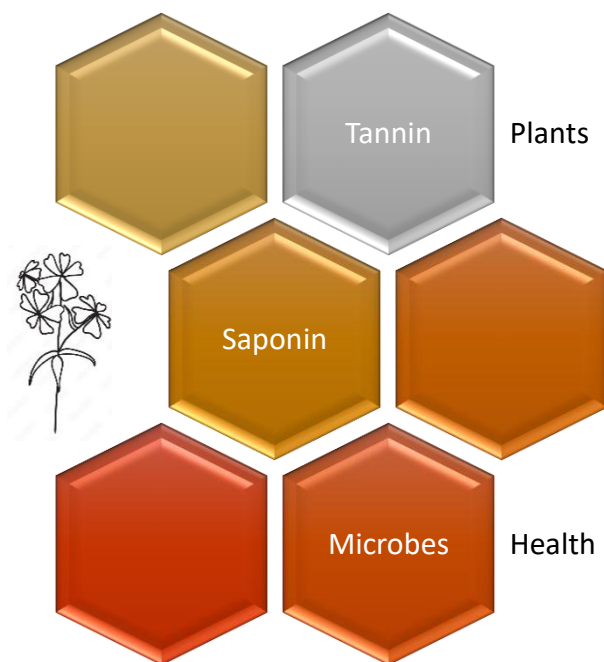


PLANTS & SECONDARY METABOLITES

VOLUME XI

Dr. Madhuri Vajha • Dr. Kugarthi Jayalakshmi • Dr. Preeti Chaturvedi



Plants & Secondary Metabolites

VOLUME 11



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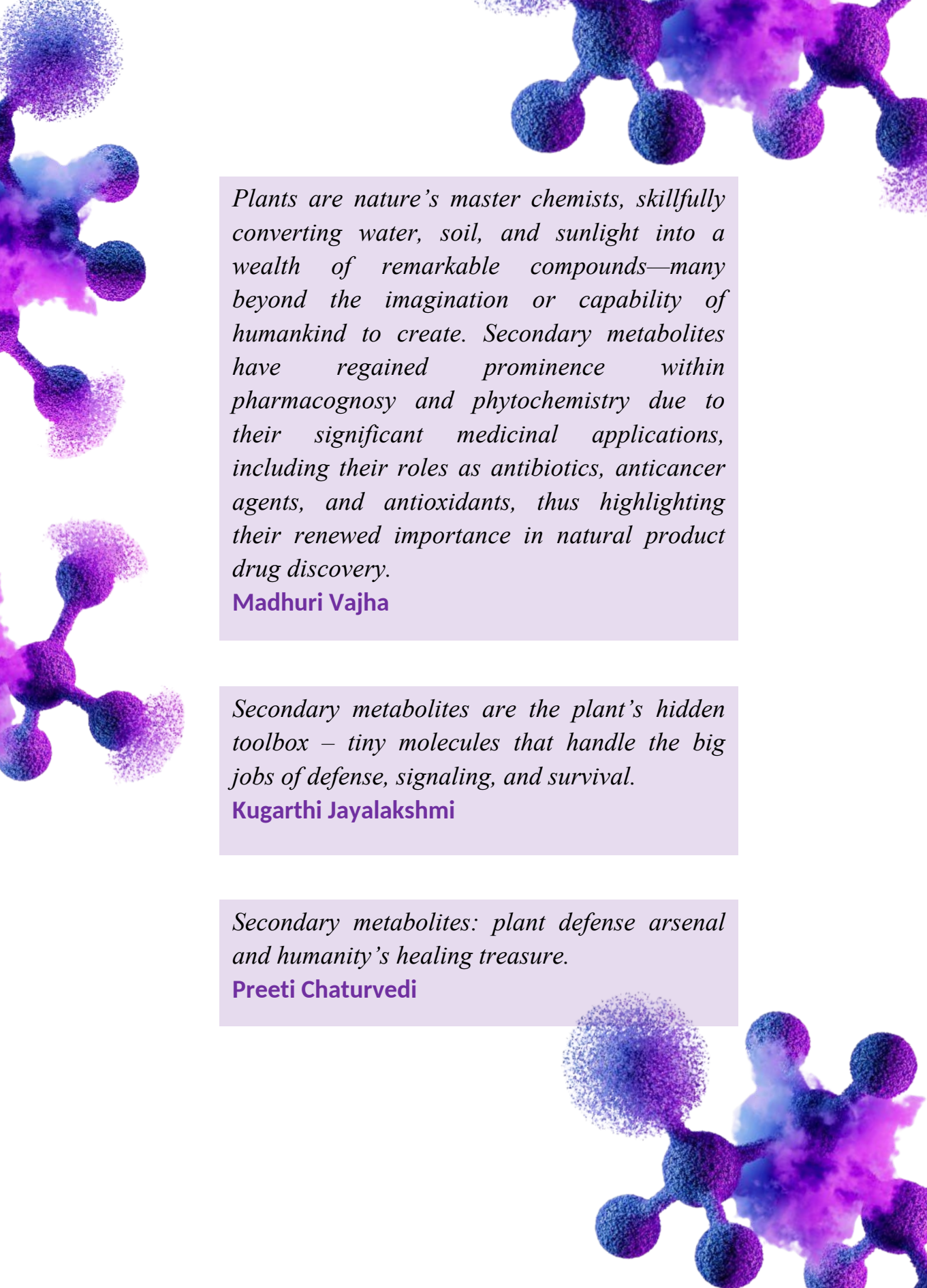
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Cover: Hexagonal structure

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The image features several decorative molecular structures in shades of blue and purple, scattered across the white background. These structures are composed of spheres (atoms) connected by lines (bonds), with some spheres having a textured, grainy appearance. They are positioned in the top-left, top-right, middle-left, and bottom-right corners, framing the central text blocks.

Plants are nature's master chemists, skillfully converting water, soil, and sunlight into a wealth of remarkable compounds—many beyond the imagination or capability of humankind to create. Secondary metabolites have regained prominence within pharmacognosy and phytochemistry due to their significant medicinal applications, including their roles as antibiotics, anticancer agents, and antioxidants, thus highlighting their renewed importance in natural product drug discovery.

Madhuri Vajha

Secondary metabolites are the plant's hidden toolbox – tiny molecules that handle the big jobs of defense, signaling, and survival.

Kugarthi Jayalakshmi

Secondary metabolites: plant defense arsenal and humanity's healing treasure.

Preeti Chaturvedi

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PREFACE

Plants have long stood at the intersection of nature and medicine, offering a silent yet powerful chemistry that continues to shape human survival and scientific curiosity. From ancient healing systems to modern pharmacological innovations, their secondary metabolites have emerged as key players in defense, communication and natural product research. This book, **“Plants & Secondary Metabolites, Volume 11”** is a compilation of research articles based on study of the phytochemicals and their pharmacology with relevance in a world facing mounting challenges of microbial resistance and ecological imbalance. This volume brings together eleven carefully curated chapters that explore a rich diversity of plant taxa from forest fruits and climbers to desert cacti and hemi-parasitic herbs, each contributing a unique profile of phytochemicals and bioactive potential. The studied species are wild and traditionally valued such as *Smilax zeylanica*, *Carissa spinarum*, *Diospyros sylvatica*, *Gouania leptostachya*, and *Striga densiflora*, to name a few. Included chapters revisit folk therapeutics and traditional knowledge systems, biochemical and antibacterial profiling while addressing the rising wave of antimicrobial resistance and reminding readers that plant based solutions may offer hope where conventional methods falter. This book serves as an invitation to observe more closely, to question more deeply, and to respect the intelligence embedded within plant systems. It is intended for researchers, students, conservationists, and scientists who seek interdisciplinary exploration between biodiversity and biotechnology, phytochemistry and pharmacology, curiosity and conservation.

(Editors)

BACKGROUND

The accelerating loss of biodiversity, alarming rise of drug resistant microbes and lifestyle related diseases are compelling scientists to turn back to nature for answers. Plants produce special chemicals called secondary metabolites that help them survive in their environment. These same compounds have shown great potential in treating infections and other health problems. However, many useful plants and their chemical properties are still not fully studied or recorded. And, much of this biochemical diversity remains underexplored and insufficiently documented. In this context, **“Plants & Secondary Metabolites”** emerges as a timely contribution, bringing together multidisciplinary research focused on the phytochemical composition and bioactive potential of diverse plant species, including climbers, forest trees, wild fruits, desert flora, hemi-parasitic herbs and lesser known plant species. This editorial book is needed because many modern medicines are slowly losing their effectiveness due to increasing drug resistance, while new diseases and infections continue to emerge. At the same time, countless plant species with healing potential remain unexplored or poorly documented. Plants produce powerful secondary metabolites that can serve as natural sources of new drugs, yet information about these compounds is scattered and incomplete. By bringing together focused research on different plant species, their phytochemical composition, and their biological activity this particular volume would help fill an important knowledge gap. It aims to provide a single, reliable platform for students, researchers, and professionals to access updated information, support further studies, and encourage the sustainable use of plant based resources in healthcare and biotechnology.

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Chapter 1

Evaluation of phytoconstituents and antibacterial activity of *Smilax zeylanica* L. (Smilacaceae)

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ABSTRACT

Herbal remedies play a vital role in traditional healthcare systems and are deeply rooted in indigenous knowledge. *Smilax zeylanica* L., commonly known as wild sarsaparilla, is a climbing shrub widely distributed across tropical regions of India and valued in Ayurveda, Siddha, and folk medicine for its diverse therapeutic uses. Traditionally, different parts of the plant have been used to treat various health problems. Present study was carried out to qualitatively analyze the phytochemical composition of *S. zeylanica* fruits and evaluate their antibacterial efficacy against *Escherichia coli*. Qualitative screening revealed that the hydroethanolic extract contained tannins, saponins, terpenoids, phenolic compounds, reducing sugars, and alkaloids. The antibacterial assay indicated a Minimum Inhibitory Concentration (MIC) of 50 mg/mL for the hydroethanolic extract, suggesting moderate antibacterial potential. These findings highlight the presence of pharmacologically important bioactive compounds in *S. zeylanica* fruits and validate its traditional use, emphasizing the need for further exploration into its therapeutic and nutraceutical properties.

Keywords: Phytochemistry, antibacterial potential, traditional medicine

INTRODUCTION

Traditionally, herbal medicines have been used intensively to treat various diseases (Rizvi *et al.*, 2022). Indigenous knowledge of traditional healers helped in treating common ailments like diarrhea, dysentery, stomach pain, cold, cough and flu (Ahmad *et al.*, 2006). With the arrival of modern medicine and rapid urbanization, the ancient medicinal practices have decreased significantly (García *et al.*, 2021). The need of this current situation indicates us towards culminating a future where the traditional knowledge associated with wild plants and their medicinal uses can be preserved. *Smilax zeylanica* (Figure 1) is one such plant in this series that steps up to its potential (Table 1). It is an evergreen climbing shrub belonging to the family Smilacaceae, commonly found in tropical and subtropical regions of India. Locally known by various names such as ‘Kantajuri,’ ‘Chobchini,’ or ‘Kumarika,’ this species has long been valued in traditional systems of medicine like Ayurveda, Siddha, and folk healing practices (Sabarisenthil and Kalaichelvan, 2017). The plant is renowned for its therapeutic versatility *i.e.* the whole plant, roots and leaves are used to treat a wide range of health disorders. Traditionally, the leaves were used as vegetable by some communities (Dhanya *et al.*, 2018). Roots and rhizomes are used in treating venereal diseases, skin diseases whereas plant is used in treatment of psoriasis, rheumatism, swellings, toothache, abscesses, dysentery, dropsy (Dhanya *et al.*, 2018; Jena *et al.*, 2011; Hossain *et al.*, 2013). Keeping the importance of *S. zeylanica*, an attempt has been made to document the general information, traditional uses, bioactive compounds and antibacterial activity.

Table 1: General information and traditional uses of *Smilax zeylanica*

Category	Details
Scientific Name	<i>Smilax zeylanica</i> L.
Family	Smilacaceae

Common name	Wild sarsaparilla, Ceylon sarsaparilla
Vernacular names	Hindi:Kumarika, Jangli Aushbah Sanskrit:Vanamadhusnahi, Chopachinee Odia:Mootri-lata Tamil:Ayadi, Malaittamarai Telugu:Kondadantena Bengali:Kumarika Marathi:Ghotvel Kannada: Kaadu Hambu Sinhala: Kabarassa, Kabarossa, Kabalossa (Sabarisenhil and Kalaichelvan, 2017).
Plant parts used	Whole plant, Root, rhizome, leaves
Traditional uses	
Root / Rhizome	Used in treating skin diseases (eczema, ulcers, psoriasis, leprosy) decoction used for rheumatism, gout, and joint pain (Sabarisenhil and Kalaichelvan, 2017).
Leaves	Consumed as vegetables (Sabarisenhil and Kalaichelvan, 2017).
Whole plant	In treating venereal diseases, psoriasis, rheumatism, swellings, toothache and abscesses, dysentery (Sabarisenhil and Kalaichelvan, 2017).

Its extensive ethnomedicinal applications highlight the deep-rooted wisdom of indigenous communities who have relied on it for generations. Recent

phytochemical studies further substantiated its pharmacological relevance (Kamble and Lobo, 2022) but much of the major experiments have been conducted on its leaves and roots while, fruits remain understudied. Therefore, through this experiment we put forth an attempt to study the phytochemical profile of the fruits of *S. zeylanica* and test their antibacterial potential through evaluating their Minimum Inhibitory Concentration (MIC) against *E. coli* that will help us validate the efficacy of folk medicinal practices associated with this plant.



Figure 1: Fruits of *Smilax zeylanica*

METHODOLOGY

Fruits of *Smilax zeylanica* were collected from Khordha, Odisha, India. The plant species (Figure 1) was identified by authors followed by referring to the published literature (Kumar *et al.*, 2022). Fruits were thoroughly

washed with water to remove dust. Further, they were extracted using maceration method with n-Hexane and Hydroethanolic for further experimental work. Detection of secondary metabolites using qualitative phytochemical analysis and estimation of Minimum Inhibitory Concentration (MIC) against *Escherichia coli* (MTCC 45) was done using standard methods (Jena *et al.*, 2025).

RESULTS AND DISCUSSION

The experimental study of *Smilax zeylanica* fruits (Figure 1) aimed to screen the bioactive compounds present in its fruits and use the results to study its antibacterial efficacy against *Escherichia coli*, common gut bacterium known to cause major gastrointestinal and urinary infections when overgrown (Zhou *et al.*, 2023). The qualitative phytochemical screening revealed that the occurrence of secondary metabolites varied with solvent polarity (Table 2). The n-hexane solvent extracted only non-polar compounds thus, only the reducing sugars were detected (Figure 3), while the hydroethanolic extract was found to be rich in several bioactive compounds (Figure 2), including tannins, saponins, terpenoids, phenolic compounds, reducing sugars, and alkaloids. The antibacterial assay using the hydroethanolic extract of *S. zeylanica* fruits showed inhibitory activity against *E. coli* (Table 3). The Minimum Inhibitory Concentration (MIC) was determined to be 50 mg/mL (Figure 4), as bacterial growth was observed at lower concentrations (25 and 12.5 mg/mL) but was inhibited at 50 mg/mL and above.

Table 2: Qualitative phytochemical analysis of *S. zeylanica*

Polarity	Extract	Detected secondary metabolites
Non-Polar	n-Hexane	Reducing sugars
Polar	Hydroethanolic	Tannin, Saponin, Terpenoids, Phenolic compounds, Reducing sugars and Alkaloids

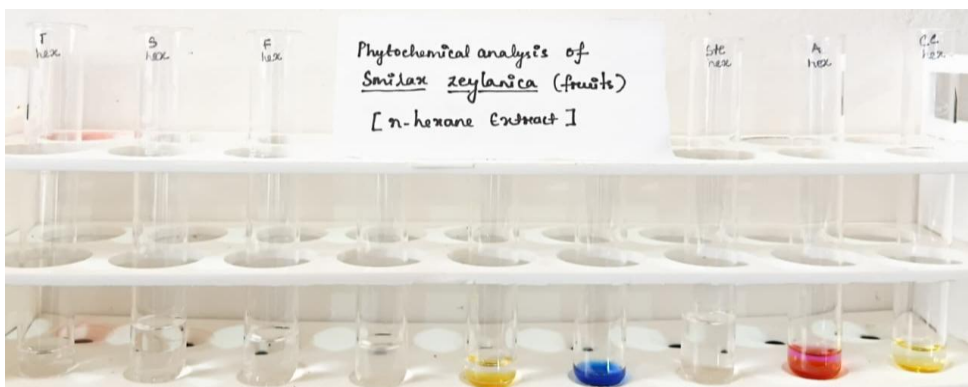


Figure 2: Phytochemical analysis of *S. zeylanica* using n-hexane extract

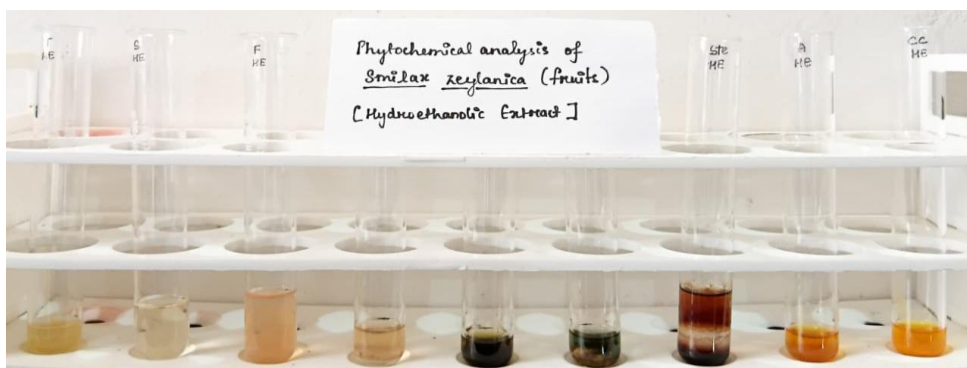


Figure 3: Phytochemical analysis of *S. zeylanica* using hydroethanolic extract

Table 3: Estimation of Minimum Inhibitory Concentration (MIC)

Hydroethanolic extract	Concentration (mg/mL)				MIC (mg/mL)
	100	50	25	12.5	
<i>Smilax zeylanica</i> (fruits)	NG	NG	G	G	50
Nutrient broth	NG	NG	NG	NG	-
Microbial broth	G	G	G	G	-

(NG: No growth of bacteria; G: Growth)

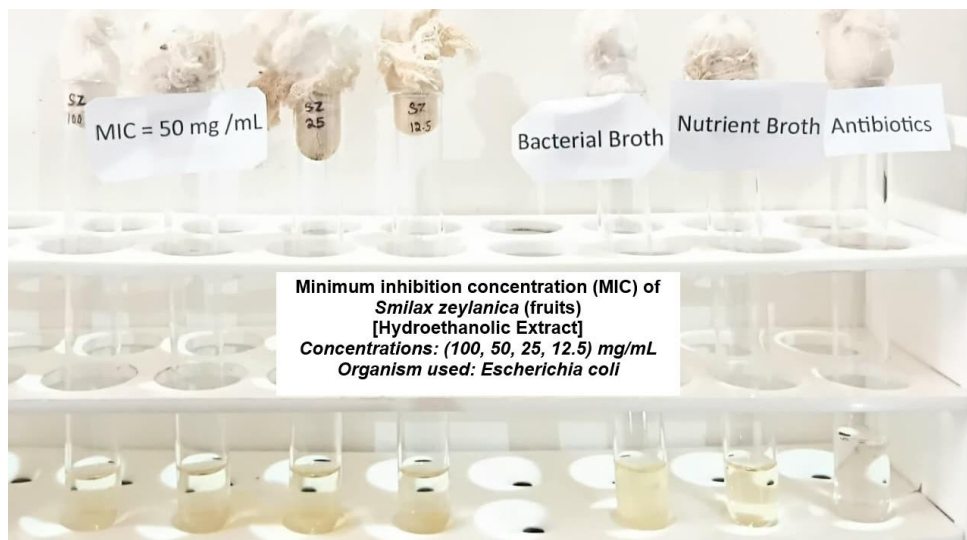


Figure 4: Minimum inhibition concentration (MIC) of fruits of *S. zeylanica*

These observations indicated that the presence of diverse secondary metabolites in the hydroethanolic extract of *S. zeylanica* contribute to its antibacterial potential against *E. coli*. If the phytoconstituents can be studied further, they can be used in developing edible plant based therapeutic agents against gastrointestinal ailments like diarrhea, dysentery, and indigestion.

CONCLUSION

This study reinforced the ethnomedicinal significance of *Smilax zeylanica*, a plant long recognized in traditional medicine for its broad spectrum of healing properties. The detection of multiple bioactive compounds such as tannins, phenolics and alkaloids in the fruit extract confirmed its potential as a source of natural therapeutic agents. Although the antibacterial activity observed was moderate, it provides a scientific basis for the plant's traditional applications in treating infectious and inflammatory conditions. Further quantitative and pharmacological studies are recommended for the isolation and characterization of the present active compounds responsible for these effects. Preserving and scientifically validating such traditional knowledge can contribute to the both sides: development of sustainable,

plant-based therapeutics and the conservation of indigenous medicinal heritage.

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Chapter 2

Study of microbial inhibition and secondary metabolites of *Naringi crenulata* (Roxb.) Nicolson (Rutaceae)

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ABSTRACT

In recent years, the global shift towards synthetic drug development has overshadowed the exploration of natural plant-based remedies, despite their long-standing contributions to traditional medicine. *Naringi crenulata* (Roxb.) Nicolson, a lesser-known member of the family Rutaceae, represents one such underexplored species with potential pharmacological importance. Present study aimed to evaluate the phytochemical composition and antibacterial activity of *N. crenulata* fruit extracts. Qualitative phytochemical screening revealed the presence of bioactive compounds such as tannins, flavonoids, alkaloids, phenols, and saponins predominantly in the hydroethanolic extract, while n-hexane extract showed limited metabolite presence. The antibacterial potential was assessed against *Escherichia coli* (MTCC 45) using the Minimum Inhibitory Concentration (MIC) method, demonstrating notable inhibition at lower concentrations in hydroethanolic extracts. These findings highlight *N. crenulata* as a promising source of natural bioactive compounds and support its potential role in developing plant based antibacterial agents.

Keywords: Phytochemicals, antibacterial activity, traditional remedies

INTRODUCTION

Today, the mainstream science gives so much attention to synthetic drug discovery that the real spirit of studying natural products is fading away (Atanasov *et al.*, 2021). The idea of discovering something new has veiled

the passion of researching the present resources we already have. While nature continues to rejuvenate the vast and largely unexplored library of flora amidst the growing pollution, human population, and destruction of natural habitats (Joppa *et al.*, 2011) we, as a generation can take initiatives to study, understand and preserve the traditional knowledge with immense therapeutic potential that is dying a slow death. *Naringi crenulata* (Figure 1), the only recognized member of the family Rutaceae under genus *Naringi*, stands as one such promising species that deserves deeper scientific exploration.

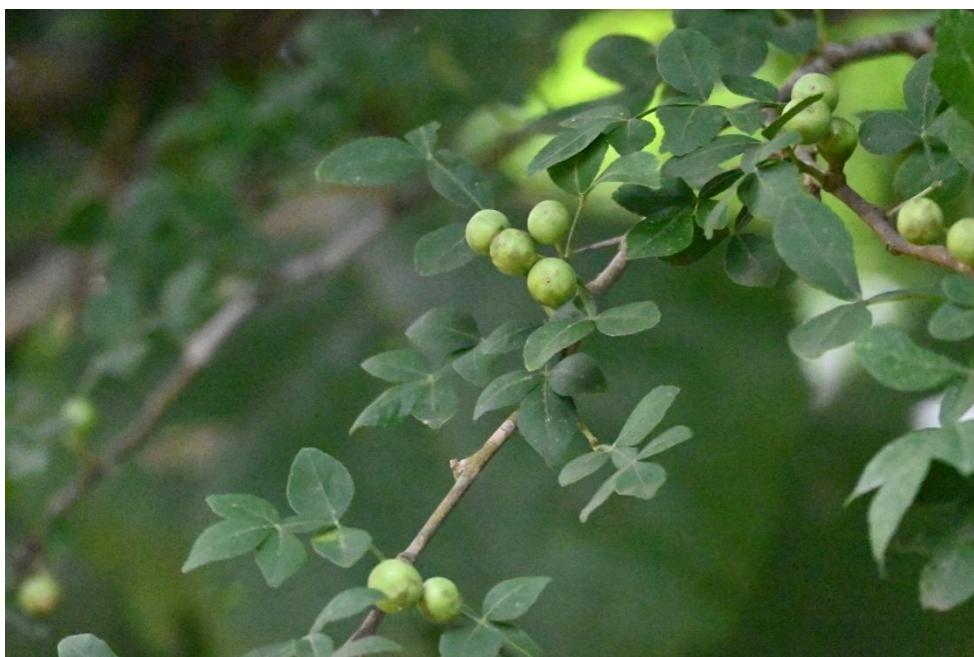


Figure 1: Fruits of *Naringi crenulata*

Traditionally used in various indigenous healing systems, this plant is reputed for its medicinal properties against several ailments (Subramanian and Ramakrishnan, 2011). Its roots have been used as a remedy for Cobra bite (Sekhar *et al.*, 2011), alleviating bodily pain (Pattanaik *et al.*, 2008), gastric problems like colic, dysentery, and vomiting (Kumar, 2006; Ramachandran, 2010). Stem is useful in acne and anti-aging treatments (Mayuree, 2009). In folk medicine, bark is used for puerperal fever and pitta while leaves as a remedy for dysentery and epilepsy (Murty, 2010; Ramani, 2010). However, systematic studies validating these claims

remain limited. This experimental study was a step towards profiling the secondary metabolites present in its fruits and evaluating its antibacterial efficacy against pathogenic bacteria, which could bridge gap between traditional knowledge and modern science thereby, opening new pathways in natural product research.

METHODOLOGY

Fruits of *Naringi crenulata* were collected from the forests of Chandaka-Dampara Wildlife Sanctuary, Odisha, India. The plant species (Figure 2) was identified by authors followed by referring to the published literature (Kumar *et al.*, 2022). Fruits were washed thoroughly under running tap water to remove soil particles and other surface contaminants. After cleaning, the fruits were air dried under shade at ambient room temperature to minimize thermal degradation of bioactive compounds. The dried material was coarsely powdered using a mechanical grinder and stored in airtight, sterile container to prevent moisture absorption and microbial contamination. Powdered fruit samples were subjected to solvent extraction using the maceration technique. Two solvent systems of differing polarity used for extraction were n-hexane (non-polar) and hydroethanol (7:3; polar)

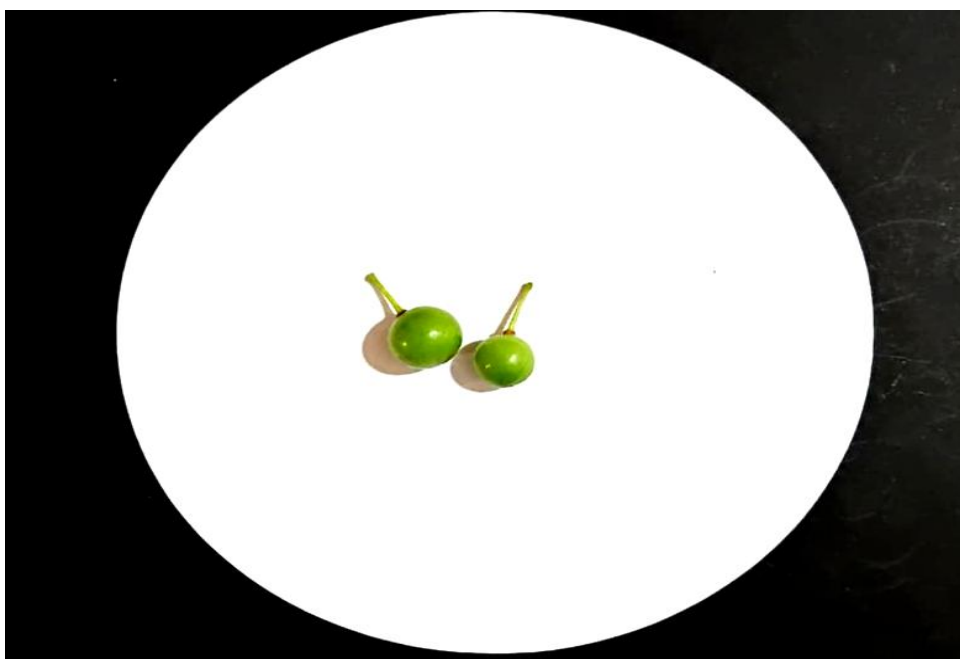


Figure 2: Fruits of *Naringi crenulata*

The extracts were filtered using Whatman No. 1 filter paper, and the filtrates were concentrated by air drying at room temperature until solvent residues were completely evaporated. The dried crude extracts were then stored under refrigerated conditions (4 °C) for two experimental setups following the standard procedures (Jena *et al.*, 2025):

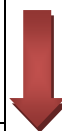
- a) Qualitative phytochemical screening to detect the presence of selected secondary metabolites, and
- b) Estimation of Minimum Inhibitory Concentration (MIC) to assess antibacterial activity against *Escherichia coli* (MTCC 45).

RESULTS AND DISCUSSION

The qualitative phytochemical screening of *Naringi crenulata* fruit extracts was done while keeping a clear view of solvent polarity on the secondary metabolite detection (Table 1; Figure 3-4). The non-polar n-hexane extract with polarity index of 0.1 appeared transparent and oily which showed the presence of only reducing sugars, indicating limited solubility of complex secondary metabolites in non-polar media.

Table 1: Phytochemical screening of *Naringi crenulata* (fruits)

Solvent	Polarity Index	Extract Color	Detected Metabolites	Extraction Efficiency	Remarks
n-Hexane	0.1	Transparent	Reducing sugars	Low	Extracted mainly lipophilic or simple carbohydrates.
Hydro ethanolic (7:3)	5.2	Pale green	Tannins, Saponins, Flavonoids and Reducing sugars	High	Extracted diverse bioactive compounds



The extraction efficiency was low; suggesting that n-hexane primarily extracted lipophilic or simple carbohydrate constituents. In contrast, the hydroethanolic extract (7:3), with a polarity index of 5.2, exhibited a pale-green coloration and tested positive for tannins, saponins, flavonoids, and reducing sugars.

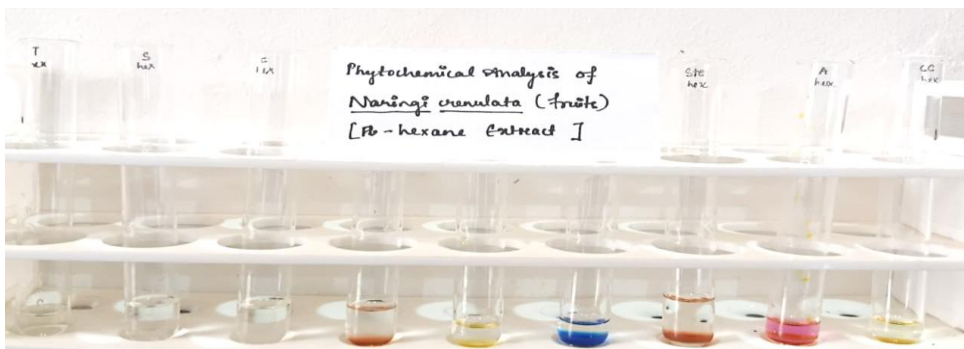


Figure 3: Phytochemical analysis of *N. crenulata* using n-hexane extract

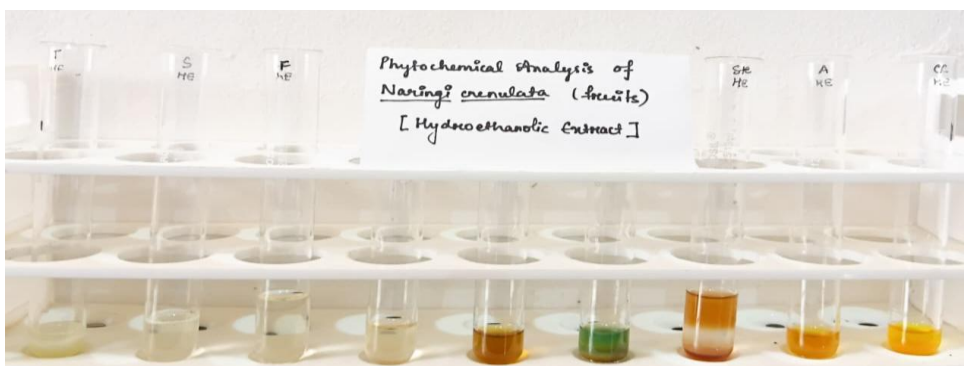


Figure 4: Phytochemical analysis of *N. crenulata* using hydroethanolic extract

The hydroethanolic extract was comparatively richer in diverse bioactive metabolites, reflecting its superior capacity to dissolve both polar and moderately non-polar bioactive compounds. Then, the efficacy of the extract was screened for studying its antibacterial potential. The minimum inhibitory concentration (MIC) of the hydroethanolic extract of *N. crenulata* fruits was evaluated against *Escherichia coli* using serial dilutions ranging from 100 to 12.5 mg/mL (Table 2).

Table 2: Estimation of Minimum Inhibitory Concentration (MIC)

Hydroethanolic Extract	Concentration (mg/mL)				MIC (mg/mL)
	100	50	25	12.5	
<i>Naringi crenulata</i> (fruits)	NG	NG	NG	NG	12.5
Nutrient broth	NG	NG	NG	NG	-
Microbial broth	G	G	G	G	-
Antibiotics	NG	NG	NG	NG	-

(NG: No growth of bacteria; G: Growth)

It exhibited a dose dependent inhibitory effect, with no visible bacterial growth (NG) observed at any of the tested concentrations (100, 50, 25, and 12.5) mg/mL, indicating effective antibacterial activity even at the lowest tested concentration. The MIC value was determined to be 12.5 mg/mL (Figure 5), showing the minimum concentration required to inhibit visible bacterial growth.



Figure 5: Minimum inhibition concentration (MIC) of fruits of *N. crenulata*

These results suggested that *N. crenulata* fruit extract possesses significant antibacterial potential, particularly against *E. coli* and the potential of the fruits to serve as an effective natural remedy against common ailments

associated with gastrointestinal and urinary tract (Zhou *et al.*, 2023). The nutrient broth (control) and antibiotics (standard) showed no growth, confirming sterility, while the microbial broth control exhibited normal growth (G), validating the experimental setup.

CONCLUSION

Amidst nature taking its course to revitalize itself, human population continues to exploit the natural resources and the need for preserving its knowledge. The findings from our present study highlighted *N. crenulata* as a promising source of natural bioactive compounds and support its potential role in developing plant based antibacterial agents. Further studies focusing on compound isolation and mechanistic insights could help establish its pharmaceutical relevance and strengthen the link between traditional knowledge and modern therapeutic innovation and preserve the nature and its essence.

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Chapter 3

Phytochemical screening and antimicrobial activity of *Carissa spinarum* L. (Apocynaceae): a wild therapeutic fruit

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ABSTRACT

In a rapidly developing world of modern science, ethnobotany plays quite an important role. Preserving and conserving traditional botanical knowledge is as important as discovering new drugs. In fact, it enriches and complements these discoveries. *Carissa spinarum*, is one such understudied species of family Apocynaceae which has been long used in folk medicinal practices. The fruits of *C. spinarum* were analysed in this context for studying its phytochemical profile and antibacterial activity. Results showed that polar solvents have diverse range of bioactive compounds in comparison to the non-polar. The efficacy was validated by performing antibacterial assay against *Escherichia coli* using hydroethanolic extract. The minimum inhibitory concentration (MIC) was determined to be 25mg/mL. Further analysis on its compound extraction and other pharmacological aspects is needed for concise evaluation and deeper insights.

Keywords: Ethnobotany, pharmacology, phytochemistry

INTRODUCTION

Ethnobotanical knowledge when transmitted across generations weaves a web of connection that comprises all the interdependent living beings including humans and plants. Traditionally, human beings used this knowledge to cure diseases and lead a sustainable lifestyle while tending to the nature for its gifts. With time, human greed grew and the urge to exploit increased. And, this over exploitation of natural resources hindered the rejuvenation capacity of the existing flora as well as the medicinal knowledge associated with it leading to the gradual decrease of traditional medicine practitioners (Nishteswar, 2014). Alongside the view to conserve and document the remaining flora, we focused on the wild edibles in this series. *Carissa spinarum* is such a member of family Apocynaceae that has long been hidden in the wilds and is understudied for its pharmacological values (Kumar, 2022). Different plant parts exhibit distinct therapeutic uses, reflecting the diverse range of phytoconstituents present in the species (Table 1). The extensive ethnomedicinal applications of *Carissa spinarum* highlight its importance as a multipurpose therapeutic plant in traditional medicine across Asia and Africa (Sharma *et al.*, 2023). Various parts of the plant like roots, leaves, bark, fruits, and even the whole plant are utilized to treat a wide range of ailments, including infectious, metabolic, and inflammatory disorders (Sharma *et al.*, 2023; Ansari and Patil, 2018). The plant is used in managing conditions such as fever, jaundice, cardiac diseases, diabetes, rheumatism, and gastrointestinal infections suggests its pharmacological potential as an antimicrobial, antioxidant, anti-inflammatory (Feyissa and Melaku, 2016), and cardioprotective agent. Moreover, its role in treating reproductive and vector-borne diseases, along with ethnoveterinary applications reflects that *C. spinarum* possesses a wide spectrum of therapeutic potential.

Table 1: Traditional medicinal uses of different parts of *Carissa spinarum*

Plant part used	Traditional medicinal uses
Whole Plant	Used to treat venereal, respiratory, and gastrointestinal infections, fever, jaundice, hepatitis, cardiac diseases, diabetes, malaria, pneumonia, chronic joint pain, asthma, rheumatism, stomachache, cough, chest complaints, sickle-cell anemia,

	hypertension, kidney complications, diarrhea, worms, eye cataracts, gastric ulcers, and cancer. Also used against microbial infections such as herpes, gonorrhea, syphilis, rabies, typhoid, jaundice, and polio. Acts as an antivenin for snake bites and used to treat infertility, asthenia, and premature ejaculation in males (Sharma et al., 2023; Ansari and Patil, 2018).
Leaves	Used as a mosquito repellent; applied in treating ulcers, rheumatism, asthma, and respiratory complaints (Ansari and Patil, 2018).
Roots	Used for treating fever, diarrhea, stomachache, worm infestation, jaundice, and as an antivenin for snake bites. Also employed to stop bleeding after delivery and to relieve muscle cramps (Sharma et al., 2023).
Bark	Used for treating gastrointestinal disorders, inflammation, and infectious diseases due to its bioactive compounds (Ansari and Patil, 2018).
Fruits	Used to treat gastric ulcers, diarrhea, and microbial infections; also recognized for their hepatoprotective, and cardioprotective properties (Sharma et al., 2023; Ansari and Patil, 2018).
Ethnoveterinary	Used to treat anaplasmosis and worm infestations in wounded animals (Sharma et al., 2023).

In recent decades, there has been renewed scientific interest in traditional medicine due to its holistic approach, cultural acceptance, and the discovery of bioactive compounds that serve as prototypes for modern drugs. In that particular context, fruits of *C. spinarum* were analysed in this study for their phytochemistry and antibacterial activity.

METHODOLOGY

Collection and identification of plant material: Mature fruits of *Carissa spinarum* were collected from the natural forest stands of the Chandaka Dampara Wildlife Sanctuary, Odisha, India. The plant species (Figure 1) was taxonomically identified by the authors. The collected specimens were assigned a voucher number and deposited in the departmental herbarium for future reference.

Preparation of plant material: The berries (Figure 2) were thoroughly washed under running tap water to remove adhering soil particles and other

surface contaminants. The cleaned fruits were air dried under shade at ambient temperature (25 ± 2 °C) for 7–10 days to minimize thermal degradation of bioactive constituents. Dried fruits were coarsely powdered using a mechanical grinder, sieved to obtain uniform particle size, and stored in sterile, airtight glass containers under dry conditions to prevent moisture absorption and microbial contamination until further analysis.



Figure 1: Fruits of *Carissa spinarum*



Figure 2: Collected fruits of *Carissa spinarum* for experimental use

Solvent extraction: The powdered fruit material was subjected to solvent extraction using the Soxhlet method (Jena et al. 2025). Two solvent systems of differing polarity were employed to ensure broad-spectrum extraction of phytoconstituents:

- a) n-Hexane
- b) Hydroethanol (7:3)

For each extraction, powdered material was placed in a thimble and was subjected to Soxhlet extraction using the two above mentioned solvents. The extracted material was collected and was placed in room temperature for evaporation of extra solvent. The remaining extracts were stored in sterile glass vials under refrigerated conditions (4 °C) until further experimental use.

Qualitative phytochemical screening: Preliminary phytochemical screening of both n-hexane and hydroethanolic extracts was performed following standard protocols (Jena *et al.*, 2025) to detect the presence of major classes of secondary metabolites.

Determination of antibacterial activity: The antibacterial potential of the extracts was evaluated against *Escherichia coli* (MTCC 45) obtained from the Microbial Type Culture Collection, Chandigarh, India. The minimum inhibitory concentration (MIC) was determined using the broth microdilution method as described by Jena *et al.*, (2025) with minor modifications.

RESULTS AND DISCUSSION

Depending on solvent polarity, the qualitative phytochemical screening of *Carissa spinarum* fruits was analyzed which detected the difference in secondary metabolite profiles (Table 2).

Table 2: Detection of secondary metabolites of *C. spinarum* fruit extract

Polarity	Solvent extract	Detected secondary metabolites	Phytochemical richness
Non-polar	n-Hexane	Reducing sugars	♦

Polar	Hydroethanolic	Tannins, Phenolic and Reducing	Saponins, compounds and sugars	◆
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(◆ = low, ◆ = high)

The non-polar n-hexane extract showed a limited phytochemical spectrum where, reducing sugars was the only detected constituent, indicating a lower phytochemical richness. In contrast, the hydroethanolic (7:3) extract demonstrated a broader range of metabolites, showing tannins, saponins, phenolic compounds, and reducing sugars. The higher metabolite diversity in the polar extract suggested that polar solvents are more effective in extracting bioactive constituents from *C. spinarum* fruits. The antibacterial potential of the hydroethanolic extract of *C. spinarum* fruits was then evaluated against *Escherichia coli* by determining the minimum inhibitory concentration (MIC) (Table 3).

Table 3: Estimation of Minimum Inhibitory Concentration (MIC)

Hydroethanolic Extract	Concentration (mg/mL)				MIC (mg/mL)
	100	50	25	12.5	
<i>Carissa spinarum</i> (fruits)	NG	NG	NG	G	25
Nutrient broth	NG	NG	NG	NG	-
Microbial broth	G	G	G	G	-
Antibiotics	NG	NG	NG	NG	-

(NG: No growth of bacteria; G: Growth)

The results showed that bacterial growth was completely inhibited (NG) at concentrations of 25 mg/mL and above, establishing MIC at 25 mg/mL (Figure 3). At lower concentrations (12.5 mg/mL), visible bacterial growth (G) was observed, confirming concentration dependent inhibitory activity. Control assays showed no bacterial growth (nutrient broth and antibiotic standards) validating the experimental conditions, whereas the microbial

broth control showed normal growth, confirming the viability of the bacterial inoculum.

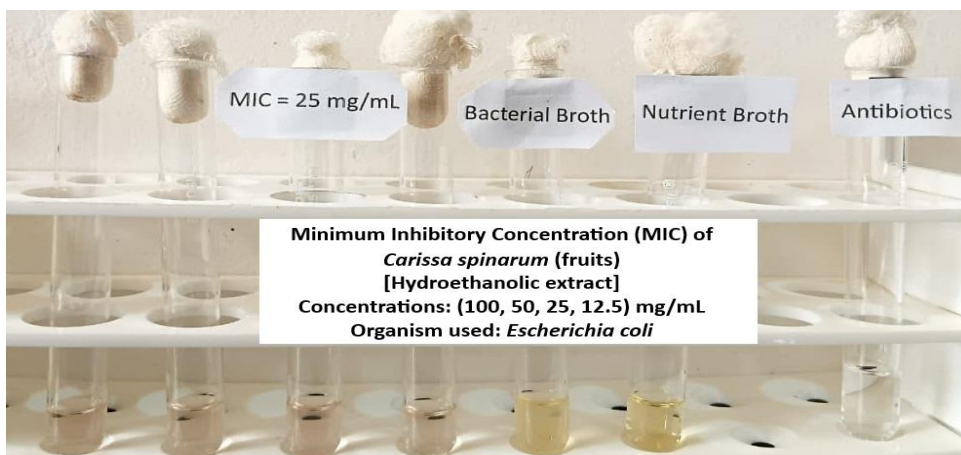


Figure 3: Minimum inhibition concentration (MIC) of fruits of *C. spinarum*

CONCLUSION

Rapid urbanization continues to exert pressure on wild habitats, while the rich knowledge of wild medicinal resources remains largely unexplored. In the present study, we profiled the phytoconstituents of *Carissa spinarum* fruits and assessed their phytochemical richness, which was further validated by determining the minimum inhibitory concentration (MIC) against *Escherichia coli*. Nevertheless, comprehensive scientific documentation, conservation of medicinal plants, and rigorous clinical evaluation are crucial to integrate traditional wisdom with modern medical science and to ensure the sustainable and responsible utilization of these bioresources in contemporary healthcare.

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Chapter 4

Desert bioactives: profiling phytochemicals and antibacterial potential in *Cereus repandus* (L.) Mill. (Cactaceae)

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ABSTRACT

Cereus repandus, a succulent tree, has long been recognized in traditional medicine for its potential health benefits. Present study aimed to profile the phytochemical composition and evaluate the antibacterial activity of its hydroethanolic fruit extract. Qualitative phytochemical analysis revealed the presence of primary metabolites, including proteins, carbohydrates, and amino acids, highlighting the nutritional value of the fruit. Secondary metabolites such as tannins, flavonoids, and reducing sugars were detected, indicating potential pharmacological properties. The antibacterial activity was assessed against *Escherichia coli*, which established a minimum inhibitory concentration (MIC) of 50 mg/mL. The extract exhibited a concentration dependent inhibition of bacterial growth, suggesting moderate antibacterial potential. The observed bioactivity is likely associated with the presence of secondary metabolites, particularly tannins and flavonoids. These findings support the therapeutic property of *C. repandus* and highlight its potential as a source of bioactive compounds for future pharmacological applications.

Keywords: Antibacterial, ethnomedicine, nutraceuticals

INTRODUCTION

Cacti are remarkable desert plants that have adapted to survive under extreme environmental conditions, storing water and nutrients within their succulent tissues (Hultine *et al.*, 2023). Many cactus species are valued for their nutritional and medicinal properties. Edible parts such as fruits and cladodes (flattened stems) are rich in nutrients including carbohydrates, amino acids, vitamins, and minerals. They also contain a wide range of bioactive compounds such as flavonoids, tannins, alkaloids, and phenolics that contribute to its pharmacological properties (Conte *et al.*, 2025). Traditionally, cacti have been consumed as food and used in folk medicine across arid regions of the America, Africa, and Asia for treating ailments like diabetes, obesity, and digestive disorders (Monteiro *et al.*, 2023). Native to the coasts of Venezuela to Colombia in the Caribbean Sea (POWO, 2025), *Cereus repandus* (Figure 1), commonly called as the Peruvian apple cactus or Cadushi by the locals, thrives in typical dry tropical habitats.



Figure 1: Fruit of *Cereus repandus* attached to the plant

Its interchangeable taxonomic identity often gets confused with the name *C. peruvianus* L. In southern part of Brazil, its cladodes formulation is known to inhibit gastric lesions and its extract is also marketed as a herbal

medicine used for weight loss (Nunes *et al.*, 2022). Its stems are reviewed (Morton, 1967) to be used as a staple food and dried stems to be used as torches, fuel and fences and when matured, thick trunks are also used for carpentry. In recent years, scientific researches have also highlighted cacti as functional foods with potential health values. Their ethnobotanical use has also been linked to today's nutraceutical and pharmaceutical applications. In that light, fruits of *C. repandus* (Figure 2) were screened for studying their phytochemical richness and antimicrobial activity against *Escherichia coli*, a gram negative bacteria associated with common gastrointestinal disorders (Petersen, 2022).

METHODOLOGY

The fruits of *Cereus repandus* were collected from nearby Athagarh areas of Cuttack district, Odisha, India. The plant species was identified by the authors (Figure 1).

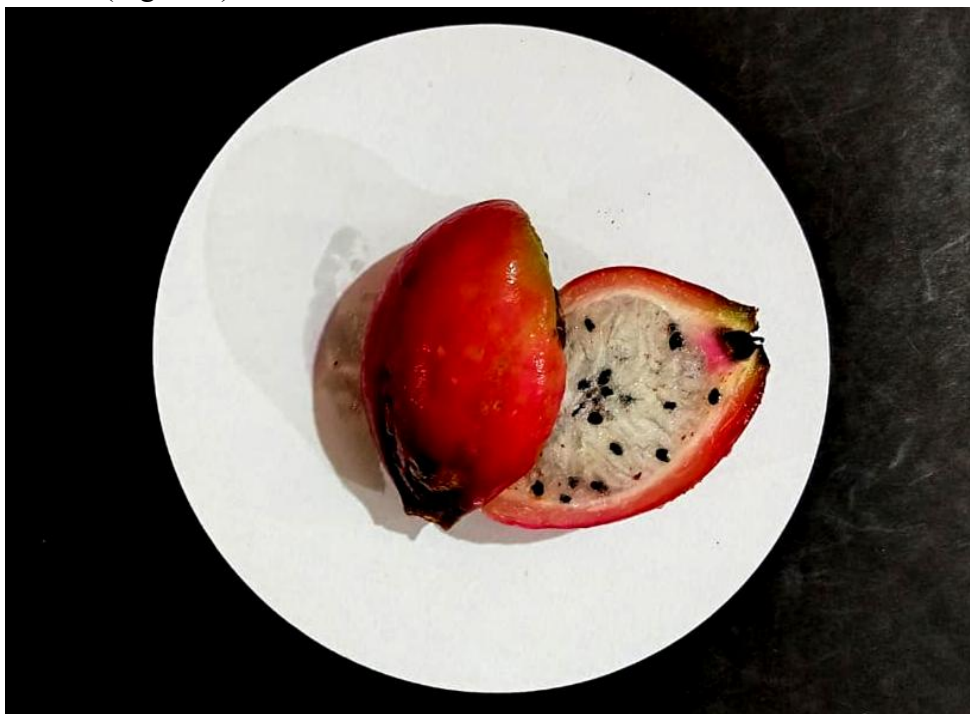


Figure 2: Collected fruit sample of *C. repandus*

The Soxhlet extraction method was adopted using hydroethanolic extract for qualitative phytochemical analysis (Table 1). Detection of primary and

secondary metabolites was conducted and antibacterial activity was studied by determining the minimum inhibitory concentration (MIC) using *Escherichia coli* using standard methods. (Devi *et al.*,2023; Jena *et al.*,2025; Sharma *et al.*,2025).

RESULTS AND DISCUSSION

The hydroethanolic extract of *Cereus repandus* fruits was analyzed for the presence of primary and secondary metabolites (Table 1). The extract contained primary metabolites including proteins, carbohydrates, and amino acids (Figure 3), indicating the nutritional and metabolic potential of the fruit. Secondary metabolites such as tannins, flavonoids, and reducing sugars were also detected (Figure 4), confirming the presence of key phytochemicals that may contribute to the pharmacological efficacy of the fruit.

Table 1: Qualitative phytochemical analysis of *Cereus repandus* for detection of primary and secondary metabolites

Extract	Category of Metabolites	Detected Bioactive Compounds	Significance
Hydroethanolic	Primary Metabolites	Proteins, Carbohydrates and Amino acids	Indicates the nutritional and metabolic potential of the fruit.
	Secondary Metabolites	Tannins, Flavonoids and Reducing sugars	Confirms the presence of key phytochemicals contributing to pharmacological efficacy.

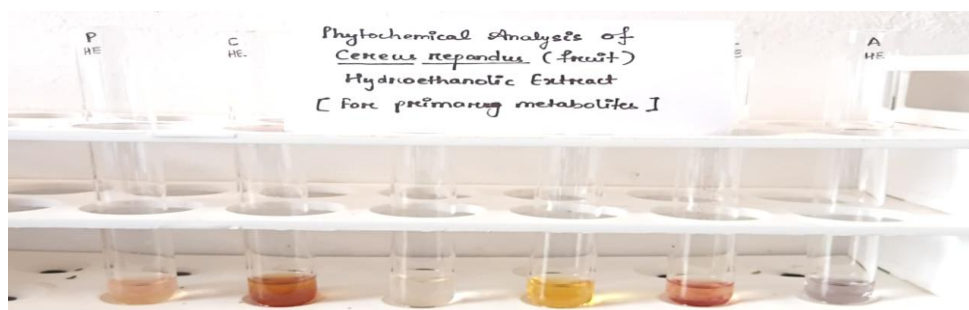


Figure 3: Detection of primary metabolites

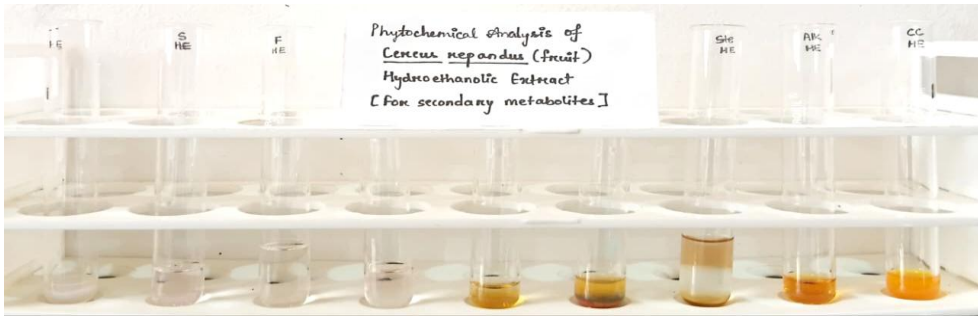


Figure 4: Detection of secondary metabolites

These findings suggest that *C. repandus* possesses both nutritional and bioactive properties, supporting its traditional and potential therapeutic applications. The antibacterial potential of the hydroethanolic extract was evaluated against *Escherichia coli* using the broth microdilution method (Table 2). The extract inhibited bacterial growth at concentrations of 50 mg/mL and above, establishing the minimum inhibitory concentration (MIC) at 50 mg/mL (Figure 5). At lower concentrations (25 and 12.5 mg/mL), visible bacterial growth was observed, indicating a concentration dependent effect. Control experiments validated the results, with nutrient broth showing no growth and microbial broth demonstrating normal bacterial proliferation, while antibiotic controls exhibited complete inhibition. These results suggest that the hydroethanolic extract of *C. repandus* fruits possesses moderate antibacterial activity, likely attributable to the detected secondary metabolites, such as tannins and flavonoids, known for their antimicrobial properties.

Table 2: Estimation of Minimum Inhibitory Concentration (MIC)

Hydroethanolic Extract	Concentration (mg/mL)				MIC (mg/mL)
	100	50	25	12.5	
<i>Cereus repandus</i> (fruits)	NG	NG	G	G	50
Nutrient broth	NG	NG	NG	NG	-
Microbial broth	G	G	G	G	-
Antibiotics	NG	NG	NG	NG	-

(NG: No growth of bacteria; G: Growth)

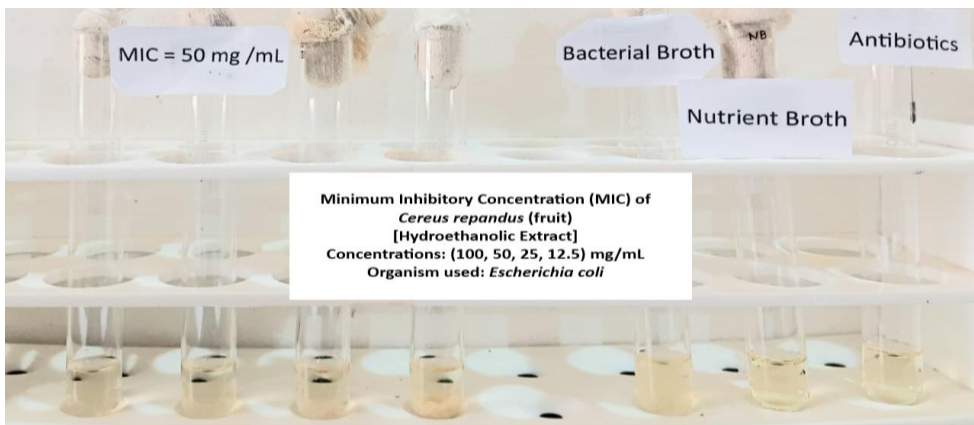


Figure 5: Determination of minimum inhibitory concentration (MIC)

CONCLUSION

The hydroethanolic extract of *Cereus repandus* fruits bespeaks dual significance: nutritional and bioactive. The presence of primary metabolites shows its metabolic and dietary value, while secondary metabolites, notably tannins and flavonoids, contribute to its moderate antibacterial activity against *E. coli*. This study validates the traditional use of *C. repandus* and highlights its potential as a natural source of bioactive compounds with pharmacological relevance. Further studies exploring other microbial strains and in vivo applications could expand its therapeutic potential and support its integration into modern medicinal frameworks.

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Chapter 5

Bioactive richness of the forest ebony: *Diospyros sylvatica* Roxb. (Ebenaceae)

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ABSTRACT

The forest ebony *Diospyros sylvatica* Roxb., a hardy tree belonging to the family Ebenaceae, thrives in dry deciduous forests and is valued for both its strong ebony wood and traditional medicinal uses associated with its genus. Present study was carried out to explore the bioactive richness of this species by analyzing the phytochemical composition and antibacterial activity of its extracts. Qualitative screening revealed the presence of important secondary metabolites such as tannins, saponins, phenolics, and reducing sugars, which are known for their medicinal properties. The hydroethanolic extract showed promising antibacterial effects, suggesting that the active compounds may help combat bacterial growth. This study highlights *D. sylvatica* as a valuable source of natural bioactive compounds with potential therapeutic applications, encouraging further scientific exploration.

Keywords: Antibacterial, ebony, secondary metabolites

INTRODUCTION

Members of the family Ebenaceae are renowned for their remarkable resistance to harsh climatic conditions and are predominantly native to dry deciduous and semi arid habitats (POWO, 2025). Their ability to thrive in such constrained environments (Wallnöfer, 2001) contributes to the

development of dense and durable wood highly valued in carpentry and internationally traded under the name ‘ebony.’ Beyond their economic and ecological significance, many species within this family possess rich ethnomedicinal histories (Ribeiro *et al.*, 2023), being used traditionally to treat a variety of ailments ranging from skin infections to gastrointestinal and respiratory disorders (Fankam *et al.*, 2025).



Figure 1: Fruits of *Diospyros sylvatica*

Among them, *Diospyros sylvatica* Roxb., commonly known as forest ebony, stands out as a lesser explored species with promising pharmacological potential. Traditionally, various parts of genus *Diospyros* have been employed in indigenous medicine for their therapeutic effects, including pharmacological properties (Rao *et al.*, 2024). Despite the traditional importance, scientific documentation on this particular species *sylvatica*'s phytochemical composition and bioactivity remains limited. Investigating the bioactive compounds present in *D. sylvatica* is therefore crucial not only for validating its ethnomedicinal relevance but also for identifying potential natural compounds that may serve as leads in modern drug discovery. The present study aims to explore the bioactive richness of *D. sylvatica* through qualitative phytochemical screening and antibacterial evaluation of its fruits (Figure 2), shedding light on its pharmacological potential and conservation value.

METHODOLOGY

The fruits of *Diospyros sylvatica* were collected from forests of Chandaka-Dampara Wildlife Sanctuary, Odisha, India. The plant species was identified by the authors (Figure 1). The maceration extraction method was adopted using hydroethanolic extract for the following experiments (Devi *et al.*, 2023; Jena *et al.*, 2025).

Detection of secondary metabolites: Detection of secondary metabolites was conducted following Devi *et al.* (2023).

Test for tannin: 1 ml of plant extract is mixed with 4-5 drops of 10% lead acetate solution. The formation of a light-yellow precipitate confirms the presence of tannins.

Test for saponin: 1 ml of plant extract is mixed with 1 ml of distilled water, and after vigorous shaking, the formation of a stable, persistent froth confirms the presence of saponins.

Test for flavonoids: To 2 ml of plant extract, a few drops of dilute sodiumhydroxide (NaOH) are added. The appearance of an intense yellow colour indicates the presence of flavonoids. Subsequent addition of 4-5 drops of dilute sulphuric acid causes the colour to fade, further confirming the presence of flavonoids.



Figure 2: Collected fruit sample of *D. sylvatica*

Test for terpenoids: A mixture of 1 ml of plant extract and 2 ml of chloroform is prepared, and an equal volume of concentrated sulphuric acid is added. The appearance of a reddish-brown coloration at the interface confirms the presence of terpenoids.

Test for phenolic compounds: 1 ml of plant extract is treated with 5 drops of 1% ferric chloride solution, resulting in the formation of a bluish-black coloration, which indicates the presence of phenolic compounds.

Test for reducing sugars: 1 ml of plant extract is added with 3 drops of Fehling's solution A and B, and kept in water bath for a few minutes. The formation of an orange-red precipitate confirms the presence of reducing sugars.

Test for steroids: 1 ml of plant extract is mixed with 2 ml of chloroform, followed by the addition of 2 ml of concentrated sulphuric acid. The resulting formation of two distinct phases, characterized by an upper red layer and a lower yellow layer with green fluorescence, confirms the presence of steroids.

Test for alkaloids: 1 ml of plant extract is mixed with 3-4 drops of Dragendorff's reagent and kept in water bath for a few minutes. The formation of an orange-red precipitate confirms the presence of alkaloids.

Antibacterial activity assessment: It was studied by determining the minimum inhibitory concentration (MIC) using *Escherichia coli* using standard methods (Jena *et al.*,2025).

RESULTS AND DISCUSSION

Phytochemical screening of *Diospyros sylvatica* fruit extracts revealed variation in metabolite composition between non polar and polar solvents (Table 1; Figure 2-3). The hydroethanolic (polar) extract detected many of the tested secondary metabolites, including tannins, saponins, phenolic compounds, reducing sugars, and alkaloids. In contrast, the n-hexane (non polar) extract displayed the presence of only reducing sugars, indicating limited solubility of polar phytoconstituents. The presence of these bioactive compounds, particularly tannins and phenolics, suggests potential antioxidant and antimicrobial properties associated with the hydroethanolic extract.

Table 1 Qualitative phytochemical analysis of *Diospyros sylvatica* using different extracts

Bioactive compounds	n-Hexane	Hydroethanolic
Tannin	Absent	Present
Saponin	Absent	Present
Flavonoids	Absent	Absent
Terpenoids	Absent	Absent
Phenolic compounds	Absent	Present
Reducing sugars	Present	Present
Steroids	Absent	Absent
Alkaloids	Absent	Present

Therefore, broth microdilution method was used to study the antibacterial potential of the hydroethanolic extract. It exhibited moderate antibacterial activity with a minimum inhibitory concentration (MIC) of 100 mg/mL (Table 2; Figure 5). No bacterial growth was observed in the antibiotic control, confirming assay validity, while the nutrient broth showed no inhibition, serving as a negative control. These observations suggested that the antibacterial property of *D. sylvatica* may be attributed to the presence of tannins, saponins, phenolic compounds, and alkaloids, which help stop bacterial growth by weakening the cell membrane and blocking vital enzymes (Vaouet *al.*,2021).

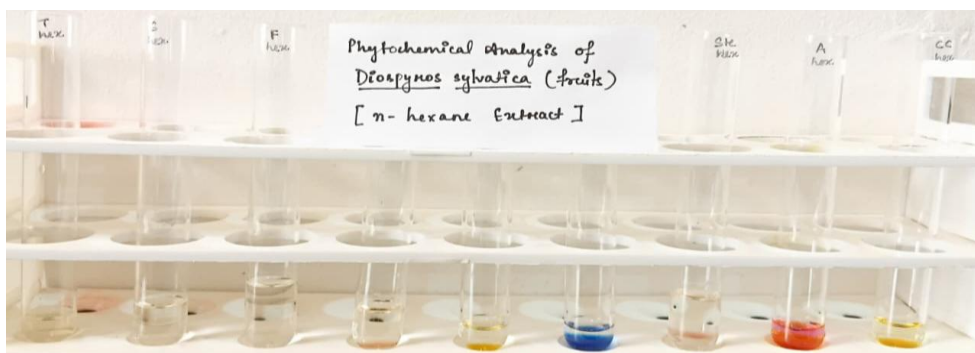


Figure 3: Detection of secondary metabolites in n-hexane extract

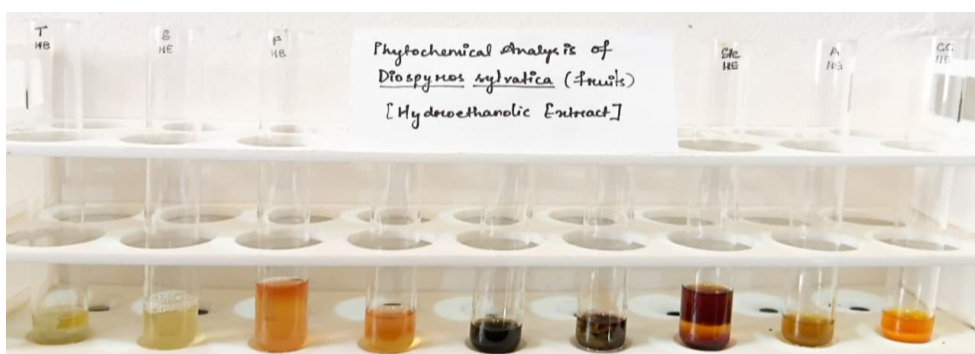


Figure 4: Detection of secondary metabolites in hydroethanolic extract

Table 2: Estimation of Minimum Inhibitory Concentration (MIC)

Extract Type	Tested Organism	Range of Concentrations (mg/mL)	MIC (mg/mL)	Antibacterial Strength
Hydroethanolic extract (<i>Diospyros sylvatica</i> fruits)	<i>E. coli</i>	12.5 – 100	100	Moderate
Antibiotic control	<i>E. coli</i>	Standard	-	Strong
Nutrient broth	-	-	-	Negative



Figure 5: Determination of minimum inhibitory concentration (MIC)

CONCLUSION

The results of this study revealed that *Diospyros sylvatica* is not only a symbol of ecological endurance but also a reservoir of valuable phytochemicals. The presence of diverse bioactive compounds and noticeable antibacterial activity indicates that this species holds great promise for developing natural remedies and plant based antibacterial agents. By bridging traditional knowledge with modern science, the study reaffirms the medicinal potential of forest ebony and underlines the need for its conservation and further pharmacological research.

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Chapter 6

Biochemical wealth and microbial defense of the forest fruit *Melia dubia* Cav. (Meliaceae)

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ABSTRACT

Plants have long served as valuable sources of natural therapeutic agents, especially in traditional medicinal systems. *Melia dubia* Cav. (Meliaceae), commonly known as the forest neem or Malabar neem was explored in this study to screen the phytochemical composition and antibacterial activity of its fruits by using solvent extraction method. Qualitative phytochemical screening revealed that the hydroethanolic extract contained several bioactive compounds, including tannins, saponins, flavonoids, terpenoids, reducing sugars and alkaloids, whereas the non-polar extract did not detect any tested metabolites. Antibacterial activity assessed against *Escherichia coli* demonstrated complete growth inhibition at 100 mg/mL concentration of the hydroethanolic extract, confirming moderate antibacterial potential. These findings support the ethnomedicinal relevance of *M. dubia* and highlight its potential as a source of natural antibacterial compounds for future pharmacological development.

Keywords: Pharmacological value, phytochemicals, traditional medicine

INTRODUCTION

Medicinal plants have been an integral part of human healthcare since ancient times, providing essential remedies for various diseases (Mahalakshmi *et al.*, 2020; Haji *et al.*, 2024; Susheela *et al.*, 2008). These ethnobotanical knowledge from across the world forms the foundation for many modern drug discoveries, particularly those addressing bacterial infections and resistance. Many contemporary pharmaceuticals have originated from plant derived compounds that were first identified through traditional medicinal practices (Nasim *et al.*, 2022). In recent years, the rise of antibiotic resistance has renewed global interest in ethnomedicine for exploring novel antimicrobial agents from natural sources (Anand *et al.*, 2019). This exploration of plant based bioactive compounds gives a promising alternative to synthetic drugs which is sustainable and less expensive. *Melia dubia* is one such multipurpose tree belonging to family Meliaceae, native to tropical and subtropical regions of Asia and Africa (Ramanan *et al.*, 2024). Traditionally, various parts of this plant including fruits, leaves, bark, and seeds have been used to treat ailments such as colic, skin infections, fever, asthma, malaria, and venereal diseases (Table 1).

Table 1: Ethnomedicinal uses of different parts of *Melia dubia*

Plant part	Traditional medicinal uses	Mode of use	Geographical reference
Fruit	Used as an anthelmintic, astringent, and for treating colic, skin diseases, sores, and scabies (Mahalakshmi <i>et al.</i> , 2020; Haji <i>et al.</i> , 2024; Susheela <i>et al.</i> , 2008).	Green fruits are made into a paste for treating skin ailments and fruit juice mixed with sulphur used for scabies.	India, Philippines (Laguna)
Leaves	Used to treat stomachache, asthma, eczema, and malaria; also as mosquito repellent and pesticide (Haji <i>et al.</i> , 2024).	Boiled leaves used orally for stomachache; burnt leaves used for repelling mosquitoes; mashed leaves mixed with kerosene applied on skin for acne, allergies, and ringworm.	India, Philippines (Mindanao), Local tribal practices

Stem Bark	Applied for skin ailments, open wounds (Haji <i>et al.</i> , 2024).	Decoction or extract of bark applied topically or consumed.	Indonesia (West Timor), Philippines
Seeds	Used as insect repellent (Haji <i>et al.</i> , 2024).	Oil extracted for topical or fumigant use.	Philippines
Wood	Valued for furniture, farm tools, and carpentry due to its durable quality (Goswami <i>et al.</i> , 2020).	Processed wood material.	India and Southeast Asia
Whole Plant	Employed traditionally to treat leprosy, eczema, asthma, malaria, fevers, venereal diseases, diabetes cholelithiasis, acariasis, and for reducing pain (Mahalakshmi <i>et al.</i> , 2020; Haji <i>et al.</i> , 2024; Susheela <i>et al.</i> , 2008).	Decoctions, poultices, or powders prepared from entire plant parts.	India, Africa, Southeast Asia



Figure 1: Fruits of *Melia dubia*

The plant is also valued for its durable timber and its ecological adaptability to dry deciduous habitats (Goswami *et al.*, 2020). Despite its extensive

traditional and economical use, the phytochemical and antibacterial potential of *M. dubia* fruits remain underexplored. Therefore, this study was undertaken to qualitatively assess its phytochemical composition and evaluate the antibacterial activity of its hydroethanolic fruit extract against *Escherichia coli*, a common multifaceted pathogenic bacterium responsible for various gastrointestinal diseases (Braz *et al.*, 2020).

METHODOLOGY

Mature fruits of *Melia dubia* were collected from the natural forest stands of Chandaka, Odisha, India and identified by the authors. The samples were given tags and were put in sterile cotton bags (Figure 2).

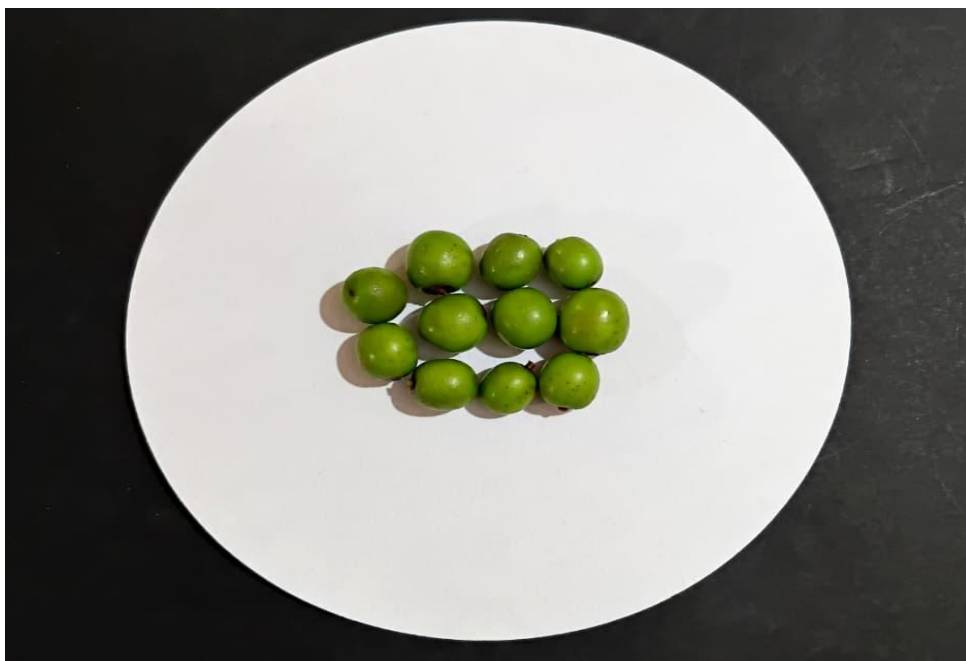


Figure 2: Collected fruit sample of *Melia dubia* for experimental use

Then, the fruits were washed thoroughly to remove debris and surface contaminants. They were extracted using the maceration method (Devi *et al.*, 2025) with two solvents of different polarity: *n*-hexane and hydroethanol (1:1). The extracts were concentrated at room temperature to remove residual solvent and stored in sterile vials at 4 °C until further use. Preliminary phytochemical screening of both extracts was carried out to detect major classes of secondary metabolites. Then, the antibacterial

potential of the extracts was assessed against *Escherichia coli* (MTCC 45) and the minimum inhibitory concentration (MIC) was determined using the broth micro dilution method with minor modifications to the standard protocols (Jena *et al.*, 2025).

RESULTS AND DISCUSSION

The qualitative phytochemical analysis of *Melia dubia* (Table 2) revealed distinct variations in the metabolite profiles depending on the polarity of the extraction solvent.

Table 2: Qualitative phytochemical analysis of *M. dubia*

Polarity	Extract	Detected secondary metabolites
Non-Polar	n-Hexane	No tested metabolites were detected
 Polar	Hydroethanolic	Tannin, Saponin, Flavonoids, Terpenoids, Reducing sugars and Alkaloids

The non-polar n-hexane extract showed negative result for all the tested secondary metabolites (Figure 3). In contrast, the polar hydroethanolic extract exhibited a rich phytochemical composition, confirming the presence of tannins, saponins, flavonoids, terpenoids, reducing sugars, and alkaloids (Figure 2). These compounds are known to possess diverse pharmacological properties (Leela *et al.*, 2016), including antimicrobial, antioxidant, and anti-inflammatory activities. The antibacterial potential of the hydroethanolic fruit extract was hence, evaluated through the determination of its Minimum Inhibitory Concentration (MIC) against *Escherichia coli* (Table 3). The extract exhibited complete inhibition of bacterial growth at the concentration of 100 mg/mL, while lower concentrations (50, 25, and 12.5 mg/mL) allowed visible bacterial growth. The nutrient broth control showed no growth, confirming sterility, whereas the microbial broth exhibited consistent bacterial proliferation. The antibiotic control displayed complete inhibition, validating the assay performance.

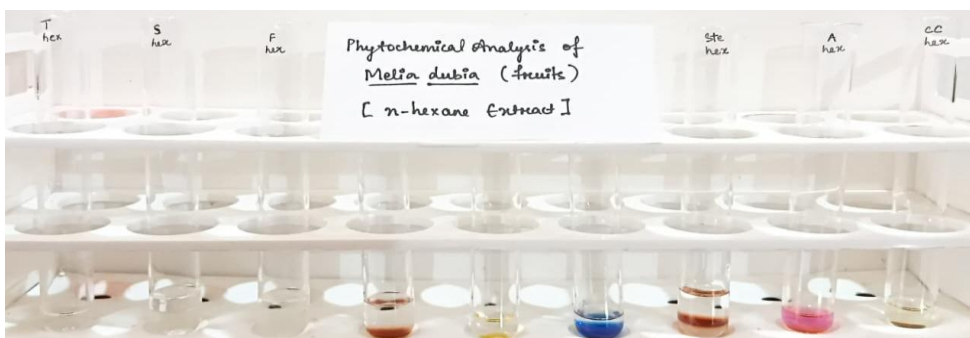


Figure 3: Detection of secondary metabolites in n-hexane extract

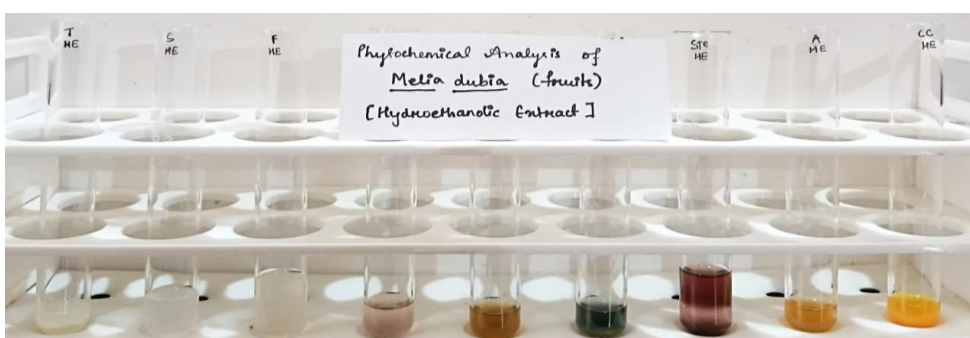


Figure 3: Detection of secondary metabolites in hydroethanolic extract

Table 3: Estimation of Minimum Inhibitory Concentration (MIC)

Sample	Extract type	Bacterial response	Minimum Inhibitory Concentration (MIC)
<i>Melia dubia</i> (fruit)	Hydroethanolic	Inhibited growth at 100 mg/mL; growth observed at lower concentrations (50, 25, 12.5) mg/mL	100 mg/mL
Nutrient Broth	-	No growth (sterile medium)	-
Microbial Broth	-	Consistent bacterial growth	-
Antibiotic (standard)	-	Complete inhibition (positive control)	-

These observations indicated that *Melia dubia* fruit possesses moderate antibacterial activity, with hydroethanolic extracts being effective than the non-polar extract due to their higher secondary metabolite content and this validates its traditional medicinal practices.

CONCLUSION

The findings of present study revealed that the fruits of *Melia dubia* are rich in diverse secondary metabolites such as tannins, flavonoids, terpenoids, alkaloids, and saponins those are recognized for their pharmacological significance. The hydroethanolic extract exhibited marked antibacterial activity against *Escherichia coli*, showing inhibition at the tested concentration of 100 mg/mL. These outcomes lend scientific support to the traditional medicinal uses of *M. dubia* and showcase its promise as a natural reservoir of bioactive molecules with antibacterial potential. To strengthen these observations, future research should focus on quantitative profiling, purification, and characterization of individual phytochemicals to better understand the pharmacological relevance of this valuable yet understudied species.

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Chapter 7

Revisiting folk therapeutics: ethnopharmacology of *Ceriscoides turgida* (Roxb.) Tirveng. (Rubiaceae)

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ABSTRACT

The increasing global interest in ethnomedicinal plants reflects an urgent need to explore traditional botanical resources for novel therapeutic compounds. Present study investigates the phytochemical composition and antibacterial potential of *Ceriscoides turgida*, member of the Rubiaceae family widely used in traditional medicine by tribal communities across India. Ethnobotanical documentation revealed diverse medicinal uses of the plant which was used as a base to study the preliminary phytochemical profile of *C. turgida* fruits. It revealed a richer profile in the polar extract, revealing the presence of tannins, saponins, flavonoids, alkaloids, terpenoids, phenolic compounds, and reducing sugars, while the non-polar extract exhibited minimal phytochemical diversity. Antibacterial assays against *Escherichia coli* (MTCC 45) demonstrated inhibitory effects of the hydroethanolic extract, suggesting the presence of bioactive metabolites with antimicrobial potential.

Keywords: Ethnomedicine, natural therapeutics, pharmaceuticals

INTRODUCTION

Modern medicine often prides itself on precision, predictability, and progress, the polished outcomes of laboratories and algorithms. Yet, behind many synthetic drugs lies an old story, one rooted in forests, villages, and the quiet knowledge of healers who observed nature long before science named its molecules. Like, aspirin from Willow bark (Desborough and Keeling, 2017), quinine from *Cinchona* (Davies and Hollman, 2002), or artemisinin from sweet wormwood (Krishna *et al.*, 2008) were not accidents of chemistry, but rediscoveries of remedies long known to communities

who relied on the flora around them. Ethnomedicine, built on centuries of lived experience, has guided our understanding of plants as a source of healing and survival (Mahapatra *et al.*, 2019). Often time, folk medicine is understood the same as traditional medicine, while the former is actually a component of the later one. It specifically represents the accumulated wisdom of indigenous and rural communities, developed through generations of observation and experience which is basically passed down orally (Telles *et al.*, 2014). Such traditional practices form the foundation of many modern pharmaceuticals today, as they often reveal plants with significant bioactive potential. In regions where access to formal healthcare is limited, folk medicine plays an essential role in primary healthcare, offering affordable and culturally accepted remedies (Zhang, 2015). Documenting and scientifically validating these traditional uses not only preserves valuable cultural heritage but also helps in the discovery of novel therapeutic compounds. *Ceriscoides turgida* (Figure 1) belonging to the family Rubiaceae, occupies an important place in the ethnomedicinal traditions of India, particularly among the tribal communities of Gujarat, Odisha, and Maharashtra. Known locally as Duduki, Katolmaram, Kharhar, and Pendra (Table 1), this species is an integral component of folk healthcare systems that rely on plant-based remedies for both acute and chronic ailments. The ethnobotanical practices surrounding this species give a deep ecological knowledge and cultural continuity in the use of native flora for healing purposes (Table 2).

Table 1: General information

Scientific Name	<i>Ceriscoidesturgida</i> (Roxb.) Tirveng. (syn. <i>Gardenia turgida</i> Roxb.)
Family	Rubiaceae
Local Names	Duduki, Katolmaram, Kharhar, Pendra
Reported ethnic distribution	Commonly used by Bhil, Dhanka and Nayaka tribes: North Gujarat, India (Jain and Srivastava, 2003), and local healers of Chandrapur District, Maharashtra, India (Shukla and Harmukh, 2020)

Among the various plant parts used, the root stands out as the most versatile and frequently used. Traditional healers prepare it in multiple forms like paste, decoction, cold infusion, powder, or juice, either administered alone or in combination with other medicinal species (Table 2). These preparations are used to treat various conditions, including digestive disorders like indigestion, stomachache (Bodele *et al.*, 2017; Jain and Srivastava, 2003), febrile illnesses for *e.g.* fever, malaria, tuberculosis (Shukla and Harmukh, 2020), inflammatory diseases like gout, rheumatism, chest pain and reproductive ailments like leucorrhea, gonorrhea, lactation insufficiency (Zilani *et al.*, 2018). Additionally, the root is applied in the management of poison related conditions such as snakebite, scorpion sting, and dog bite, reflecting its perceived detoxifying and restorative properties.



Figure 1: Fruit of *Ceriscoides turgida*

The fruits and seeds also hold significant ethnomedicinal value. Fruit pulp and extracts are used to relieve headache, eye irritation, and mammary gland inflammation, while seed pastes are used in treatment against food poisoning (Shukla and Harmukh, 2020). Such diverse applications point to the plant's likely antimicrobial, anti-inflammatory, and detoxifying potential. Thus, from an ethnopharmacological perspective, *C. turgida* represents a promising candidate for bioprospecting and drug discovery, as its broad traditional applications suggests the presence of multiple bioactive metabolites. However, despite its widespread folk use, scientific validation remains limited, with few modern pharmacological investigations exploring its phytochemical composition and mechanism of action.

Table 2: Traditional medicinal uses of *Ceriscoides turgida*

	Form of preparation	Ailments treated	Additional ingredients (if any)	Mode of administration & duration
Seeds	Ground into paste	Used to treat food poisoning among Bhil, Dhanka, and Nayaka tribes (Jain and Srivastava, 2003)	-	-
Fruits	Fresh fruit, pulp or paste	Applied for eye disorders, fever, mammary gland inflammation. For headache: pulp applied on forehead (Zilani <i>et al.</i> , 2018)	-	Topical (for fever/headache), oral (for internal ailments)
Roots	Decoction, cold infusion, paste, powder, or juice	Leucorrhoea (root boiled with <i>Aloe vera</i> & <i>Smilax zeylanica</i>) (Zilani <i>et al.</i>, 2018) Indigestion in children, fever, jaundice (Bodele <i>et al.</i>, 2017; Shukla and Harmukh, 2020) Dog bite, scorpion sting, snake bite (Zilani <i>et al.</i>, 2018; Shukla and Harmukh, 2020)	Commonly combined with <i>Phoenix acaulis</i> , <i>Cyperus rotundus</i> , <i>Euphorbia hirta</i> , <i>Diospyros melanoxylon</i> , <i>Cordia macleodii</i> , <i>Cassia fistula</i> , <i>Abelmoschus moschatus</i> , <i>Thespesia lampas</i> ,	Internal use as decoction or pill; external for headache; usually taken once or twice daily for 2–15 days, depending on ailment

		For Headache: juice dropped in ear, paste applied externally (Shukla and Harmukh, 2020)	<i>Blumealacera</i> , <i>Piper longum</i>	
		Stomachache, chest pain, gout, tuberculosis		
		Kidney stones, gonorrhoea, diminished lactation, toothache, cough & cold (Shukla and Harmukh, 2020)		
Whole Plant / General Use	Extracts or mixtures with other herbs	Used to treat snake bites, epilepsy, stomachache, rheumatic pain, scorpion sting (Zilani <i>et al.</i> , 2018; Shukla and Harmukh, 2020)	Used singly or in combination with other local herbs	Internal administration (liquid or powder form)

In that light, this study explores its phytochemical profile and potential antibacterial activity through estimating its inhibitory concentration. This may aid as a framework for further pharmacological and therapeutical evaluation and standardization of the species.

METHODOLOGY

Plant collection and identification: Mature fruits of *Ceriscoides turgida* were plucked from naturally growing populations within the Chandaka areas, Odisha, India. The species was taxonomically authenticated by the authors through morphological comparison with standard botanical descriptions (Saxena and Brahmam, 1995).

Preparation of plant material: The freshly collected fruits (Figure 2) were thoroughly washed with running tap water to remove adhering soil and surface contaminants. After cleaning, the fruits were shade dried for a short period to eliminate surface moisture while preserving natural metabolites. The partially dried material was then coarsely chopped and macerated directly for extraction without prior pulverization to minimize the loss of volatile or heat-sensitive constituents (Jena *et al.*, 2025).

Extraction procedure: The extraction of bioactive compounds was carried out by cold maceration using solvents of differing polarity to ensure broad spectrum recovery of phytoconstituents using standard protocol (Devi *et al.*, 2023). Approximately 50 g of fresh fruit material was soaked separately in *n*-hexane (non-polar) and hydroethanol (7:3, polar) in sterile conical flasks. The mixtures were kept for 72 hours at room temperature with occasional stirring to enhance solvent penetration.



Figure 2: Collected fruits of *Ceriscoides turgida* for experimental use

After the extraction period, the mixtures were filtered through Whatman No. 1 filter paper to separate the liquid extracts from plant residues. The filtrates were then air dried at ambient temperature to allow complete

solvent evaporation. The concentrated crude extracts were weighed and stored in airtight, sterile vials under refrigerated conditions (4 °C) until further use.

Phytochemical screening: Both n-hexane and hydroethanolic extracts were subjected to qualitative phytochemical analysis using standard phytochemical assays to identify the presence of key secondary metabolites such as tannins, saponins, terpenoids, phenolics, flavonoids, alkaloids, and reducing sugars. The intensity of coloration or precipitate formation in each reaction was used as an indicator of compound presence (Jena *et al.*, 2025).

Assessment of antibacterial activity: The antibacterial efficacy of the extracts was assessed against *Escherichia coli* (MTCC 45), a standard laboratory strain obtained from the Microbial Type Culture Collection (MTCC), Chandigarh, India. The minimum inhibitory concentration (MIC) was determined using the broth microdilution technique with serial dilutions of the extracts prepared in nutrient broth following standard methods (Jena *et al.*, 2025). Each assay was performed and bacterial growth was monitored visually after incubation at 37°C for 24 hours. The lowest concentration showing complete inhibition of visible growth was recorded as the MIC value, indicating the minimum inhibitory concentration of the extract against *E. coli*.

RESULTS AND DISCUSSION

A clear contrast was observed between the extracts obtained with non-polar and polar solvents (Table 3). The n-hexane extract showed negligible phytochemical content, indicating its ineffectiveness in isolating key constituents from the fruit material. In comparison, the hydroethanolic extract (1:1) displayed a broad spectrum of secondary metabolites, including tannins, saponins, flavonoids, terpenoids, phenolics, reducing sugars, and alkaloids. The substantial recovery of metabolites in the hydroethanolic medium reflected that the solvent has capacity to dissolve compounds of varying polarity, therefore, captured a wider range of bioactive molecules (Figure 3 and 4).

Table 3: Detection of secondary metabolites in fruit extract of *C. turgida*

Solvent Extract	Polarity	Number of metabolites detected	Major phytochemical Classes	Extraction efficiency
n-Hexane	Non-polar	0	None	Poor
Hydroethanol (1:1)	Polar	7	Tannins, Saponins, Flavonoids, Terpenoids, Phenolics, Reducing sugars, Alkaloids	Good

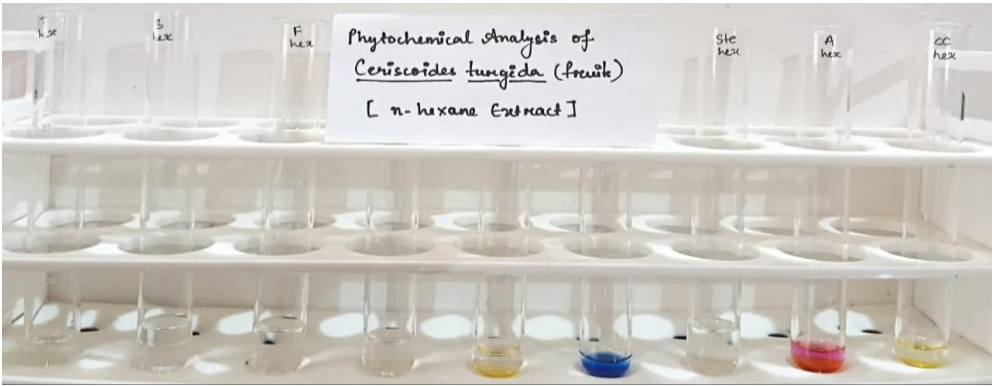


Figure 3: Phytochemical analysis of non-polar extract



Figure 4: Phytochemical analysis in polar extract

The antibacterial potential of the hydroethanolic extract was tested against *Escherichia coli* (MTCC 45) using the broth dilution method (Table 4). Noticeable inhibition of bacterial growth occurred only at the highest concentration (100 mg/mL), while lower concentrations (50, 25, and 12.5 mg/mL) showed no inhibitory effect (Figure 5).

Table 4: Estimation of Minimum Inhibitory Concentration (MIC)

Hydroethanolic Extract	Concentration (mg/mL)				MIC (mg/mL)
	100	50	25	12.5	
<i>Ceriscoides turgida</i> (fruits)	NG	G	G	G	100
Nutrient broth	NG	NG	NG	NG	-
Microbial broth	G	G	G	G	-
Antibiotics	NG	NG	NG	NG	-

(NG: No growth of bacteria; G: Growth)

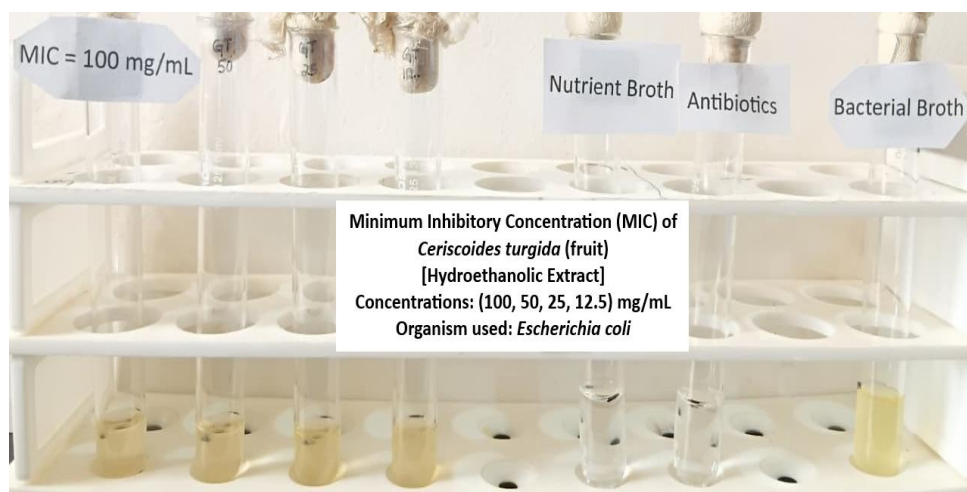


Figure 5: Minimum inhibition concentration (MIC) of fruits of *C. turgida*. Control assays behaved as expected, confirming the validity of the results. The observed inhibition at higher doses suggests that the extract contains compounds with mild antibacterial potential, which may act synergistically

at sufficient concentration. Although the activity was modest, it supports the ethnomedicinal relevance of *C. turgida*.

CONCLUSION

Modern drug discovery often focuses on speed and uniform results, sometimes forgetting the long history of traditional healing practices. Ethnomedicine is not just a list of herbal cures; it carries the knowledge and experiences of many generations. By combining this traditional wisdom with modern scientific research, we can develop safer and more sustainable medicines while also protecting valuable plant diversity. The frequent and consistent use of *Ceriscoides turgida* among different tribal communities shows its trusted healing value. In this study, the hydroethanolic fruit extract of this plant showed strong phytochemical richness and a moderate antibacterial activity with minimum inhibitory concentration (MIC) at 100mg/mL, supporting its traditional use. The future of medicine may depend on learning from such traditional systems, turning old knowledge into new discoveries that connect nature with science.

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Chapter 8

The chemistry of a borrowed life: bioactive potential of the hemi-parasitic herb *Striga densiflora* (Benth.) Benth. (Orobanchaceae)

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ABSTRACT

In the quiet scrublands of Chandaka, Odisha, *Striga densiflora* thrives as a seemingly ordinary hemi-parasitic plant, yet within its delicate structure lays a reservoir of unexplored chemistry. This study sought to uncover its hidden bioactive potential through a comparative solvent extraction approach. Whole plants were gently washed, shade dried and macerated in solvents of varying polarity to observe how nature's chemistry unfolds under different conditions. The non-polar extract revealed no major secondary metabolites. In contrast, the polar extract tested positive for tannins, saponins, phenolics, alkaloids, and reducing sugars. When challenged against *Escherichia coli*, a common and resilient bacterial strain, the hydroethanolic extract displayed complete inhibition of growth at all tested concentrations. The minimum inhibitory concentration (MIC) was determined to be 12.5 mg/mL. These results suggest that *S. densiflora* harbors promising antibacterial constituents, its potential veiled in polarity and revealed through thoughtful extraction. This work opens a window to the latent therapeutic promise of the plant and invites deeper exploration into its pharmacological essence.

Keywords: Antibacterial, semi parasite, therapeutics

INTRODUCTION

In nature, every plant plays an important role in keeping the environment balanced. While trees and shrubs are easily noticed, small herbs also help in

maintaining the ecosystem by supporting soil health, providing food, and regulating natural cycles (Guo *et al.*, 2023). Among these herbs, there is a small and special group belonging from the parasitic type. These plants are often considered harmful because they depend on other plants, called hosts, to survive. However, parasitic plants are also examples of how nature evolves in unique ways to adapt and survive in difficult conditions (Bouwmeester *et al.*, 2021). Parasitic plants are mainly divided into two types, holoparasites and hemiparasites (Ishida and Costa, 2024). Holoparasites are completely dependent on their host plants as they cannot produce their own food due to the absence of chlorophyll. On the other hand, hemi-parasitic plants are partly independent. They attach to host plants for water and minerals but can still make their own food through photosynthesis. This makes them more adaptable and resilient in changing environments. *Striga densiflora* (Figure 1) is one such hemi-parasitic herb which is normally found in seasonally dry tropical regions (POWO, 2025). Some of its reported habitats include upper Gangetic, Karnataka, Tamil Nadu Plains, Odisha and Deccan Peninsula (Lyngdoh *et al.*, 2023). It can grow in harsh conditions using its root as the mode of parasitism (Lyngdoh *et al.*, 2023) and adjust well to environmental changes. Although it is often ignored as a weed, it may contain valuable chemical compounds that have medicinal importance because the members of the Orobanchaceae family, to which *S. densiflora* belongs, are well known not only for their parasitic lifestyle but also for their significance in traditional medicine. Despite their dependence on host plants, several species in this family are valued for their healing properties. For instance, as reported by a survey (Jaiswal *et al.*, 2021), *Aeginetia indica* stems are used to relieve coughs, while *Buchnera hispida* leaves are ground into a paste to treat scabies and eczema. The flowers of *Centranthera indica* are used as a diuretic, and *Orobanche cernua* stems are applied to reduce swelling. Likewise, *Striga asiatica* flower infusions are traditionally used to eliminate stomach parasites. These examples show that even parasitic plants, often viewed as harmful, possess rich medicinal potential. An important indication to how these plants are used as effective folk medicinal practices may link to the fact that, hemi-parasitic plants interact closely with other species and face environmental stress, they often produce different secondary metabolites or natural

chemicals that help them defend and survive (Behera *et al.*,2023). And, many of these compounds are known to show antibacterial and other health related properties. But, despite its presence in many parts of India, *Striga densiflora* has not been studied much for its chemical or medicinal properties. This study aims to fill that gap by examining its phytochemical composition and testing its antibacterial activity. By understanding how this hemi-parasitic plant produces and uses these compounds, we can explore its potential as a natural source of antimicrobial agents.



Figure 1: *Striga densiflora* in its habitat

METHODOLOGY

Plant Collection and Identification: Whole plants of *Striga densiflora* (Figure 1) were collected from the Chandaka village of Khordha, Odisha, India. The plant species was taxonomically verified using relevant published floras and identification keys (Kumar *et al.*, 2018; Balkrishna *et al.*, 2018).



Figure 2: Plant parts of *S. densiflora*

Preparation of Plant Material: Collected plants (Figure 2) were rinsed thoroughly under running tap water to remove adhering soil and surface impurities. The cleaned samples were shade dried briefly to eliminate excess surface moisture while retaining volatile constituents. The partially dried plants were then coarsely chopped (Figure 3) and subjected directly to maceration (Devi *et al.*, 2023).

Extraction of Bioactive Compounds: Extraction was performed through cold maceration using solvents of varying polarity to ensure comprehensive recovery of phytoconstituents following standard procedures (Devi *et al.*,

2023). Approximately 40g of fresh plant material was soaked separately in n-hexane (non-polar) and hydroethanol (1:1) in sterilized conical flasks. The mixtures were left undisturbed for 72 h at room temperature with occasional stirring to facilitate solvent penetration. After maceration, each extract was filtered and were air dried at room temperature to allow complete solvent evaporation. The concentrated crude extracts were weighed, transferred into sterile airtight glass bottles and stored for following experiments.



Figure 3: coarsely chopped plant parts for experimental use

Preliminary Phytochemical Screening: Both n-hexane and hydroethanolic extracts were analyzed qualitatively for the presence of major secondary metabolites, including tannins, saponins, terpenoids, phenolics, flavonoids, alkaloids, reducing sugars and carbonyl compounds using established phytochemical assays (Jena *et al.*, 2025). The development of characteristic color reactions or precipitates in each test was interpreted as a positive indication of the respective compound group.

Evaluation of Antibacterial Activity: The antibacterial potential of the plant extracts was evaluated against *Escherichia coli* (MTCC 45), a

standard laboratory strain obtained from the Microbial Type Culture Collection (MTCC), Chandigarh, India. The minimum inhibitory concentration (MIC) was determined using the broth microdilution method with serial dilutions of each extract prepared in nutrient broth (Jena *et al.*, 2025). Tubes were inoculated with bacterial suspension and incubated at 37 °C for 24 h. Growth inhibition was assessed visually, and the lowest extract concentration exhibiting no visible turbidity was recorded as the MIC, representing the minimum concentration required to inhibit *E. coli* growth completely.

RESULTS AND DISCUSSION

Qualitative phytochemical analysis of hydroethanolic extract of *Striga densiflora* showed solvent dependent activity (Table 1). Non polar n-hexane extract detected none of the tested secondary metabolites. Whereas polar hydroethanolic extract (1:1) detected tannins, saponins, phenolics, reducing sugars and alkaloids (Figure 4 and 5). It showed that polar solvent is able to extract diverse range of metabolites in comparison to non-polar solvent indicating its higher phytochemical richness.

Table 1: Solvent dependent phytochemical analysis of *S. densiflora*

Polarity	Solvent extract	Detected secondary metabolites	Phytochemical richness
Non-polar	n-Hexane	No tested metabolites were detected	◆
Polar	Hydroethanolic	Tannins, Saponins, Phenolics, Reducing sugars and Alkaloids	◆

(◆ = low, ◆ = high)

Its efficacy was then tested for antibacterial activity determining its minimum inhibitory concentration (MIC) against *Escherichia coli*. Control assays behaved as expected, microbial broth showed consistent bacterial growth and nutrient broth showed no bacterial growth, proving sterility. Antibiotics standard, validated the efficacy of the assay. The hydroethanolic extract showed no bacterial growth at any of the tested concentrations (100, 50, 25 and 12.5) mg/mL. Therefore, the lowest tested value 12.5 mg/mL (Figure 5) was established as the minimum inhibitory concentration (MIC).

This validated the phytochemical richness of the hydroethanolic extract and the presence of the tested group of bioactive compounds (Table 2). This also implied that the species may be effective against bacterial infections associated with gastrointestinal and urinary tract aligning with the traditional medicinal practices within its genus (Jaiswal *et al.*, 2021). And, these findings can be used for further continuation of detailed research related to its chemical and molecular characterization.



Figure 3: Phytochemical analysis of non-polar extract

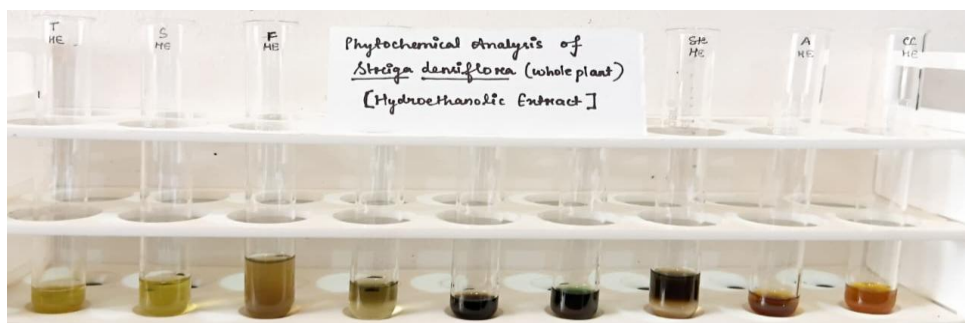


Figure 4: Phytochemical analysis in polar extract

Table 2: Estimation of Minimum Inhibitory Concentration (MIC)

Hydroethanolic Extract	Concentration (mg/mL)				MIC (mg/mL)
	100	50	25	12.5	
<i>Striga densiflora</i> (Whole	NG	NG	NG	NG	12.5

plant)					
Nutrient broth	NG	NG	NG	NG	-
Microbial broth	G	G	G	G	-
Antibiotics	NG	NG	NG	NG	-

(NG: No growth of bacteria; G: Growth)



Figure 5: Determination of minimum inhibitory concentration (MIC)

CONCLUSION

The journey into chemistry of *Striga densiflora* reveals the dynamics of polarity and potential. While the non-polar extract remained inert, the polar hydroethanolic fraction unfolded group of diverse metabolites including phenolics, alkaloids, tannins and saponins those are capable of halting bacterial growth. The complete inhibition of *E. coli* at low concentrations signals not only the richness of its phytochemical composition but also its potential as a natural antibacterial source. The findings remind us that even the most overlooked species in the wild may hold molecular treasures of medicinal importance. Future work, guided by isolation, characterization, and mechanistic studies may illuminate how these compounds function and how *S. densiflora* could contribute to plant-based antimicrobial therapies.

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Chapter 9

Climbing towards cure: phytochemical and antibacterial exploration of *Gouania leptostachya* DC. (Rhamnaceae)

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ABSTRACT

Lianas being famous for their entwining vines but less studied in light of their pharmacological potential. *Gouania leptostachya* (Rhamnaceae) is one such liana known for its traditional medicinal uses across tropical regions of Asia. Present study explores the phytochemical composition and antibacterial potential of its leaf extracts. The phytochemical screening showed that the hydroethanolic extract was richer in secondary metabolites, including tannins, saponins, phenolic compounds, and reducing sugars, while the non-polar extract contained only reducing sugars. When tested against *Escherichia coli* to validate its folk medicinal practices, the hydroethanolic extract exhibited notable antibacterial activity, with a minimum inhibitory concentration (MIC) of 12.5 mg/mL. Observations suggested that the polar extract of *G. leptostachya* leaves holds promising antibacterial properties, possibly linked to the presence of phenolic and tannin compounds. This study provides a scientific basis for the plant's traditional use and supports its potential as a natural source of bioactive compounds.

Keywords: Bioactivity, folk medicine, liana

INTRODUCTION

In tropical forests, lianas (long-stemmed woody vines) form an important part of the forest structure. These plants grow from the ground and climb trees or other supports using tendrils, hooked spines, or climbing roots to

reach sunlight in the upper canopy (Rowe, 2018). Unlike epiphytes that live on other plants, lianas stay rooted in the soil while extending high into the forest layers (Ceballos *et al.*, 2025). Their presence often reflects the health and maturity of a forest ecosystem. Although they compete with trees for light, water, and nutrients, and sometimes slow their growth by adding weight, lianas also play vital ecological roles (De Deurwaerder *et al.*, 2024). They connect tree canopies, creating natural bridges that allow animals to move easily through the forest, and influence forest regeneration and diversity (Schnitzer and Bongers, 2002). In addition to their ecological functions, many lianas have cultural and medicinal importance (Devarakonda *et al.*, 2022). Communities living in tropical regions have long used them in traditional healing, food, and daily practices (Dunget *al.*, 2015). Thus, lianas are not only a structural element of forests but also a source of knowledge and health for people who live close to them. *Gouania leptostachya* (Figure 1) in that context was studied for correlating its ethnomedicinal practices with today's modern medicine.



Figure 1: Leaves and inflorescence of *Gouania leptostachya*

Being a native species in the Indian subcontinent and Western Malaysia, this Slender Spiked *Gouania* belongs to family Rhamnaceae. It typically grows in wet tropical biomes and has ethnobotanical relevance which makes it an integral but lesser-known part of the folk medicinal practices (Gumisiriza *et al.*, 2024). Its leaves, stems, and roots are prepared as poultices, extracts, decoctions, herbal baths, and smoke inhalations for the management of ailments including sores, wounds, gastrointestinal disorders, postpartum complications, inflammatory diseases, and fever

(Table 1). Thus, its potential pharmacological relevance has been assessed in this study to support its traditional therapeutic reputation.

Table 1: Traditional ethnomedicinal uses of *G. leptostachya*

Plant parts used	Mode of use	Ethno-medicinal applications	Associated communities/ regions	Source(s)
Leaves	Poultice applied externally/ topically	Treatment of eczema (local name: <i>Raktapitchali</i>)	India (Odisha, Jharkhand, Uttarakhand, West Bengal)	Devarakonda <i>et al.</i> , (2022); Pradhan and Badola, (2008); Uprety <i>et al.</i> , (2016)
Leaf	Extract applied externally	Treatment of wounds	India (Himachal Pradesh)	Sharma <i>et al.</i> , (2024)
Leaves and stems	Decoction or cold infusion taken orally	Relief from stomachache and diarrhea	Indonesia	Gumisiriza <i>et al.</i> , (2024)
Whole plant (mainly leaves)	Herbal bath formula and food supplement	Postpartum care, treatment of convulsions in newborns, numbness, fainting, antispasmodic conditions and general inflammation	Mien tribe, Northern Thailand, Vietnam, Bhutan, Nepal	Panyaphu <i>et al.</i> , (2011); Dung <i>et al.</i> , (2015); Gumisiriza <i>et al.</i> , (2024)
Roots	Roots burned; smoke inhaled	Treatment of fever	Rural communities of North Andaman, India	Prasad <i>et al.</i> , (2008)

METHODOLOGY

Leaves of *Gouania leptostachya* (Figure 2) were collected from Chandaka Khordha, Odisha, India, and identified by the authors. The collected samples were properly tagged and placed in cotton bags to prevent contamination during transport.



Figure 2: Leaves of *G. leptostachya*

In the laboratory, the leaves were washed thoroughly under running tap water followed by distilled water to remove adhering dust, debris, and surface contaminants. Cleaned leaves were shade dried at ambient temperature (25 ± 2 °C) for 7-10 days to preserve thermolabile phytoconstituents and then finely powdered using a mechanical grinder. The powdered material was subjected to solvent extraction by the maceration method (Devi *et al.*, 2025) using two solvents of different polarity, n-hexane and hydro-ethanol (1:1), to ensure a broad spectrum of phytochemical recovery. The mixtures were agitated intermittently for 48 hours and filtered through Whatman No. 1 filter paper, after which the filtrates were concentrated at room temperature to evaporate residual solvent. The obtained crude extracts were stored in sterile glass vials under

refrigeration (4°C) until further analysis. Preliminary qualitative phytochemical screening was performed on both extracts following standard procedures to detect the presence of major classes of secondary metabolites such as tannins, flavonoids, terpenoids, reducing sugars, saponins, alkaloids, carbonyl compounds and phenolic compounds. The antibacterial potential of the extracts was subsequently evaluated against *Escherichia coli* (MTCC 45). The minimum inhibitory concentration (MIC) was determined by the broth microdilution method following standard protocols with minor modifications (Jena *et al.*, 2025) to assess the concentration-dependent antibacterial efficacy of the extracts.

RESULTS AND DISCUSSION

The qualitative phytochemical screening of *Gouania leptostachya* leaf extracts revealed the presence of key secondary metabolites that varied according to solvent polarity (Table 2). The non-polar n-hexane extract detected reducing sugars (Figure 3), indicating a limited phytochemical yield. Meanwhile, the polar hydroethanolic extract exhibited a richer phytochemical profile, containing tannins, saponins, phenolic compounds, and reducing sugars (Figure 4). This suggests that polar solvents are more efficient in extracting diverse bioactive compounds from *G. leptostachya* leaves, reflecting their higher phytochemical richness. The antibacterial activity of its hydroethanolic leaf extract was tested against *E. coli* (MTCC 45). The extract effectively inhibited bacterial growth at all tested concentrations, with the minimum inhibitory concentration (MIC) recorded at 12.5 mg/mL (Table 3). The results were consistent across all replicates. Quality control checks verified sterility in the nutrient broth, viability of the microbial culture, and complete inhibition in the antibiotic control.

Table 2: Detection of secondary metabolites of *G. leptostachya* leaf extract

Polarity	Solvent extract	Detected secondary metabolites	Phytochemical richness
Non-polar	n-Hexane	Reducing sugars	◆
Polar	Hydroethanolic	Tannins, Saponins, Phenolic compounds and Reducing sugars	◆

(◆ = low, ◆ = high)



Figure 3: Detection of secondary metabolites in n-hexane extract

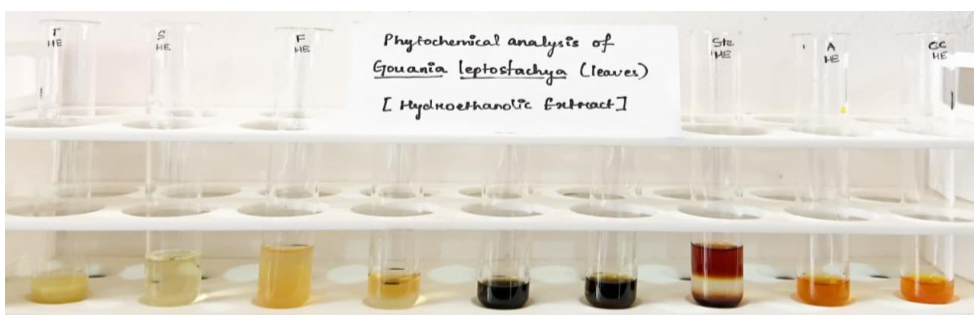


Figure 4: Detection of secondary metabolites in hydroethanolic extract

Table 3: Estimation of Minimum Inhibitory Concentration (MIC)

Sample	Extract	Concentration (mg/mL)	Result	Replicates (n)	QC note
<i>G. leptostachya</i> (Leaves)	Hydroethanolic	100	NG	3	consistent
		50	NG	3	consistent
		25	NG	3	consistent
		12.5 (MIC)	NG	3	consistent
Nutrient broth	-	-	NG	3	sterility
Microbial broth	-	-	G	3	culture viable
Antibiotic	-	-	NG	3	positive control

(G= Growth, NG= No growth QC = Quality control)

CONCLUSION

Gouania leptostachya is a plant with valuable bioactive potential, particularly evident in its hydroethanolic leaf extract, as observed in the experimental study above. The presented results align with its long-standing traditional uses. While the current findings are preliminary, they open the scope for further research on isolating specific compounds and understanding their mechanisms of action. As a forest liana with deep ethnobotanical roots, *G. leptostachya* continues to prove how traditional knowledge and modern science can complement each other in exploring nature's pharmacy.

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Chapter 10

Natural antibacterial potential of *Grewia rhamnifolia* Roth (Malvaceae): insights from phytochemical analysis

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ABSTRACT

Antibiotic resistance has become a major global problem, leading researchers to explore medicinal plants as natural antibacterial agents. This experiment focused on the fruits of *Grewia rhamnifolia*, a wild plant belonging to the Malvaceae family known for its therapeutic properties. Fruit extracts were prepared using the Soxhlet extraction method with contrasting solvents and tested for their chemical composition and antibacterial activity. The hydroethanolic extract showed the presence of several important compounds such as tannins, phenolics, alkaloids, and reducing sugars, suggesting it was the most effective solvent for extracting active ingredients. The antibacterial test against *Escherichia coli* showed that the extract could stop bacterial growth at a concentration of 100 mg/mL. These results indicate that *G. rhamnifolia* fruits contain useful natural compounds with potential antibacterial properties. This study supports the traditional use of this plant and highlights its possible role in developing new plant-based medicines.

Keywords: Ethnomedicine, antibiotic resistance, plant-based therapeutics

INTRODUCTION

Today, the search for natural antibacterial agents has gained considerable global attention due to the crisis of increasing antibiotic resistance (Angelini, 2024). However, traditional knowledge systems known as modern-day ethnobotany and ethnomedicine have long recognized the therapeutic potential of plants, providing a solid foundation for a new era of drug discovery (McClatchey *et al.*, 2009). Worldwide, numerous indigenous communities have historically relied on medicinal plants to treat infectious diseases, guided by generations of experiential knowledge from

traditional healers and folk medicine practitioners. These plant-based remedies constitute a diverse group of bioactive compounds like flavonoids, phenolics, alkaloids, tannins and many more that add to their antibacterial potency (AlSheikh *et al.*, 2020). This brings us to the pretext that wild and underexplored plants having medicinal uses can be used for developing safer and sustainable natural antibacterial agents. *Grewia rhamnifolia* (Figure 1) is one such wild climbing shrub found in seasonally dry tropical biomes native to India and Sri Lanka (POWO, 2025).



Figure 1: A twig of *Grewia rhamnifolia*

The leaves of this species are ovate-lanceolate with serrulate or crenulate margins, an acuminate apex, and a rounded or obtuse base. They are typically 3-nerved, occasionally exhibiting two additional smaller lateral nerves, with 3-5 secondary veins, and are nearly glabrous. The flowers are large, white to yellowish in colour, and borne in terminal or leaf-opposed umbels containing few blossoms. Floral buds are ovoid, distinctly ribbed, and covered with dense tomentose and hirsute hairs. The gonophore is short, and the style is stout with a four-lobed stigma. The drupe is depressed-globose, hairy, and yellow tomentose, containing several seeds;

the fruiting pedicels are stout and firm, which adds to its distinguishable characteristics (Saxena and Brahmam, 1994). A notable fact that aligns with its morphology is that typical members of the family Malvaceae, belonging to the genus *Grewia*, exhibit a diverse range of medicinal properties (Table 1), which makes them an integral part of folk medicine in their native habitats (Suguna and Umesha, 2022). The present study suggests that *G. rhamnifolia* (Figure 2) may possess comparable pharmacological potential similar to this trend.

Table 1: Traditional therapeutic applications of some selected species of genus *Grewia*

Species	Plant part used	Therapeutic applications	Source(s)
<i>Grewia asiatica</i>	Leaves	Applied on skin for anti-toxic and connective effects.	Morton, (1987)
	Roots and bark	Used for stiffness, astringent and stomachic properties; treats blood, heart, and respiratory problems.	
	Bark	Used as a demulcent, febrifuge, and to relieve bowel looseness.	Waliullah <i>et al.</i> , (2011)
	Unripe fruit	Mentioned in Ayurveda for curing Vata, Pitta, and Kapha imbalances; used for wounds, fever, ulcers, menstrual disorders, and diabetes.	Morton, (1987)
	Fruit	Reduces inflammation, soothes throat infections, and is used to expel dead fetuses.	Gupta <i>et al.</i> , (2006)
<i>Grewia abutilifolia</i>	Whole plant	Treats malaria, smallpox, cough, bladder and intestinal disorders, eczema, dysentery, typhoid fever, rheumatism, infertility, and abscesses.	Rafe <i>et al.</i> , (2018)
<i>Grewia</i>	Leaves, root and	Juice consumed with other herbs for	Dey and De,

<i>gamblei</i>	bark	snakebite treatment.	(2011)
<i>Grewia disperma</i>	Roots	Used to control bleeding, treat bronchitis, cough, and cold.	Ullah <i>et al.</i> , (2012)
	Bark	Applied for boils.	
	Fruits	Used as a cardi tonic.	
<i>Grewia tenax</i>	Roots	Treats jaundice, asthma, and pulmonary infections.	Aadesariya <i>et al.</i> , (2017)
	Leaves	Used for trachoma (eye infection).	
	Leaves and fruits	Decoction and juice are taken to increase haemoglobin in anaemic patients.	
<i>Grewia tiliaefolia</i>	Leaves and bark	Decoction used to treat snakebite.	Dharmasoth and Rao, (2019)
	Root powder	Used for sprains, ulcers, burning sensations, and skin diseases.	

As this species remains scientifically understudied, the present study was undertaken to qualitatively assess its phytochemical composition and evaluate the antibacterial activity of its fruit extracts, which can provide a base for its further exploration.

METHODOLOGY

Fruits of *Grewia rhamnifolia* were collected from Chandaka, Khordha, Odisha, India and were taxonomically identified by the authors. The collected samples were properly tagged and placed in cotton bags to prevent contamination during transport (Figure 3). The solvent extraction methods employed for isolating bioactive constituents from medicinal plants largely depend on the type of solvent used and the application of heat. The finely ground fruit samples of *G. rhamnifolia* were enclosed in a porous cellulose thimble and placed in the extraction chamber of the Soxhlet apparatus. The n-hexane and hydro-ethanol solvents, upon heating in the round-bottom flask, vaporized and ascended into the thimble chamber, where they

condensed and gradually filtered through the plant matrix, dissolving the desired phytoconstituents, respectively.



Figure 2: Fruit of *Grewia rhamnifolia*

When the solvent volume reached the siphon arm, it was automatically siphoned back into the boiling flask, and this cyclic operation was repeated several times to ensure exhaustive extraction (Jena *et al.*, 2025).



Figure 3: Collected fruit sample of *G. rhamnifolia*

The antibacterial potential of the extracts was subsequently evaluated against *Escherichia coli* (MTCC 45). The minimum inhibitory concentration (MIC) was determined by the broth microdilution method following standard protocols with minor modifications (Jena *et al.*, 2025) to assess the concentration-dependent antibacterial efficacy of the extracts.

RESULTS AND DISCUSSION

The qualitative analysis of *Grewia rhamnifolia* fruit extracts showed a clear influence of solvent polarity on the type and abundance of secondary metabolites extracted (Table 2). The non-polar solvent system (n-hexane) mainly extracted fat-soluble compounds and simple sugars, showing the presence of only reducing sugars. This indicated that n-hexane was not efficient in recovering a wide range of phytoconstituents due to its low polarity. In contrast, the hydroethanolic solvent system, with its higher polarity, extracted a broader spectrum of bioactive compounds, including tannins, phenolics, alkaloids, and reducing sugars. This suggested that mixed polar solvents like aqueous-ethanol combinations are more suitable for isolating different phytochemicals, which are typically polar or semi-polar in nature.

Table 2: Solvent-dependent secondary metabolite screening of fruits of *G. rhamnifolia*

Solvent system	Relative polarity	Nature of extracted compounds	Detected bioactive compound	Inference
n-Hexane	Non-polar	Fat-soluble, non-polar compounds	Reducing sugars	Inefficient for extracting a diverse array of metabolites.
Hydroethanolic	Polar	Polar and semi-polar compounds	Tannins, Phenolic compounds, Reducing sugars and Alkaloids	Effective solvent for extracting secondary metabolites.

The antibacterial efficacy of the hydroethanolic extract of *G. rhamnifolia* fruits was assessed by determining its minimum inhibitory concentration (MIC) against *Escherichia coli* (Table 3).

Table 3: Estimation of Minimum Inhibitory Concentration (MIC)

Hydroethanolic extract	Concentration (mg/mL)				MIC (mg/mL)
	100	50	25	12.5	
<i>Grewia rhamnifolia</i> (fruits)	NG	G	G	G	100
Nutrient broth	NG	NG	NG	NG	-
Microbial broth	G	G	G	G	-
Antibiotics	NG	NG	NG	NG	-

(NG: No growth of bacteria; G: Growth)

The results showcased that bacterial growth was inhibited only at the concentration of 100 mg/mL, while growth was consistent at all the other lower tested concentrations, indicating the MIC value to be 100 mg/mL. The absence of bacterial growth in the antibiotic control validated the assay conditions, while nutrient and microbial broths served as appropriate negative and positive controls, respectively. In one of the folkloric medicinal plant studies conducted by Senthil *et al.*, (2015), the fruit juice of *G. rhamnifolia* was documented to be taken orally for treating stomachache and for alleviating digestive problems. The observed antibacterial potential through this experimental set-up can be attributed towards dual directions in that context. One, as a collateral to the antibacterial activity of *G. rhamnifolia* fruit extract to be effective against *E. coli* and the other towards the presence of phytochemicals such as tannins and phenolic compounds, which are known to disrupt bacterial cell membranes and interfere with enzymatic activity (Takó *et al.*, 2020), giving a valid reason for its antibacterial potency.

CONCLUSION

Nowadays, the modern science of drug discovery is rapidly running toward the development of easily accessible, more effective and powerful drug compositions. This not only helps modern healthcare but also gives rise to more complex problems like antibiotic resistance. Natural antibacterial agents in that aspect can prove a good alternative. *Grewia rhamnifolia*, a potential natural antibacterial agent, was assessed for its phytochemical profile, which revealed the presence of tannins, phenolic compounds, reducing sugars and alkaloids. This was validated through studying its antibacterial activity by determining its minimum inhibitory concentration (MIC) against *E.coli*, which was found to be 100mg/mL. These findings encourage further isolation and characterization of bioactive compounds of this species for a better understanding of their mechanisms of action and to explore their potential in developing alternative antibacterial formulations.

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Chapter 11

The rising tide of antimicrobial resistance: causes, consequences and potential solutions

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ABSTRACT

Antimicrobial resistance (AMR) has emerged as a defining challenge of modern medicine, threatening to reverse decades of therapeutic progress. The phenomenon, driven by the evolutionary adaptability of microorganisms and exacerbated by human misuse of antimicrobial agents, represents a multidimensional crisis that spans biology, health systems, agriculture, economics, and policy. Present study examines the escalating threat of AMR by exploring its underlying causes, far-reaching consequences, and feasible solutions within a global “One Health” framework. The study highlights the ecological, social, and economic repercussions of rising resistance and the emerging recognition of AMR as a silent pandemic. The study also outlines potential solutions, ranging from stewardship programs and regulatory reforms to innovative therapies and public awareness initiatives. The overarching argument emphasises that AMR is not a future threat but an immediate reality requiring urgent, coordinated, and sustained global action.

Keywords: AMR, drugs, one health, pathogenic microbes

INTRODUCTION

Antimicrobial resistance refers to the ability of microorganisms to withstand the effects of drugs that were once effective against them. This resistance develops through natural selection, genetic mutation, or horizontal gene transfer, enabling pathogens to survive and multiply despite exposure to antimicrobial agents (Salam *et al.*, 2023; Figure 1). In practical terms, AMR renders many common infections increasingly difficult or impossible to treat, turning minor ailments into life-threatening conditions (Muteeb *et al.*, 2023). The growing prevalence of resistant pathogens has created a major global health concern that transcends national borders and healthcare systems. The discovery of penicillin by Alexander Fleming in 1928 revolutionised modern medicine, heralding the antibiotic era (Lobanovska and Pilla, 2017). However, even in his Nobel lecture, Fleming warned of the potential misuse of antibiotics, leading to resistance a prophecy now realised (Rosenblatt-Farrell, 2009). The decades following World War II witnessed the discovery of numerous antibiotic classes, resulting in a golden age of antimicrobial therapy (Adedeji, 2016). Yet, excessive use in humans, animals, and agriculture, coupled with a decline in the development of new antibiotics, has led to a critical imbalance. The same drugs that once symbolised scientific triumph are now losing their potency, as resistant pathogens outpace pharmaceutical innovation (Brüssow, 2024). Unlike acute health crises such as COVID-19, antimicrobial resistance spreads quietly, without public panic or immediate visibility. Its cumulative impact, however, is profound. Resistant infections cause prolonged illnesses, increased hospital stays, and elevated mortality rates (Adebisi *et al.*, 2021). The inability to treat routine infections jeopardises modern medical procedures such as surgeries, chemotherapy, and organ transplants, all of which depend on effective antimicrobial prophylaxis (Chinemerem *et al.*, 2022). The silent spread of resistance genes across borders underscores that AMR is not confined to any single region or species; it is a planetary health issue that challenges global sustainability. In recent years, the burden of antimicrobial resistance has grown exponentially (Salam *et al.*, 2023). Multidrug-resistant tuberculosis, methicillin-resistant *Staphylococcus aureus* (MRSA), and carbapenem-

resistant *Enterobacteriaceae* have become emblematic of the crisis. Estimates suggest that millions of deaths annually are attributable to resistant infections, with the majority occurring in low- and middle-income countries (Marino *et al.*, 2025).

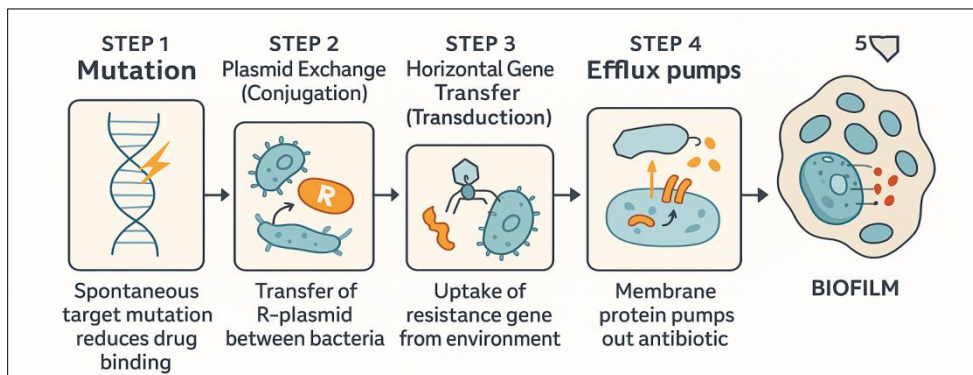


Figure 1: Mechanisms of microbial resistance development

In many regions, inadequate healthcare infrastructure, poor sanitation, and unregulated access to antibiotics contribute to the rapid spread of AMR. Additionally, international travel and trade facilitate the global dissemination of resistant strains, blurring the boundaries between local and global outbreaks (Endale *et al.*, 2023). The complexity of AMR arises from its deeply interconnected causes. Beyond biological evolution, resistance is influenced by sociocultural practices, economic pressures, and environmental degradation (Larsson and Flach, 2022). The unregulated use of antibiotics in livestock and aquaculture fosters resistance in animal populations, which can transfer to humans through food chains or environmental contamination (Manyi-Loh *et al.*, 2018). Furthermore, pharmaceutical manufacturing waste containing antibiotic residues further pollutes our water systems, creating environments that promote the growth of resistant bacteria. AMR thus epitomizes a systems-level problem that demands a holistic understanding and coordinated global action (Kotwani *et al.*, 2021). Traditional approaches that focus solely on medical interventions are insufficient. Addressing the AMR crisis requires a “One Health” perspective, which acknowledges the intrinsic links between human, animal, and environmental health (Danasekaran, 2024). To effectively combat resistance development, integrated surveillance, rational drug use,

improvements in sanitation, and educational campaigns must operate in synergy. Ultimately, tackling the problem of AMR involves not just microbiology but also issues of governance, awareness, and equity as it is about microbiology.

CAUSES AND DRIVERS OF ANTIMICROBIAL RESISTANCE

Antimicrobial resistance (AMR) does not arise from a single source but from a convergence of biological adaptation, human behaviour, agricultural practice, and policy shortcomings. Its drivers operate at multiple scales, from molecular genetics within microbes to global trade and governance failures. Understanding these interconnected causes is essential for designing meaningful interventions (Ferraz, 2024). Microorganisms possess remarkable genetic plasticity that enables them to adapt rapidly to hostile environments. When exposed to antimicrobial agents, selective pressure favours the survival of resistant variants, which then proliferate. Resistance can emerge through several mechanisms, each conferring unique adaptive advantages. Random mutations in microbial DNA can alter drug targets, metabolic pathways, or membrane permeability. These mutations may reduce a drug's binding affinity, deactivate its enzymatic target, or prevent its entry into the cell. In bacterial populations that reproduce quickly, even a single advantageous mutation can dominate within hours under antibiotic pressure (Salam *et al.*, 2023). Perhaps the most powerful driver of AMR is the exchange of genetic material between microorganisms. Through conjugation, transformation, or transduction, bacteria can acquire resistance genes carried on plasmids, transposons, or integrons. This means that resistance developed in one species such as environmental *Pseudomonas*, can transfer to a human pathogen like *Escherichia coli*. The “resistome,” a collective gene pool of resistance determinants, circulates freely across microbial communities in soil, water, and the human microbiome (Iskandar *et al.*, 2022). Many microbes form biofilms, protective matrices of polysaccharides and proteins that shield bacterial cells from antibiotics. Within biofilms, slow-growing or dormant “persister” cells evade antimicrobial action, only to repopulate once treatment ceases. This physiological tolerance differs from genetic resistance but contributes significantly to treatment failure in chronic

infections (Iskandar *et al.*, 2022). Exposure to non-antibiotic compounds such as heavy metals, disinfectants, or biocides can co-select for resistant strains. Likewise, a single resistance mechanism, such as efflux pumps, can expel multiple drug classes simultaneously, leading to cross-resistance. These intertwined pathways illustrate why resistance emerges even in environments not directly exposed to antibiotics (Endale *et al.*, 2023).

Human and clinical factors: Human medical practices are the primary contributors to AMR. The overuse and misuse of antibiotics in healthcare settings accelerate the development and spread of resistance. Antibiotics are often prescribed for viral infections, such as colds or influenza, where they offer no benefit. In many regions, patients can purchase antibiotics without a prescription, leading to incomplete or inappropriate treatment courses. Every unnecessary exposure to antibiotics strengthens selective pressure, raising the likelihood that resistant mutants will survive. In low-resource settings, the lack of rapid and accurate diagnostic tools forces clinicians to rely on empirical treatment (Castro-Sanchez *et al.*, 2016). As a precaution, broad-spectrum antibiotics are administered even when the cause of infection is uncertain. This indiscriminate use eliminates susceptible microbes while leaving resistant populations to thrive. Healthcare facilities, particularly intensive care units, serve as hubs for resistant pathogens. Inadequate infection prevention measures, poor hand hygiene, contaminated equipment, and overcrowded wards facilitate cross-infections. Resistant strains such as Methicillin-resistant *Staphylococcus aureus* (MRSA) and *Clostridioides difficile* often spread within hospitals, compounding patient morbidity and healthcare costs. Patients who discontinue their treatment prematurely, once their symptoms subside, allow partially resistant microbes to survive and multiply (Castro-Sanchez *et al.*, 2016). Similarly, sub-therapeutic dosing or counterfeit drugs with insufficient active ingredient content create ideal conditions for the selection of resistance. The movement of people across borders further spreads resistant organisms internationally. A patient treated with antibiotics abroad may return home carrying multi-resistant strains, effectively globalising local outbreaks. The interconnected nature of healthcare systems ensures that resistance knows no geographic boundaries (Endale *et al.*, 2023).

Agricultural and environmental factors: Antimicrobials have become integral to modern food production, yet their indiscriminate use outside human medicine profoundly influences resistance evolution (Li *et al.*, 2023). Antibiotics are widely administered to animals not only for therapeutic purposes but also as growth promoters and prophylactics. Continuous low-dose exposure in feed creates optimal conditions for resistance selection within animal microbiota (Laborda *et al.*, 2022). Resistant bacteria or resistance genes can then transfer to humans via direct contact, contaminated meat, or environmental runoff. Fish farming operations often rely on antibiotics to prevent disease outbreaks in dense populations. Similarly, certain crops are treated with antibacterial agents to control plant pathogens. These practices introduce substantial amounts of antimicrobial residues into aquatic and soil environments, fostering resistant microbial communities (Zeng *et al.*, 2025). Effluents from drug manufacturing, hospitals, and municipal waste streams carry unmetabolized antibiotics into rivers and soils. In these habitats, sub-inhibitory concentrations of antimicrobials exert chronic selection pressure, enriching for resistant bacteria even in the absence of disease (Laborda *et al.*, 2022). Such environmental reservoirs act as breeding grounds where resistance genes can recombine and later re-enter human or animal populations. Wild animals exposed to human waste or agricultural effluents can acquire and disseminate resistant bacteria through migratory routes. This ecological connectivity underscores that AMR extends beyond anthropogenic boundaries; it permeates entire ecosystems (Laborda *et al.*, 2022).

Socioeconomic and policy drivers: Hidden beneath the biological and behavioral layers of AMR lie deep structural inequities and policy failures that perpetuate resistance on a global scale. In some regions, antibiotics are scarce, leading to under-treatment, while in others, they are easily accessible over the counter. The lack of strong regulatory frameworks allows counterfeit or substandard drugs to circulate, increasing the risk of resistance. Economic constraints often compel patients to purchase incomplete doses, resulting in incomplete treatment. To effectively contain AMR, it is essential to gather data on antibiotic use and resistance patterns. Many countries lack functional surveillance systems and inconsistently enforce regulations. Without evidence-based policies, antibiotics continue

to be misused across different sectors, and resistant outbreaks often go undetected until they escalate. Additionally, the antibiotic development pipeline has stagnated because new drugs offer low commercial returns compared to treatments for chronic-disease. As a result, pharmaceutical companies are reluctant to invest in costly research for medicines intended for short-term use, especially when they are subject to stewardship guidelines. This economic disincentive has resulted in a global reliance on aging classes of antibiotics. The flow of goods, animals, and people facilitates international spread of resistant strains. Food exports that are contaminated with resistant bacteria or resistance genes can create new ecological niches in far-off markets. At the same time, global trade agreements often overlook public-health safeguards, prioritizing economic interests over the responsible use of antimicrobials. Social perceptions about antibiotics influence their consumption. In many societies, antibiotics are perceived as quick fixes for any illness, which reinforce their demand and misuse (Capuozzo *et al.*, 2024). A lack of understanding about resistance mechanisms perpetuates behaviors that inadvertently fuel the crisis. Therefore, education and cultural change are therefore as vital as scientific discovery. These factors are interconnected within a complex web of causality. Biological evolution is influenced by human behavior, while human misuse is shaped by socioeconomic pressures. Environmental contamination provides the backdrop for the ongoing circulation of resistance. This interplay blurs the boundaries between clinical, agricultural, and ecological issues. No single intervention, whether scientific or regulatory, can succeed in isolation. An effective strategy must address the underlying network of interactions that sustain antibiotic resistance (Singer *et al.*, 2025).

CONSEQUENCES AND IMPACTS OF ANTIMICROBIAL RESISTANCE

Antimicrobial resistance (AMR) has become one of the gravest global health challenges, with repercussions extending far beyond clinical medicine. Its impacts are multifaceted, spanning healthcare systems, economies, ecosystems, and societies. As infections resistant to treatment grow in prevalence, the world faces a scenario where once manageable

diseases could again become fatal. Therefore, the consequences of AMR are not just a biomedical issue; they represent a significant threat to human development, environmental stability, and social equity (de Kraker, 2023; Figure 2).

Clinical and public health burden: The most immediate consequence of antimicrobial resistance is the increasing difficulty in treating infectious diseases. Infections that were once easily curable now require longer, more complex, and often less effective treatment regimens. Patients infected with resistant organisms experience prolonged illness, recurrent infections, and higher rates of complications. Common bacterial diseases, such as pneumonia, urinary tract infections, and sepsis, have become progressively harder to manage, especially in hospital settings. Multidrug-resistant pathogens such as *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Mycobacterium tuberculosis*, and *Neisseria gonorrhoeae* are causing global concern. These “superbugs” have developed resistance to multiple classes of antibiotics, limiting available treatment options. In extreme cases, infections become entirely untreatable. The emergence of pan-resistant strains indicates a potential collapse of modern infectious disease control (Prestinaciet al., 2015).

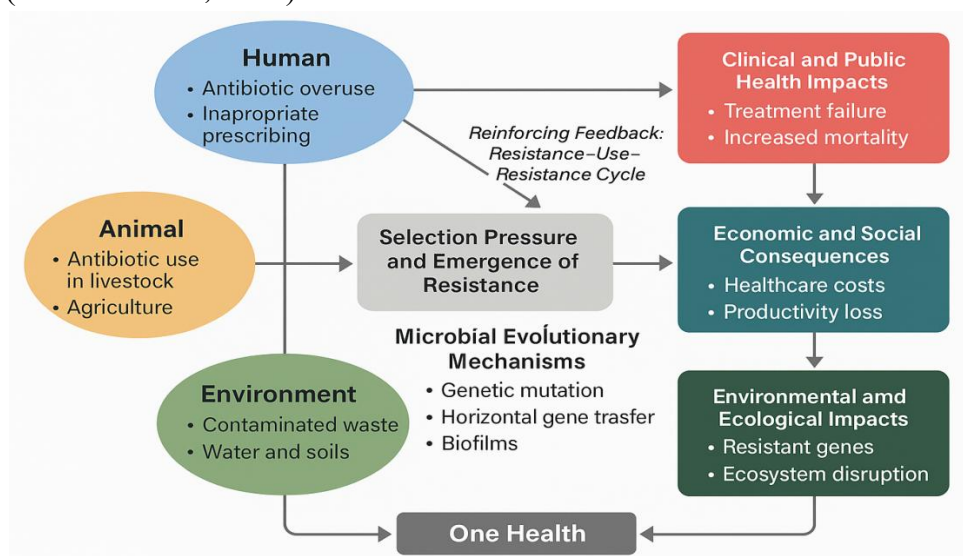


Figure 2: Conceptual framework of antimicrobial resistance drivers and consequences

Prolonged hospitalisation and healthcare strain: AMR increases the length and cost of hospital stays. Patients infected with resistant pathogens often require isolation, specialised care, and combination therapies, which strain limited healthcare resources. Hospital-acquired infections further compound the problem, as resistant bacteria can spread between patients and persist on medical surfaces. Intensive care units and post-surgical wards have become hotspots for these resistant outbreaks, leading to higher treatment costs and increased mortality rates (Dadgostar, 2019).

Impact on modern medical procedures: The success of advanced medical interventions, including organ transplants, cancer chemotherapy, and major surgeries, depends heavily on the effective use of antibiotics for prophylaxis. As antibiotic resistance diminishes this protection, even routine procedures can expose patients to severe infections. Without dependable antimicrobials, the safety of childbirth, invasive diagnostics, and wound care is compromised. The threat of untreatable infection could force healthcare systems to limit the use of life-saving technologies that have become standard practice (Dhole *et al.*, 2023).

Vulnerability of high-risk populations: Certain groups face a disproportionate burden of morbidity related to AMR. Newborns, the elderly, immunocompromised individuals, and patients with chronic diseases are particularly vulnerable. In developing countries, limited access to diagnostics and second-line medications exacerbates mortality among these populations. The spread of resistance in conditions such as neonatal sepsis, tuberculosis, and malaria indicates an alarming setback in global health achievements made over the past half-century.

Escalating healthcare costs: The financial impact of antimicrobial resistance is immense. Infections that are resistant to treatment require longer hospital stays, more expensive drugs, and additional diagnostic tests. The transition from affordable, first-line antibiotics to costly last-resort therapies significantly inflates treatment expenses for both patients and healthcare systems. In countries with out-of-pocket healthcare models, the financial burden often drives families into poverty (Oliveira *et al.*, 2024).

Loss of productivity and economic output: In addition to direct medical expenses, AMR undermines labour productivity. Prolonged illness,

disability, and premature death lead to decreased workforce participation, especially in low and middle income countries where infectious diseases remain prevalent. The agriculture and livestock sectors also suffer from reduced productivity and export losses due to resistant infections. Collectively, these impacts erode economic growth, increase inequality, and threaten food security (Naylor *et al.*, 2025).

Macroeconomic instability: At the macroeconomic level, the widespread effects of AMR can mirror those of global financial crises. If resistance continues unchecked, it could reduce global GDP, disrupt trade, and weaken healthcare-dependent industries. The financial strain on health systems diverts resources from other development priorities such as education, sanitation, and infrastructure. This creates a vicious cycle: weak health infrastructures contribute to the increase in resistance, which in turn undermines national economies (Naylor *et al.*, 2025).

Impact on pharmaceutical innovation: The economic impact extends to pharmaceutical development. As older drugs lose efficacy, the cost of developing new antimicrobials rises sharply due to scientific, regulatory, and market barriers. Unfortunately, low profitability associated with antibiotics discourages private investment in antibiotic research. This leads to an innovation gap precisely when new drugs are urgently needed; the pipeline remains nearly empty. Without economic incentives, the world faces a dwindling arsenal against evolving pathogens (Dutescu and Hillier, 2021)

Alteration of microbial ecosystems: The spread of antimicrobial agents into natural environments disrupts microbial communities that play vital roles in ecological balance. Antibiotic residues in soil and water select for resistant bacteria even in non-clinical settings. These resistant microbes, in turn, can transfer resistance genes to pathogenic species, closing the loop between environmental contamination and human infection. Soil microbiota, essential for nutrient cycling and plant health, are particularly vulnerable. The loss of microbial diversity weakens soil fertility and resilience, potentially impacting agricultural productivity. In aquatic systems, antibiotic pollution fosters resistant bacteria that can colonise fish

and aquatic plants, creating reservoirs that feed back into human food chains.

Bioaccumulation and persistence: Antibiotics and resistant bacteria can persist in sediments and aquatic organisms, leading to long-term ecological contamination. Wastewater treatment plants often fail to fully remove antibiotic residues, which leads to continuous exposure of microbial populations to sub-lethal concentrations of these drugs. This persistent low-level exposure maintains selection pressure indefinitely, ensuring that resistance remains a permanent environmental feature.

Impact on wildlife and biodiversity: Wildlife can act as carriers of antibiotic-resistant bacteria, especially species that inhabit near human settlements or that consume contaminated water and waste. Migratory birds can transport resistant genes across continents. The ecological spread blurs the line between environmental and clinical resistance, underscoring the planetary dimension of the problem. Additionally, the alteration of natural microbiomes may also influence disease dynamics in wild animal populations, leading to unknown consequences for biodiversity (Elsohaby *et al.*, 2021).

Societal and ethical dimensions: Antimicrobial resistance exacerbates existing health inequalities. Wealthier nations can afford advanced diagnostics, combination therapies, and infection control measures, while poorer countries face limited treatment options and weaker surveillance systems (Pokhare *et al.*, 2019). This disparity means that the burden of resistance falls disproportionately on those least able to respond, transforming AMR into a question of global health justice. In many developing regions, the lack of access to reliable antibiotics coexists with rampant overuse of counterfeit or substandard drugs. As a result, these communities experience both undertreatment and misuse, a paradox that perpetuates suffering and economic vulnerability. Addressing AMR without tackling these inequities would be incomplete and ethically flawed.

Public perception and behavioural barriers: AMR remains an abstract concept for much of the public. Unlike contagious epidemics with visible symptoms, resistance develops silently, and its consequences unfold gradually. This invisibility undermines public engagement and policy

urgency. Misconceptions about antibiotics, such as the belief that they cure viral infections, persist even among educated populations. Without social awareness, even the best scientific solutions risk failure (Naing *et al.*, 2021).

Global interdependence and responsibility: Resistance knows no borders; when one nation misuses antimicrobials, it can jeopardise the health of others. This reality emphasises the need for global solidarity and shared responsibility. However, achieving coordinated action remains challenging in a world of uneven resources, conflicting priorities, and political fragmentation. Therefore, ethical stewardship must extend beyond national self-interest and embrace a collective vision for our planet (Petersen *et al.*, 2023).

Implications for sustainable development: The rise of AMR poses a direct threat to global efforts toward achieving sustainable development. Several of the United Nations Sustainable Development Goals (SDGs), including those related to health, hunger, clean water, and economic growth, are undermined by resistance. Without effective antibiotics, progress in reducing maternal and child mortality, controlling infectious diseases, and ensuring food security will stall or reverse. The environmental impacts of antibiotic pollution also jeopardise goals related to ecosystem protection and clean water management. In this sense, AMR represents not just a medical emergency but a systemic development crisis. It challenges humanity's ability to sustain health, food production, and environmental stability simultaneously. Addressing it requires integrated governance that aligns health, agriculture, industry, and environmental policy under a unified sustainability framework (Jasovský *et al.*, 2016).

Global and regional perspectives on antimicrobial resistance: Antimicrobial resistance (AMR) has transcended its origins as a localised medical issue into a global crisis that requires unified international action. Resistance knows no borders; microbes and genes move freely across regions through trade, migration, and the environment. Consequently, the fight against AMR depends not only on national policies but on coordinated global governance. This section provides an overview of international

frameworks, regional dynamics, and the evolving landscape of AMR surveillance and response across different continents (Tang *et al.*, 2023).

GLOBAL ACTION PLANS AND INITIATIVES

The WHO recognised AMR as a significant threat to global health security and launched the Global Action Plan on Antimicrobial Resistance (GAP-AMR) in 2015. The plan outlines five strategic objectives:

- 1) Enhance awareness and understanding of AMR
- 2) Strengthen surveillance and research efforts
- 3) Reduce the incidence of infections through improved sanitation and hygiene
- 4) Optimise the use of antimicrobials in both human and animal health
- 5) Develop sustainable investments in countermeasures

The plan encourages countries to develop National Action Plans (NAPs) align with these objectives. By 2024, most WHO member states had either drafted or implemented such plans, however, the progress made varies widely. High-income nations tend to emphasise stewardship and research, while low- and middle-income countries face challenges in surveillance, regulation, and resource mobilization. The fight against AMR has expanded beyond the health sector. The Tripartite collaboration between the WHO, the Food and Agriculture Organization (FAO), and the World Organization for Animal Health (OIE) promotes a One Health approach, which integrates human, animal, and environmental health strategies. In 2022, the United Nations Environment Programme (UNEP) joined this coalition, forming the Quadripartite Alliance, to ensure environmental dimensions of resistance are fully addressed. This alliance coordinates global advocacy, supports surveillance programs, and guides countries in implementing risk-based AMR control measures. It also underscores that environmental stewardship, such as managing pharmaceutical waste and agricultural runoff, is inseparable from human health interventions. Established in 2020, the Global Leaders Group brings together heads of state, ministers, and scientific experts to sustain political momentum and accountability in addressing AMR. Its mission is to elevate AMR on the global development agenda, advocate for funding mechanisms,

and promote equitable access to antimicrobials and diagnostics (Elbehiry *et al.*, 2025).

International collaboration with development partners: International development organisations such as the World Bank, the Global Fund, and the United Nations Development Programme (UNDP) increasingly incorporate AMR within their health and sustainability portfolios. The World Bank estimates that uncontrolled AMR could reduce global GDP by several percentage points, highlighting its potential economic devastation. Meanwhile, global initiatives like the Fleming Fund and the AMR Multi-Partner Trust Fund support laboratory strengthening, data systems, and capacity building in low-resource settings (Wernli *et al.*, 2022).

Regional trends and responses: Although, AMR is a global issue, its manifestation and response differ significantly across regions due to differences in healthcare systems, agriculture, regulation, and economic capacity. Understanding these regional nuances is essential for tailoring effective interventions (Oliveira *et al.*, 2024).

Surveillance networks and data systems: Reliable data are the backbone of AMR control. Accurate information on resistance trends and antimicrobial consumption is crucial for policymaking (Mori *et al.*, 2025).

The Global antimicrobial resistance and use surveillance system (GLASS): WHO's GLASS initiative, launched in 2016, represents the first standardised global system for collecting and sharing AMR data. GLASS harmonises reporting from participating countries, enabling comparisons and tracking of resistance patterns worldwide. Although participation has been increasing steadily, challenges remain in ensuring data quality, representativeness, as well as integrating across human, animal, and environmental sectors (Ajulo and Awosile, 2024).

Regional and national surveillance: In addition to GLASS, many countries maintain regional systems. Europe's EARS-Net, the U.S. National Antimicrobial Resistance Monitoring System (NARMS), and Canada's CIPARS are well-established models. In Asia and Africa, newer networks are emerging, supported by the Fleming Fund and other international donors. The expansion of digital health technologies, genomic sequencing,

and data-sharing platforms is improving real-time monitoring and outbreak detection (Karpel *et al.*, 2017).

Data gaps and limitations: Despite some progress, global data on AMR remain fragmented. Many low-income countries lack the infrastructure needed for routine microbial culture or susceptibility testing. Even when data are available, they often do not represent infections at the rural or community level. Additionally, there is limited integration of veterinary and environmental data, which hinders comprehensive One Health analysis. Bridging these gaps is essential for achieving global equity and ensuring scientific accuracy (Nazir *et al.*, 2025).

Lessons from the COVID-19 pandemic: The COVID-19 pandemic has provided important insights into the interconnectedness of global health crises. It highlighted both the strengths and weaknesses of international health coordination, lessons that are directly applicable to AMR. During the pandemic, the widespread use of antibiotics in COVID-19 patients, often administered without confirmed bacterial co-infection, led to increased resistance rates in several countries. The crisis also exposed vulnerabilities in supply chains, surveillance, and public communication, which are similar to those encountered in managing AMR. However, it also accelerated innovations such as genomic surveillance, international data sharing, and investment in diagnostics—all of which can strengthen AMR control. The pandemic reinforced the importance of global solidarity, rapid response mechanisms, and transparent data sharing. Just as viruses spread globally, so do resistant bacteria and genes. The international mobilisation against COVID-19 provides a template for the coordinated, cross-sectoral action required to combat AMR, though this effort must be sustained beyond acute crisis moments (Khoo and Lantos, 2020).

POTENTIAL SOLUTIONS AND FUTURE DIRECTIONS

The growing tide of antimicrobial resistance (AMR) demands an integrated, multi-sector approach that looks to the future. Although this crisis has developed over several decades, it is not impossible to tackle. The solution involves a combination of responsible antimicrobial use, scientific innovation, improved governance, and global cooperation within a unified “One Health” framework. The next section examines the key strategies for

managing and reducing AMR, emphasising both immediate actions and long-term plans essential for sustainable control (Puri *et al.*, 2025).

Antimicrobial stewardship programs: The core principle of AMR containment is stewardship, which involves the responsible management of existing antimicrobials to maintain their effectiveness. Antimicrobial stewardship programs (ASPs) are designed to ensure that the correct drug is administered at the appropriate dose and for the right duration, only when necessary. By optimising the use of antimicrobials, these programs help minimise pressure on microbes and reduce the development of resistance (Bankar *et al.*, 2022).

Clinical stewardship initiatives: Hospitals and healthcare institutions play a pivotal role in antimicrobial stewardship programs (ASPs). Structured ASPs promote evidence-based prescribing through established protocols, formularies, and review systems. Key strategies for effective stewardship include:

1. Implementing diagnostic stewardship to confirm bacterial infections before prescribing antibiotics.
2. Conducting regular audits and providing feedback on antibiotic use patterns.
3. Restricting access to high-risk broad-spectrum antibiotics.
4. Promoting infection prevention measures, such as hand hygiene and environmental sanitation.

In high-income settings, electronic prescribing systems and decision-support tools assist physicians in adhering to guidelines. In resource-limited contexts, stewardship efforts may focus more on training healthcare workers and ensuring access to quality drugs (Tinker *et al.*, 2021).

Community and pharmacy-based interventions: Stewardship must also extend beyond hospitals. Community-level strategies, especially in outpatient clinics and pharmacies, are crucial since most antibiotics are used outside of hospital settings. Educational campaigns, pharmacist counseling, and public awareness initiatives can help reduce self-medication and over-the-counter sales of antibiotics. Empowering pharmacists to act as

gatekeepers in antibiotic dispensing has proven effective in several regions (Zerbinato *et al.*, 2025).

Behavioral and cultural change: Sustainable stewardship requires a shift in societal attitudes toward antibiotics. To reduce the common belief that every illness needs medication, we need long-term public education efforts. Incorporating awareness of antimicrobial resistance (AMR) into school curricula, mass media, and health literacy programs can foster responsible antibiotic use culture. Therefore, stewardship is as much a social movement as it is a medical initiative (Shutt *et al.*, 2025).

Novel therapeutics and technologies: Stewardship can help delay the development of resistance, but innovation is essential for keeping pace with it. The global shortage of new antimicrobials is due to both scientific challenges and economic disincentives. However, emerging technologies and unconventional approaches offer hope for a new era of strategies to combat infections. There is renewed urgency in the search for new classes of antibiotic. Advances in genomics, synthetic biology, and high-throughput screening have accelerated the identification of novel compounds. Exploring the soil microbiome and utilizing AI-assisted drug discovery are uncovering previously untapped natural and synthetic molecules. Additionally, structural modifications of existing antibiotics, such as β -lactamase inhibitors, can restore activity against resistant strains. Bacteriophages represent a promising alternative to traditional antibiotics. Phage therapy offers specificity, targeting only pathogenic bacteria without disturbing normal microbiota. With advances in genetic engineering, these phages can be tailored to bypass bacterial defense mechanisms. Clinical interest in phage therapy has resurged, especially for treating multi-resistant infections where antibiotics fail. Antimicrobial peptides (AMPs), which are naturally occurring molecules found in animals and plants, present another frontier in drug development. They disrupt microbial membranes, making it harder for resistance to develop. Additionally, host-directed therapies that enhance immune defenses, rather than targeting microbes directly, may reduce selective pressure and extend the efficacy of existing drugs (Elshobary *et al.*, 2025).

CRISPR-Cas and genetic tools: Gene-editing technologies, such as CRISPR-Cas systems, can specifically target and disable resistance genes in bacterial populations. These precision tools have the potential to restore bacterial susceptibility or prevent the horizontal transfer of resistance traits. Although still in experimental stages, CRISPR-based antimicrobials represent a significant advancement in the fight against AMR (Tao *et al.*, 2022).

Probiotics and microbiome restoration: Maintaining a healthy microbiome provides natural resistance against harmful pathogens. Probiotics and fecal microbiota transplantation have shown potential in restoring gut flora that has been disrupted by antibiotic use. By supporting microbial balance, these approaches may decrease the recurrence of infections and help control the spread of antibiotic resistance (Patangia *et al.*, 2022).

Nanotechnology and drug delivery innovations: Nanoparticle-based drug delivery systems can enhance the effectiveness of antibiotics by improving target specificity and reducing the necessary dosage. Nanomaterials with intrinsic antimicrobial properties, such as silver or graphene-based compounds, can also complement conventional therapies. These technologies connect material science and medicine, offering versatile tools to combat resistant pathogens (Parvin *et al.*, 2025).

POLICY, GOVERNANCE, AND EDUCATION

Effective containment of antimicrobial resistance (AMR) relies on strong policy frameworks that regulate the production, sale, and use of antibiotics. Governments need to establish strict licensing systems for antimicrobials, monitor sales data, and impose penalties for illegal distribution. It is equally important to strengthen drug quality control laboratories and take action against counterfeit medicines. Since resistance knows no borders, global governance mechanisms must ensure accountability and equity. International agreements similar to climate treaties, could formalize national commitments to control AMR. These frameworks should strike a balance between access to and stewardship of antibiotics, ensuring that life-saving medications remain available to everyone while preventing misuse. Additionally, governments and international donors must realign incentives

for the research and development of new antibiotics. Push mechanisms, such as grants and public–private partnerships, can help reduce research costs. On the other hand, pull incentives like market entry rewards and patent extensions can make antibiotic innovation financially viable. At the same time, separating profits from sales volume ensures that new antibiotics remain available as last-resort options rather than being marketed excessively. Education is fundamental for long-term control of AMR. It is crucial to train healthcare professionals, veterinarians, and pharmacists in responsible prescribing practices. Additionally, community education campaigns should demystify antibiotics, emphasizing that not all infections require them. Empowering local leaders, schools, and media can turn awareness into action. Policy and governance should be guided by reliable data. Investing in surveillance systems, laboratory networks, and digital reporting tools enhances evidence-based decision-making. Furthermore, data transparency builds public trust and encourages international collaboration (Rogers *et al.*, 2019).

RESEARCH AND INNOVATION FOR THE FUTURE

Artificial intelligence (AI) and machine learning hold immense potential for predicting resistance trends, designing new molecules, and guiding treatment decisions. AI-driven platforms can analyse large genomic and epidemiological datasets, providing insights into emerging threats before they spread widely. Whole-genome sequencing is transforming the tracking of resistance genes. By identifying transmission chains and evolutionary pathways, genomic tools facilitate targeted interventions. Integrating these technologies into national surveillance programs ensures the availability of real-time, actionable intelligence. No single country can address antimicrobial resistance (AMR) in isolation. International research collaborations that pool expertise, data, and funding are vital for accelerating discoveries. These collaborative platforms can standardise methodologies, prevent duplication of efforts, and ensure equitable access to innovations across different regions. However, technical solutions alone are not enough. Understanding cultural attitudes, prescribing behaviors, and public perceptions is crucial for designing interventions that resonate with people. Behavioral science can help inform communication strategies and

encourage populations to use antibiotics more responsibly (Branda and Scarpa, 2024).

Pathways to a sustainable AMR future: The path forward must combine innovation with accountability. Stewardship and surveillance provide the foundation, while research and policy provide the necessary tools. Public engagement is essential for ensuring sustainability. Future success depends on integrating these pillars into cohesive global systems that overcome disciplinary and geographic boundaries. The ultimate goal is not to eliminate microbial resistance, an impossible task, but to restore balance between humans and microorganisms. By promoting responsible use, encouraging robust innovation, and fostering shared global responsibility, humanity can safeguard the effectiveness of antimicrobials for generations to come (Aslam *et al.*, 2024).

CONCLUSION

Antimicrobial resistance (AMR) has emerged as a major challenge of modern medicine, threatening to reverse decades of progress in scientific and public health. This crisis is complex and is influenced by factors such as microbial evolution, human misuse of antibiotics, reliance on agricultural practices, and neglect of environmental concerns. The rising rates of illness, economic losses, and ecological disruption highlight the urgent need for coordinated global action. Tackling AMR requires a comprehensive One Health approach that unites stewardship, innovation, governance, and education across human, animal, and environmental sectors. The future hinges on striking a balance between preserving existing antimicrobials and pursuing new solutions through research, technology, and responsible policies. Only through global solidarity and sustained commitment can we protect the effectiveness of these life-saving drugs and ensure a resilient and sustainable future for generations to come.

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EDITOR'S PROFILE



Dr. Madhuri Vajha, Assistant Professor, Department of Biosciences and Biotechnology, University College of Arts and Science, Krishna University, Machilipatnam. She completed her Master's in Life Sciences from Hyderabad Central University, Hyderabad, her M.Phil. in Plant Biotechnology from the University of Delhi, New Delhi, and her Ph.D. (2001) in Biotechnology from Acharya Nagarjuna University, Guntur. She secured first division

with distinction at both graduation and post-graduation levels and has qualified the UGC-NET. With overall 34 years of teaching (for M.Sc. Biotechnology and Botany students) and research experience, she has also served as Head of the Department and Women Cell Coordinator at Andhra Loyola College, Vijayawada. Her major research interests include plant tissue culture, secondary metabolite production, chemical and molecular fingerprinting, and isolation and purification of phytoconstituents of medicinal plants. She has more than 30 research publications in national and international journals of repute and has authored three books. She has organized conferences and workshops sponsored by INSA and APCOST, delivered guest lectures and invited talks in various colleges and universities, and presented more than 100 papers in national and international conferences. Currently, she is working on a research project sponsored by RUSA. Every year, Dr. Madhuri supervises the project work of a minimum of six M.Sc. students as principal investigator. Her ongoing work focuses on mangrove plant collection, taxonomical identification, herbarium maintenance, sample drying, phytochemical analysis, and chromatography, particularly on *Avicennia*, *Rhizophora*, *Bruguiera*, and their species.

Dr. Kugarthi Jayalakshmi, former faculty in the Department of Biochemistry, Sri Padmavathi Mahila Viswavidyalayam, Tirupati-517502, pursued her B.Sc. (2003), B.Ed. (2005), M.Sc. (2007), and Ph.D. (2017) in Biochemistry from Sri Venkateswara University, Tirupati, securing distinction at graduation and first division in post-graduation. She was the topper in SVUCET-2005 and secured the first rank in SVU-RCET-2009. She has been engaged in teaching and research in biochemistry for the last 18 years. Biochemistry, pharmacology and toxicology, and conservation biology of medicinal plants are the key research areas of her interest. She has successfully developed protocols for several medicinal plants, viz., *Rhinacanthus nasutus*, and has effectively bioprospected to identify bioactive natural products from various medicinal species. She has published 15 research articles in reputed national and international journals, numerous book chapters, authored three books and has one editorial book to her credit.



Dr. Preeti Chaturvedi, Professor & Head, Department of Biological Sciences, G.B. Pant University of Agriculture & Technology, Pantnagar. She has completed her B.Sc. (1994), M.Sc. (1996), and Ph.D. (2001) from Kurukshetra University, all in first division with distinction at graduation and post-graduation level. She received the CSIR JRF during 1998–2000. She has been engaged in teaching and research in botany for the last 25 years. Bioprospecting, biodiversity, and conservation biology of medicinal plants and bryophytes are key research areas of her



interest. She has successfully developed micropropagation protocols for several high value medicinal plants of Himalaya viz., *Aconitum balfourii*, *Picrorrhiza kurroa*, *Polygonatum verticillatum*, *Rheum emodii* and *Arnebia benthamii*. She has biopropected Himalayan herbs and cryptogams, particularly bryophytes, to identify bioactive natural products. Dr. Preeti has more than 80 research publications in reputed national and international journals and one edited book to her credit. She has successfully completed five research projects. She has supervised twenty-three research students, including 10 Ph. D. and 13 M.Sc. scholars as principal advisor, and more than 20 as co-advisor.



Dr. Madhuri Vajha • Dr. Kugarthi Jayalakshmi • Dr. Preeti Chaturvedi

'Plants & Secondary Metabolites, Volume 11' offers a comprehensive exploration of ten lesser-known plants, unveiling their botany, phytochemistry, traditional medicinal uses, and potential pharmacological applications, making it an invaluable resource for researchers and botanists.



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