



Natural Inhibitors from *Polyalthia longifolia* Target NDM-1 and DNA Gyrase B in Multidrug-Resistant *Klebsiella pneumoniae* and *Acinetobacter baumannii*: An Integrated Experimental and Computational Study

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ABSTRACT:

Background: *Acinetobacter baumannii* and *Klebsiella pneumoniae* are WHO critical-priority pathogens with widespread multidrug resistance, posing a significant threat to global health. This study evaluated the antibacterial activity of solvent fractions of *Polyalthia longifolia* leaves and examined the molecular docking, pharmacokinetic, and toxicity profiles of its phytochemicals against NDM-1 and DNA gyrase B.

Results: All fractions exhibited antibacterial activity, with zones of inhibition ranging from 18.33 ± 0.33 to 23.00 ± 0.58 mm. The aqueous fraction was most active (*A. baumannii*: 22.33 ± 0.33 mm; *K. pneumoniae*: 23.00 ± 0.58 mm) and showed the lowest minimum inhibitory concentration (6.25 mg/mL). High-performance liquid chromatography identified Quercetin, Apigenin, and catechin as major bioactive constituents. Docking revealed that mangiferin (-9.263 kcal/mol), myricetin (-8.703 kcal/mol), and Baicalin (-8.411 kcal/mol) bound NDM-1 more strongly than reference drugs, while Quercetin (-7.400 kcal/mol), catechin (-7.262 kcal/mol), and Apigenin (-7.216 kcal/mol) showed high affinity for DNA gyrase B. ADME profiling indicated good oral bioavailability, moderate lipophilicity, and minimal CYP450 interference. Toxicity predictions confirmed low hepatotoxicity, cardiotoxicity, and mutagenic risks.

Conclusion: *P. longifolia* leaves possess potent antibacterial metabolites. Mangiferin, Quercetin, and myricetin showed strong inhibitory potential with favorable pharmacokinetic and safety profiles, supporting their promise as leads against multidrug-resistant *K. pneumoniae* and *A. baumannii*.

KEYWORDS:

Polyalthia longifolia, antibiotic resistance, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, NDM-1, DNA gyrase B, phytomedicine.

1. Introduction

Antimicrobial resistance (AMR) is widely recognized as one of the greatest threats to global health, with the World Health Organization describing it as a “silent pandemic” projected to cause 10 million deaths annually by 2050 if left unaddressed (1). Multidrug-resistant (MDR) bacteria, defined as organisms resistant to at least one agent in three or more antimicrobial classes, pose particular challenges to modern medicine (2). Among these, *Klebsiella pneumoniae* and *Acinetobacter baumannii* are classified as critical priority pathogens due to their high resistance levels and their association with severe clinical infections, including pneumonia, bloodstream infections, urinary tract infections, and wound sepsis (3–8).

Understanding the factors that drive resistance in these pathogens is essential for developing effective interventions. Mechanisms such as indiscriminate antibiotic use, horizontal gene transfer, biofilm formation, and efflux pump activity collectively limit the effectiveness of conventional therapies (5,9,10). Consequently, the rise of MDR pathogens has placed substantial strain on healthcare systems worldwide, particularly in low- and middle-income countries where access to novel antimicrobials is limited (11). The slowdown in new antibiotic development, due to high costs, long development timelines, and low returns on investment, further underscores the urgent need

for alternative therapeutic strategies (12).

Medicinal plants offer a promising source of structurally diverse bioactive compounds with antimicrobial potential. Historically, natural products have provided the foundation for many frontline antibiotics, and contemporary research continues to validate their importance in drug discovery (13–15). Phytochemicals such as alkaloids, flavonoids, terpenoids, phenolics, and tannins exhibit antibacterial, antifungal, anti-inflammatory, and antioxidant properties, highlighting their potential as templates for novel antimicrobial agents (16,17). These characteristics make plant-derived compounds particularly attractive for combating MDR pathogens and addressing the limitations of conventional antibiotics.

Among the many medicinal plants with antimicrobial potential, *Polyalthia longifolia* (family Annonaceae), commonly known as the Ashoka tree, has emerged as a particularly promising candidate. Its selection is based on both its rich phytochemical composition and its historical use in managing infections. Traditionally used across Asia and Africa, various plant parts—including leaves, bark, and seeds—have been employed to treat infections, fever, wound healing, and gastrointestinal disorders (18,19). Ethnobotanical surveys further highlight that leaf decoctions are widely used to treat bacterial infections (20), reflecting both cultural relevance and practical accessibility in resource-limited settings.

2. Materials and Methods

Test Microorganisms

Multidrug-resistant clinical strains of *Klebsiella pneumoniae* and *Acinetobacter baumannii* were used, selected due to their classification as critical-priority pathogens by the World Health Organization. Bacterial inocula were standardized to $\sim 1 \times 10^6$ CFU/mL using a 0.5 McFarland turbidity standard prepared by mixing 0.05 mL of 1% barium chloride dihydrate with 9.95 mL of 1% sulfuric acid. Strains were subcultured on nutrient agar, incubated at 37 °C for 18 hours, and suspended in sterile saline to match the McFarland standard visually (21).

Plant Material, Extraction, and Fractionation

Air-dried leaves of *Polyalthia longifolia* (syn. *Monoon longifolium*), Annonaceae, were collected and authenticated, and a voucher specimen was prepared. Crude ethanolic extraction was performed using maceration (22).

Briefly, 520 g of powdered leaves were soaked in 3 L of ethanol for three days with occasional shaking, filtered through muslin and Whatman No. 1 paper, concentrated, and stored at –20 °C. Fractionation was conducted via liquid–liquid extraction (23). The crude Extract was dissolved in water (1:10, w/v) and sequentially partitioned with n-hexane, a 1:1 n-hexane: ethyl acetate mixture, ethyl acetate, and water to yield four fractions: F1 (n-hexane), F2 (n-hexane: ethyl acetate), F3 (ethyl acetate), and F4 (aqueous). All fractions were concentrated, freeze-dried, and stored at 4 °C for further analysis. This polarity-gradient approach facilitates the enrichment of metabolites according to their solubility and chemical characteristics, enabling targeted evaluation of bioactivity.

Antibacterial Assays

The agar well diffusion method was used to evaluate antibacterial activity (23). Mueller–Hinton agar plates were inoculated with standardized bacterial suspensions. Wells (6 mm) were loaded with 100 μ L of Extract (100 mg/mL prepared in 5% DMSO), while amoxicillin or Ofloxacin served as positive controls based on the confirmed susceptibility of the multidrug-resistant (MDR) isolates to these antibiotics. Plates were allowed to pre-diffuse for 15 minutes at room temperature and subsequently incubated at 37 °C for 24 hours. Zones of inhibition were measured in millimeters. Minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) were determined using the broth dilution method followed by subculturing. Serial dilutions of the extracts (100–3.125 mg/mL) were prepared in Mueller–Hinton broth, inoculated with 0.5 mL of standardized bacterial suspension, and incubated at 37 °C for 24 hours. The MIC was defined as the lowest concentration showing no visible bacterial growth, while the MBC was defined as the lowest concentration yielding no growth upon subculture.

HPLC Profiling

Approximately 2 g of Extract was mixed with 20 mL of 1:1 acetonitrile–methanol, agitated for 30 minutes, and the organic phase was transferred to a 25 mL volumetric flask. Analysis was performed on an Agilent 1200 RP–HPLC system using a Hypersil BDS C18 column (250 mm \times 4.0 mm i.d.) with a mobile phase of 0.1% formic acid in water (A) and acetonitrile (B), gradient elution, 0.6 mL/min flow rate, 20 μ L injection, and 280 nm detection. Compounds were identified by comparing retention times and UV spectra with standards (23).

Generation and Preparation of Compound Library

Twelve (12) phytochemical compounds identified from *Polyalthia longifolia* by HPLC analysis were selected for *in silico* screening. The corresponding chemical structures of these HPLC-identified compounds, along with that of the reference drug, were retrieved from the PubChem database (<https://pubchem.ncbi.nlm.nih.gov>) in Structure Data File (SDF) format. All molecules were imported into the Schrödinger workspace (Schrödinger, 2021) and prepared using the LigPrep module to optimize molecular geometry, assign appropriate protonation states at physiological pH, and generate relevant tautomers and stereoisomers for subsequent computational analyses.

Protein Retrieval and Preparation

The X-ray crystallographic structures of the target proteins—*Klebsiella pneumoniae* metallo- β -lactamase-1 (NDM-1, PDB ID: 4EYB) and *Acinetobacter baumannii* DNA gyrase B (PDB ID: 7PQI)—were obtained from the RCSB Protein Data Bank. The selection of reference ligands for *in silico* screening was based on their mechanistic relevance to the chosen protein targets and known resistance pathways rather than phenotypic susceptibility profiles. Accordingly, Ofloxacin and novobiocin were used as standard inhibitors due to their established interactions with DNA gyrase B and ATP-binding enzymes, respectively. Protein preparation and grid generation were performed using the Schrödinger Protein Preparation Wizard with the OPLS4 force field.

Structure-based Virtual Screening

Prepared compounds from *P. longifolia*, along with the standard ligand, were docked against the target proteins using the extra precision (XP) Glide protocol in Maestro (Schrödinger Suite, 2021). XP docking was employed due to its high accuracy in ranking ligand binding affinities, albeit with longer computational time (23).

Binding Energy Calculations

Docked protein-ligand complexes were further refined using the local optimization feature in Prime. The binding free energy (Δ_{bind}) of each

complex was estimated through MM/GBSA calculations with the OPLS4 force field, providing quantitative insights into the stability and affinity of ligand interactions.

Statistical Analysis

All experimental data were processed using SPSS v22. One-way ANOVA was performed to compare group means, followed by Duncan's New Multiple Range Test for post hoc analysis. Statistical significance was considered at $p \leq 0.05$.

3. Results

Antibacterial Activity of *P. longifolia*

The antibacterial activity of the different solvent fractions of *P. longifolia* against multidrug-resistant *Acinetobacter baumannii* and *Klebsiella pneumoniae* is presented in Table 1. All fractions demonstrated inhibitory effects, with inhibition zones ranging between 18.33 ± 0.33 mm and 23.00 ± 0.58 mm. The aqueous fraction (F4) produced the highest zones of inhibition against both test organisms (22.33 ± 0.33 mm for *A. baumannii* and 23.00 ± 0.58 mm for *K. pneumoniae*), followed by the n-hexane fraction (F1). The ethyl acetate fraction (F3) exhibited the lowest activity, particularly against *A. baumannii*. The aqueous fraction exhibited the lowest MIC (6.25 mg/mL) against both *A. baumannii* and *K. pneumoniae*, suggesting the greatest potency. The ethyl acetate and n-hexane: ethyl acetate fractions recorded higher MICs of 25 mg/mL against *A. baumannii*. In contrast, all fractions except Fraction 4 required 12.5 mg/mL to inhibit *K. pneumoniae*. The aqueous fraction again demonstrated the lowest MBC against *A. baumannii* (12.5 mg/mL), whereas the ethyl acetate fraction was most effective against *K. pneumoniae* (12.5 mg/mL). Fractions 1 and 2 exhibited higher MBCs (25 – 50 mg/mL).

Phytochemical Profile by HPLC

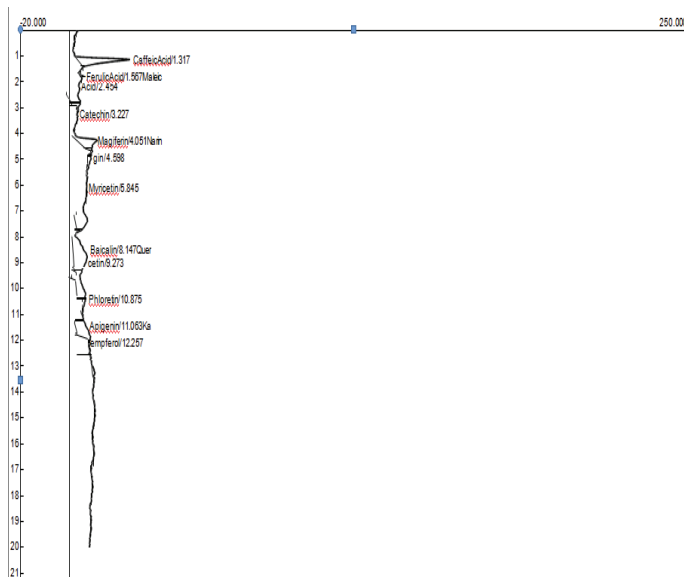
The HPLC chromatographic analysis (Table 2, Figure 1) revealed the presence of several bioactive compounds in the *P. longifolia* leaf extracts, notably Quercetin, Apigenin, catechin, and kaempferol.

Table 1: Antibacterial Activity of *P. longifolia* Extracts

Test organisms	Zone of Inhibition (mm)				MIC (mg/mL)				MBC (mg/mL)			
	F1	F2	F3	F4	F1	F2	F3	F4	F1	F2	F3	F4
<i>A. baumannii</i>	21.33 ± 0.67	19.33 ± 0.58	18.33± 0.33	22.33± 0.33	12.5	25	25	6.25	50	50	25	12.5
<i>K. pneumoniae</i>	22.67 ± 0.67	21.67 ± 0.58	21.33± 0.67	23.00± 0.58	12.5	12.5	12.5	6.25	25	25	12.5	25

Legend: F1- n-hexane fraction, F2- n-hexane/ethyl acetate fraction, F3- ethyl acetate fraction, and F4- aqueous fraction.

RetTime [min]	Type	Area [mAU*s]	Amt/Area [mg/L]	Amount [mg/L]	Grp	Name
1.317	VV E	20.25056	1.00097e-1	2.02702		Caffeic Acid
1.567	VV E	28.07921	4.69604e-3	1.31861e-1		Ferulic Acid
2.454	VV E	40.72340	3.20764e-2	1.30626		Maleic Acid
3.227	VV E	36.74120	1.7158e-2	1.13671		Catechin
4.051	VB	1399.65674	6.70379e-3	9.38301		Mangiferin
4.598	BB	142.88849	4.25662e-2	6.08223		Naringin
5.845	BB	80.81638	1.42089e-2	1.14831		Myricetin
8.147	VV X	1.19665e-1	7.75186	9.27626e-1		Baicalin
9.273	MM	20.02323	2.00894e-2	4.02254e-1		Quercetin
10.875	VV X	1.47642e-2	19.68298	2.90603e-1		Phloretin
11.063	MM	10.13986	8.18996e-2	8.30450e-1		Apigenin
12.257	MM	20.87885	3.63575e-2	7.59102e-1		Kaempferol

Table 2: HPLC-Identified Compounds of *Polyalthia longifolia* Leaf Extracts**Figure 1: Chromatogram of *Polyalthia longifolia* Leaf Extract**

Molecular Docking Interaction of *P. longifolia* with *K. pneumoniae* NDM-1

The binding affinities of the identified phytochemicals toward NDM-1 were compared

with standard drugs (Ofloxacin and novobiocin). Among the tested compounds, mangiferin (-9.263 kcal/mol), myricetin (-8.703 kcal/mol), and Baicalin (-8.411 kcal/mol) exhibited stronger binding affinities than Ofloxacin (-6.327 kcal/mol) and oxacillin (-6.286 kcal/mol) (Figure 2). These top-ranking ligands showed multiple hydrogen bonds with key active site residues, including GLN123, ASN220, and ASP124 (Figure 4, Table 3). Hydrophobic interactions were primarily observed with residues such as MET67, LEU65, ILE35, and TRP93, while mangiferin and Baicalin displayed π - π stacking with PHE70. The high binding affinities suggest potential inhibition of the bacterial β -lactamase enzyme comparable to or greater than that of the reference drug.

Molecular Docking Interaction of *P. longifolia* with *A. baumannii* DNA Gyrase B

For *A. baumannii*, Quercetin (-7.4 kcal/mol), catechin (-7.262 kcal/mol), and Apigenin (-7.216 kcal/mol) demonstrated the highest binding affinities compared to the standard novobiocin (-6.111 kcal/mol) (Figure 3). These compounds formed multiple hydrogen bonds and hydrophobic interactions with key residues such as ASP87, THR279, and VAL57 (Figure 5, Table 4). Kaempferol and myricetin also interacted favorably, forming π -cation or hydrogen bonds within the catalytic pocket, suggesting competitive inhibition potential against DNA gyrase B.

ADME and Drug-Likeness Properties

The ADME profiles of the top bioactive compounds are presented in Table 5. Most phytochemicals complied with Lipinski's rule of five, indicating good oral bioavailability and pharmacokinetic potential. Compounds such as Quercetin, myricetin, and kaempferol displayed moderate lipophilicity (iLOGP \approx 1.1–2.0) and acceptable polar surface areas (TPSA \leq 150 Å²).

High gastrointestinal absorption was predicted for most compounds, particularly Apigenin, kaempferol, and catechin. The compounds

exhibited variable CYP enzyme inhibition, with limited interactions with CYP2C9 and CYP2C19, suggesting low metabolic interference.

Toxicity Prediction

The toxicity profiles (Table 6) revealed that all tested compounds were non-carcinogenic and exhibited low hepatotoxicity and cardiotoxicity

risks (low hERG inhibition). None of the lead compounds showed significant Ames mutagenicity or acute oral toxicity, indicating favorable safety margins. Among all, mangiferin, Quercetin, and myricetin presented the most promising safety-efficacy balance, supporting their potential as lead candidates for further development against multidrug-resistant *K. pneumoniae* and *A. baumannii*.

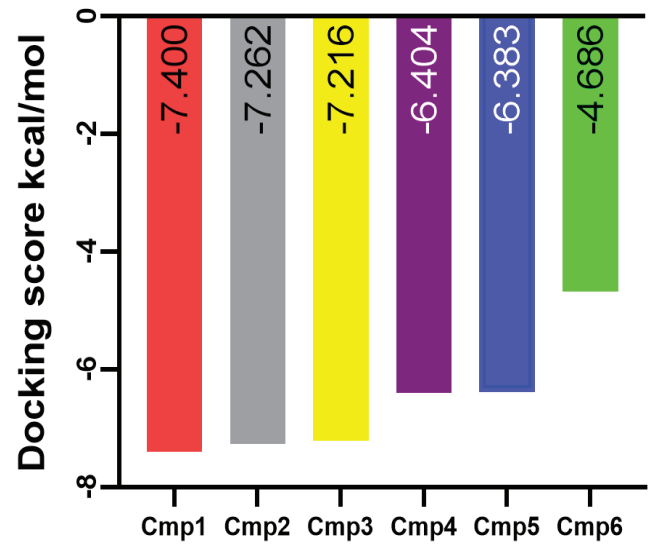
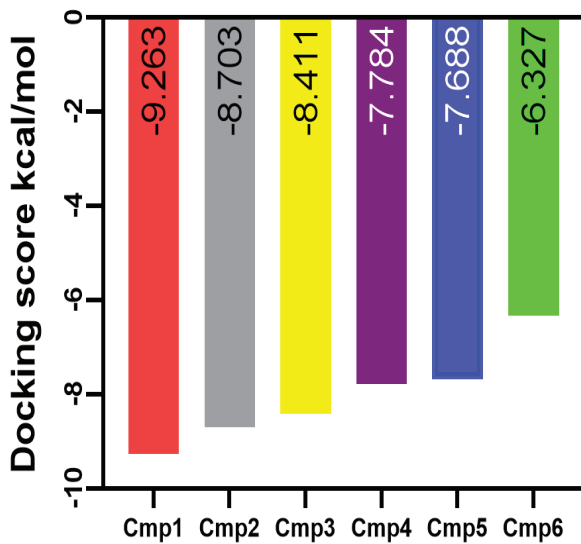
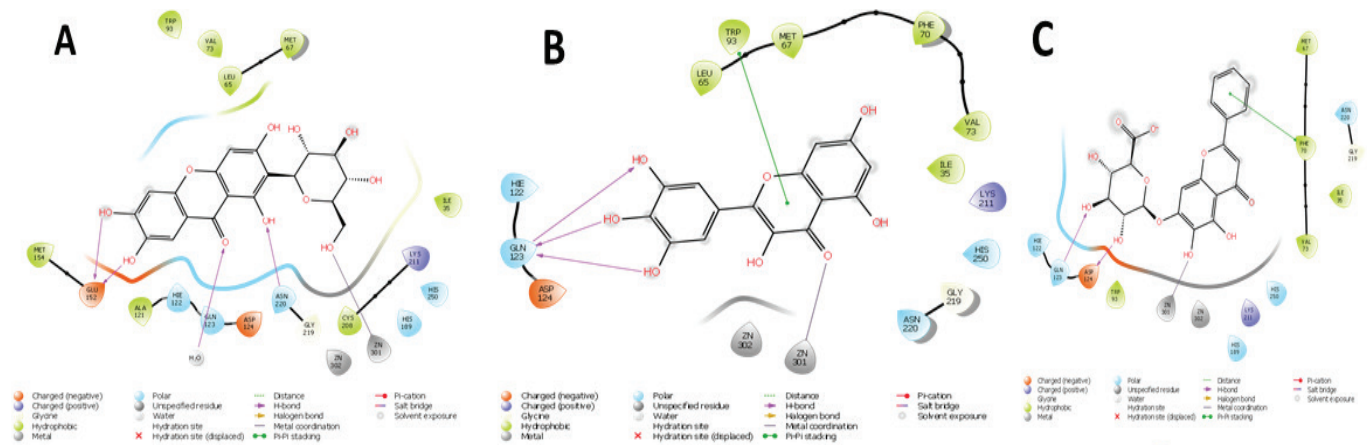


Figure 2: Graphical representation of the binding affinity calculation of the lead compounds from *P. longifolia* against *K. pneumoniae* NDM-1

Figure 3: Graphical representation of the binding affinity calculation of the lead compounds from *P. longifolia* against *A. baumannii* DNA gyrase B

Legend: cmp 1= Mangiferin cmp 2= Myricetin cmp 3= Baicalin cmp 4= Quercetin cmp 5= Maleic acid cmp 6= Ofloxacin

Legend: cmp 1= Quercetin cmp 2= Catechin cmp 3= Apigenin cmp 4= Kaempferol cmp 5= Myricetin cmp 6= Novobiocin



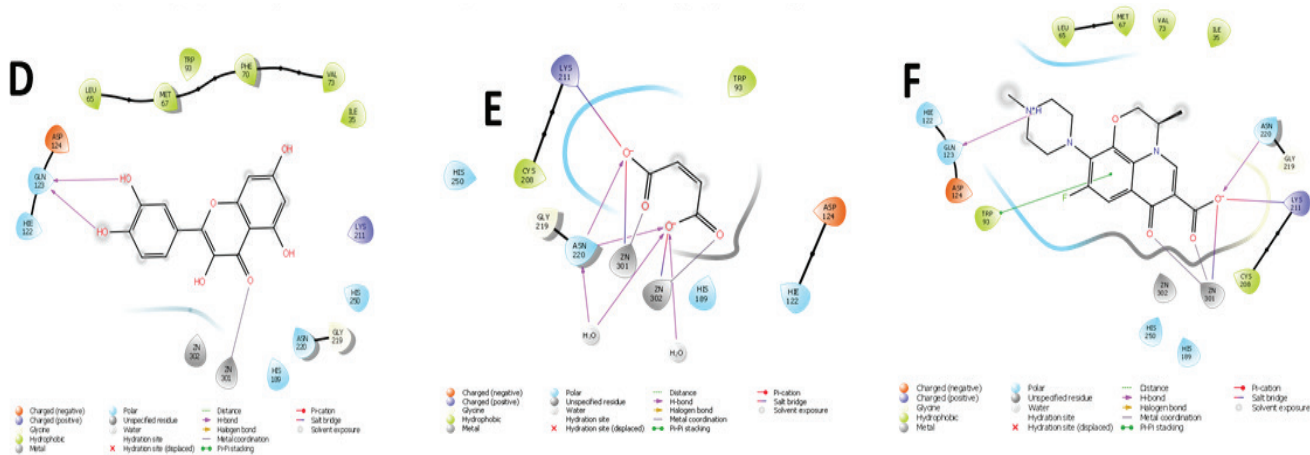


Figure 4: 2D Interaction between *P. longifolia* lead compounds and *Klebsiella pneumoniae* protein. Legend : (A) Mangiferin; (B) Myricetin; (C) Baicalin; (D) Quercetin; (E) Maleic acid; (F) Ofloxacin (standard).

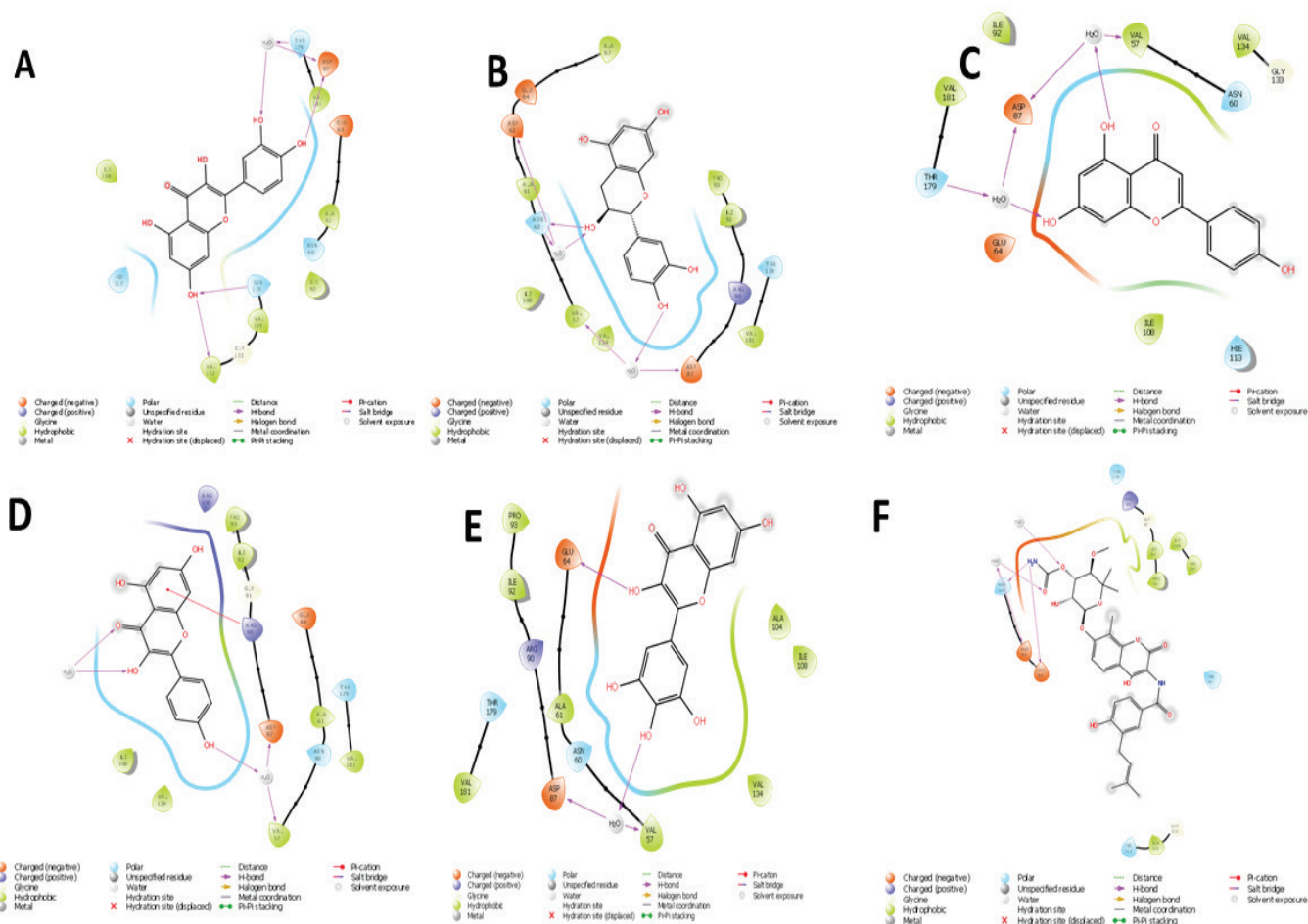


Figure 5: 2D interaction between lead compounds and *Acinetobacter baumannii* protein Legend: (A) Quercetin; (B) Catechin; (C) Apigenin; (D) Kaempferol; (E) Myricetin; (F) Novobiocin (standard).

Table 3: Hydrogen Bonds and Hydrophobic Interactions of the Lead Phytochemicals from *P. longifolia* with *K. pneumoniae*

Compound Name	H-Bond	Hydrophobic interactions	Other Interactions
Mangiferin	GLU152, ASN220	MET154, ALA121, CYS208, ILE35, LEU65, MET67, VAL73, TRP93	NONE
Myricetin	GLN123	TRP93, LEU65, MET67, PHE70, VAL73, ILE35	Pi-Pi stacking: TRP93
Baicalin	GLN123, ASP124	MET67, PHE70, VAL73, ILE35	Pi-Pi stacking: PHE70
Quercetin	GLN123	LEU65, MET67, TRP93, PHE70, VAL73, ILE35	NONE
Maleic acid	ASN220	TRP93, CYS208	Salt bridge: LYS211, ZN302, ZN302
Ofloxacin	GLN123, ASN220	LEU65, MET67, VAL73, ILE35, TRP93, CYS208	Salt bridge: LYS211, ZN301, Pi-Pi stacking: TRP93

Table 4: Hydrogen Bonds and Hydrophobic Interactions of the Lead Phytochemicals from *P. longifolia* with *A. baumannii*

Compound Name	H-Bond	Hydrophobic interactions	Other Interactions
Quercetin	THR279, ASP87, SER135, VAL132	VAL181, ALA61, ILE92, VAL134, VAL132, ILE108	NONE
Catechin	ASP63, ASN60, ASP87, VAL57	ALA67, PRO93, ILE92, ALA61, ILE108, VAL57, VAL134, VAL181	NONE
Apigenin	ASP87, THR179, VAL57,	VAL57, ILE92, VAL134, VAL181, ILE108	NONE
Kaempferol	ASP87, VAL57,	PRO93, ILE92, ALA61, ILE108, VAL134, VAL57, VAL181	Pi cation: ARG90
Myricetin	GLU64, ASP87, VAL57	ALA61, VAL57, VAL134, ILE108, ALA104, ILE92, PRO93, VAL181	NONE
Novobiocin	ASN60, GLU64	ILE92, ILE108, VAL107, PRO93, ALA114	NONE

Table 5: Drug likeness and ADME profile of the top bioactive compounds of *P. longifolia*

Compound Name	MW	HBA	HBD	TPSA	iLOGP	ROV	ESOL Log S	GIA	CYP2C19 inhibitor	CYP2C9 inhibitor
Quercetin	302.04	7	5	131.36	1.447712	0	-3.72159	0.133589	0.005855004	0.432249367
Ofloxacin	361.14	7	1	75.01	-0.11273	0	-1.97932	3.46E-06	2.59E-05	5.96E-06
Novobiocin	612.23	13	6	200.01	1.790881	1	-4.47123	0.122134	0.711179674	0.007009505
Myricetin	318.04	8	6	151.59	1.115212	0	-3.44294	0.31806	0.002221007	0.995218813
Mangiferin	422.08	11	8	201.28	0.059778	1	-3.15526	0.751839	1.91E-08	0.000311245
Maleic acid	116.01	4	2	74.6	-0.02442	0	0.404371	0.949129	3.26E-10	5.12E-05
Kaempferol	286.05	6	4	111.13	1.965317	0	-3.64796	0.015143	0.132401496	0.79935813
Catechin	290.08	6	5	110.38	1.172588	0	-2.58137	0.016103	9.82E-06	2.47E-06
Baicalin	446.08	11	6	187.12	1.300846	1	-2.30448	0.008194	6.57E-06	7.80E-07
Apigenin	270.05	5	3	90.9	2.980917	0	-4.21599	0.001684	0.112379447	0.002128024

Legend: MW= molecular weight, HBA= Hydrogen bond acceptor , HBD= Hydrogen bond donor, ROV=, GIA= Gastrointestinal absorption, BA= bioavailability

Table 6: Toxicity profile of the top bioactive compounds of *P. longifolia*

Compounds	Ames	hERG	Hepatotoxicity	Carcinogenicity	LD50(mg/kg)
Quercetin	0.586042	0.052722	0.337382	0.600177	['-']
Ofloxacin	0.920446	0.405136	0.988498	0.76824	[(9, 8, 7, 6, 5, 4, 25, 16, 15, 13, 12, 11)]
Novobiocin	0.748943	0.141221	0.88874	0.34689	['-']
Myricetin	0.657129	0.040223	0.325381	0.501712	['-']

Mangiferin	0.845841	0.015823	0.498865	0.282849	['-']
Maleic acid	0.207986	0.036178	0.242399	0.021734	['-']
Kaempferol	0.545969	0.069277	0.386179	0.715984	['-']
Catechin	0.458893	0.1343	0.556749	0.226083	['-']
Baicalin	0.499818	0.009341	0.428817	0.045225	['-']
Apigenin	0.617563	0.099782	0.435063	0.793352	['-']

Legend: Ames = Mutagenicity potential, hERG= Cardiotoxicity, LD50= Acute oral toxicity

• Abbreviations

- **ADME** – Absorption, Distribution, Metabolism, and Excretion
- **AMES** – Mutagenicity potential (Ames test)
- **ATP** – Adenosine Triphosphate
- **CYP** – Cytochrome P450 enzymes
- **DMSO** – Dimethyl sulfoxide
- **DNA** – Deoxyribonucleic acid
- **F1–F4** – Extract fractions (F1: n-hexane, F2: n-hexane:ethyl acetate, F3: ethyl acetate, F4: aqueous)
- **HPLC** – High-Performance Liquid Chromatography
- **hERG** – Human Ether-à-go-go-Related Gene (Cardiotoxicity potential)
- **iLOGP** – Lipophilicity prediction index
- **LD50** – Median lethal dose (Acute oral toxicity)
- **MBC** – Minimum Bactericidal Concentration
- **MIC** – Minimum Inhibitory Concentration
- **MDR** – Multidrug-resistant
- **NDM-1** – New Delhi Metallo-β-lactamase-1
- **PDB** – Protein Data Bank
- **TPSA** – Topological Polar Surface Area
- **XP Glide** – Extra Precision Glide docking protocol

β-lactam – Beta-lactam antibiotics

4. DISCUSSION

This study evaluated the antibacterial activity of different solvent fractions of *Polyalthia longifolia* leaves against multidrug-resistant *Acinetobacter baumannii* and *Klebsiella pneumoniae*, two critical-priority nosocomial pathogens (8,24). The rising prevalence of these resistant bacteria underscores the urgent need for alternative therapeutics, particularly natural products with established bioactive efficacy.

Antibacterial screening revealed variable inhibitory potencies among the solvent fractions. The aqueous fraction consistently produced the largest zones of inhibition and

the lowest MIC and MBC values against both pathogens, indicating a higher concentration of polar antibacterial constituents. HPLC profiling confirmed the presence of Quercetin, rutin, and other phenolic compounds, which are known to act synergistically to enhance antibacterial activity. These findings align with previous reports demonstrating that polar extracts of *Polyalthia longifolia* exhibit broad-spectrum antibacterial activity largely attributed to flavonoids, phenolics, and glycosides (25–27). Flavonoids such as Quercetin have been reported to disrupt bacterial membrane integrity, inhibit nucleic acid synthesis, and interfere with energy metabolism (27), thereby supporting the observed potency of the aqueous fraction.

In addition to polar phytochemicals, non-polar and moderately polar fractions of *P. longifolia* in the present study also exhibited antibacterial activity, albeit to a lesser extent. The n-hexane fraction showed appreciable inhibitory effects, particularly against *Klebsiella pneumoniae*, suggesting the involvement of lipophilic constituents such as terpenoids and fatty acids with membrane-disrupting and quorum-sensing inhibitory properties (28,29). Notably, clerodane-type diterpenoids previously isolated from *P. longifolia* have been reported to possess significant antibacterial activity, supporting the bioactivity observed in non-polar fractions. Faizi et al. (30) demonstrated that clerodane diterpenoids isolated from *P. longifolia* exhibited marked antimicrobial effects against pathogenic bacteria, highlighting the contribution of diterpenoid scaffolds to the plant's antibacterial profile.

The ethyl acetate fraction also demonstrated notable antibacterial activity and recorded the lowest MBC value against *K. pneumoniae*, emphasizing the bactericidal potential of moderately polar metabolites, including terpenoids, phenolic acids, and other semi-polar compounds. Collectively, these results underscore the influence of solvent polarity on phytochemical extraction efficiency and antibacterial efficacy, and further corroborate earlier reports that both polar phenolics and non-

polar diterpenoids contribute to the antimicrobial potential of *P. longifolia* (31).

Variability in bacterial susceptibility was evident, with *K. pneumoniae* being more sensitive than *A. baumannii*, consistent with the latter's robust efflux pumps and biofilm-mediated resistance (7,32). Fractionation preserved antibacterial efficacy, with the aqueous fraction achieving inhibition zones of 22.3 mm (*A. baumannii*) and 23.0 mm (*K. pneumoniae*), MICs of 6.25 mg/mL, and MBCs as low as 12.5 mg/mL, comparable to previous studies using crude extracts (26,33). The strong performance of the aqueous fraction likely reflects synergistic interactions among diverse metabolites (15).

At the molecular level, resistance in *K. pneumoniae* and *A. baumannii* is largely mediated by β -lactamases and DNA gyrase enzymes (34,35). The metallo- β -lactamase NDM-1 hydrolyzes β -lactam antibiotics (36,37), while Ofloxacin inhibits bacterial replication via stabilization of the DNA-DNA gyrase complex. DNA gyrase B in *A. baumannii* catalyzes ATP-dependent negative supercoiling of DNA, and Novobiocin competes at its ATP-binding site (38-40). Docking of *P. longifolia* phytochemicals against these targets provides mechanistic insight into their observed antibacterial activity.

Docking analyses revealed that Mangiferin, Myricetin, and Baicalin exhibited stronger binding affinities toward NDM-1 than Ofloxacin. Mangiferin (-9.263 kcal/mol) formed key hydrogen bonds with GLU152 and ASN220 and hydrophobic contacts with MET154, ALA121, CYS208, ILE35, LEU65, MET67, VAL73, and TRP93, stabilizing the complex. Myricetin (-8.703 kcal/mol) and Baicalin (-8.411 kcal/mol) showed robust interactions via hydrogen bonds, hydrophobic contacts, and π - π stacking, consistent with previous findings that hydroxyl-rich flavonoids enhance binding to target enzymes (41). Quercetin (-7.784 kcal/mol) and Maleic acid (-7.688 kcal/mol) demonstrated moderate binding, while reference antibiotics Oxacillin (-6.286 kcal/mol) and Ofloxacin (-6.327 kcal/mol) displayed weaker affinities. These findings indicate that natural compounds may demonstrate superior inhibitory interactions compared to standard drugs, in agreement with previous studies (22,42).

For *A. baumannii*, Quercetin exhibited the highest binding affinity (-7.400 kcal/mol), forming multiple hydrogen bonds with THR279, ASP87, SER135, VAL132, and ILE108, complemented by hydrophobic interactions. These results suggest that the natural compounds adopt favorable

conformations within the receptor's active site, enabling stable and meaningful interactions, consistent with previous findings (43,44). Catechin (-7.262 kcal/mol) and Apigenin (-7.216 kcal/mol) displayed comparable stabilizing interactions, while Kaempferol (-6.404 kcal/mol) and Myricetin (-6.383 kcal/mol) engaged in hydrogen bonding, hydrophobic contacts, and π -cation interactions with ARG90. By contrast, reference antibiotics Novobiocin (-4.686 kcal/mol) and Ofloxacin (-4.415 kcal/mol) showed lower docking scores, reflecting weaker binding tendencies and highlighting the potential of these natural compounds as effective inhibitors.

The correlation between *in silico* binding affinities and *in vitro* antibacterial outcomes reinforces the predictive accuracy of docking results. The aqueous fraction's superior potency is likely attributable to hydrophilic flavonoids, including Quercetin and Mangiferin, which interact favorably with both NDM-1 and DNA gyrase B, supporting dual inhibitory mechanisms that impair β -lactam hydrolysis and DNA replication.

ADMET profiling confirmed the pharmacological potential of the lead phytochemicals. Most compounds complied with Lipinski's Rule of Five, indicating favorable oral bioavailability and membrane permeability (45). Moderate lipophilicity (iLOGP: -0.024 to 2.98) supported membrane transport while maintaining solubility. Gastrointestinal absorption was high, and limited CYP450 inhibition suggested minimal metabolic interference. Notably, Myricetin and Catechin exhibit significant antioxidant and antibacterial activity with negligible CYP450 inhibition (46,47), consistent with the present study's findings. In contrast, Baicalin and Mangiferin showed restricted bioavailability due to high TPSA and numerous hydrogen bond donors, reflecting pharmacokinetic limitations typical of glycosylated polyphenols (41,48). Toxicity predictions indicated low mutagenic, hepatotoxic, and cardiotoxic risks for the natural compounds, whereas reference antibiotics Ofloxacin and Novobiocin displayed higher hepatotoxicity and Ames values, corroborating clinical reports of dose-related hepatocellular injury (49).

Overall, the combined *in silico* and *in vitro* evidence indicates that *P. longifolia* bioactive compounds exhibit dual antibacterial mechanisms—targeting β -lactamase and DNA gyrase B enzymes—similar to Novobiocin and Ofloxacin, while maintaining superior safety and pharmacokinetic profiles.

5. Conclusion

Polyalthia longifolia leaf fractions exhibit significant antibacterial activity against multidrug-resistant *A. baumannii* and *K. pneumoniae*, with the aqueous fraction showing the highest efficacy. The n-hexane fraction also demonstrated notable activity, highlighting contributions from both polar and non-polar phytochemicals. HPLC analysis identified flavonoids, phenolic acids, and alkaloids—including Mangiferin, Myricetin, Baicalin, Catechin, and Quercetin—as key bioactive compounds likely acting synergistically.

Molecular docking revealed strong binding affinities of these phytochemicals to clinically relevant bacterial targets (NDM-1 and DNA gyrase

B), surpassing or matching standard antibiotics and supporting dual inhibitory potential observed *in vitro*. ADMET profiling confirmed favorable pharmacokinetic and safety profiles, with good oral bioavailability, low CYP450 inhibition, and minimal toxicity, though some polyhydroxylated flavonoids showed limited gastrointestinal absorption.

These findings underscore the therapeutic potential of *P. longifolia* as a source of bioactive compounds with dual antibacterial mechanisms, combining cell wall disruption and DNA replication inhibition. Further *in vitro* and *in vivo* validation, along with optimization for solubility and absorption, is essential to translate these findings into clinically useful antimicrobial therapies.

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