studies. GC–MS analyses provided preliminary metabolite profiles (Fig. 5), but further purification and structural elucidation of active compounds are required to confirm their specific bioactivities.

Future research should expand spatial and temporal sampling, include additional mangrove species, and incorporate rigorous quantitative assays to validate bioactivity. Integrating metabolomics, proteomics, and genomics approaches could elucidate the molecular basis of bioactive compound production. These efforts would strengthen the potential for developing natural product-based pharmaceuticals, cosmetics, and industrial enzymes from Merauke's unique mangrove ecosystem.

## Conclusion

This study identified five mangrove species along the Merauke Coast and confirmed the presence of major secondary metabolite groups with strong antioxidant potential, particularly in *A. ilicifolius* and *H. tiliaceus*. Molecular identification revealed three dominant symbionts, *Pseudoalteromonas maricolaris, P. piscicida*, and *Photobacterium ganghwense,* which exhibited moderate antibacterial and diverse enzymatic activities. GC-MS analysis identified key lipidic metabolites, including oleic acid, methyl oleate, and linoleic acid, supporting their relevance for pharmaceutical and cosmetic applications. Overall, mangroves and their microbial symbionts from Merauke represent a valuable biological resource for developing marine biotechnology based natural products.

## DECLARATIONS

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