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Comparative GC–MS Profiling of Smilax Zeylanica and Argemone Mexicana: Phytochemical Characterization and Potential Antimicrobial Properties

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ABSTRACT: The increasing prevalence of antimicrobial resistance (AMR) has intensified the search for novel bioactive compounds from medicinal plants. The present study investigated the phytochemical composition of *Smilax zeylanica* L. and *Argemone mexicana* L. leaves using gas chromatography–mass spectrometry (GC–MS), with particular emphasis on metabolites associated with antimicrobial potential. Fresh leaves of both plants were collected, authenticated, shade-dried, powdered, and extracted separately using petroleum ether through Soxhlet extraction. The concentrated extracts were subjected to GC–MS analysis, and constituent identification was performed by comparing retention times, molecular masses, fragmentation patterns, and mass spectra with the Wiley and National Institute of Standards and Technology (NIST) databases. GC–MS analysis revealed a diverse array of phytoconstituents in both medicinal plants. The *S. zeylanica* extract contained 15 identified compounds, including D-limonene, ascaridole, citral, carotol, longifolene, caryophyllene, trans-geranylgeraniol, phytol, fatty acids, ar-turmerone, and squalene. The *A. mexicana* extract exhibited a broader chemical profile comprising 30 identified compounds and derivatives, including phytol, n-hexadecanoic acid, linoleic acid, α -linolenic acid, methylated fatty acids, longifolene, 2,4-di-tert-butylphenol, dodecanoic acid, tetradecanoic acid, and squalene. Several identified metabolites have previously been associated with antimicrobial, antioxidant, and anti-inflammatory activities. The findings demonstrate substantial chemical diversity in both plants and provide a basis for further pharmacological investigation. Future studies involving antimicrobial assays, compound isolation, toxicity evaluation, and mechanistic validation are necessary to establish the therapeutic significance of these phytoconstituents.

1. INTRODUCTION

Antimicrobial resistance is a very serious public health concern worldwide. The overuse and misuse of antibiotics lead to the development of antibiotic resistance in bacteria. Antimicrobial resistance may result from mutations in the microbial genome, thereby reducing the effectiveness of antibiotics against resistant pathogens. Antibiotic resistance among pathogenic microorganisms, including fungi, bacteria, and viruses, is reaching dangerously high levels worldwide. New resistance mechanisms are emerging and spreading globally, threatening our ability to treat common infectious diseases. The increasing incidence of AMR infections is making treatment more difficult; therefore, the discovery of new antimicrobial agents is a global need. Medicinal plants are well known as important sources of several life-saving drugs. A large proportion of the world's population depends on medicinal plants for the treatment of various diseases. Several medicinal plants belong to the *Papaveraceae* family, which comprises 775 species in 42 genera. *Argemone mexicana* also belongs to the *Papaveraceae* family and is commonly known as Mexican prickly poppy. It is indigenous to South America but is widely distributed in many tropical and

subtropical countries, including India. The phytoconstituents of *A. mexicana* have been reported to possess gastrointestinal, wound-healing, cytotoxic, anti-inflammatory, anti-stress, anti-allergic, fungitoxic, anticancer, and antidiabetic activities, among others (Iqbalet al., 2021; Braderet al., 2014; Moreet al., 2017).

In addition to plant metabolites, plant-associated microorganisms contribute significantly to secondary metabolite production and the medicinal properties of plants (Aly et al., 2013; Brahmachari et al., 2013; Kusari et al., 2013; Gandhi et al., 2015). Endophytes are bacterial or fungal microorganisms that live within plant tissues without causing apparent harm or damage to the host plant (Hardoim et al., 2008, 2015; Bhattacharjee et al 2010; Ludwig-Muller et al., 2014). The symbiotic relationship between plants and endophytes may range from mandatory to facultative (Lorena et al., 2021). Mandatory endophytes spend their entire life cycle within the plant, whereas obligatory or facultative endophytes can survive outside the plant. Some bacterial strains, such as *Bacillus* sp. and *Pseudomonas* sp., promote induced systemic resistance in plants against pathogens, whereas fungal endophytes inhibit pathogenic growth through the production of various secondary metabolites, including alkaloids, flavonoids, phenols, and others (Nie et al., 2017). In our previous study, a consortium of bacterial and fungal endophytes triggered induced systemic resistance in *A. mexicana* as well as in the model plant *Arabidopsis thaliana* (Singh et al., 2021). Endophytes contribute to cellular defence responses, oxidative bursts, the formation of defense-related enzymes, and the production of essential secondary metabolites in host plants (Rania et al., 2016; Ludwig-Muller, 2015; Rahman et al., 2014; Ahn et al., 2007; Wojtaszek, 1997). The study of novel metabolites and microbial strains may therefore provide valuable opportunities in various fields of agriculture and pharmacology.

Typhoid is one of the major health problems in the developing world. It spreads rapidly within populations where sanitation and access to clean water are inadequate (Wainet al., 2015). The infection can spread from the intestine through the bloodstream to the intestinal lymph nodes, liver, and spleen, where bacterial populations may increase. (Majowicz et al., 2010) reported that the morbidity and mortality associated with the disease may affect over 90 million people worldwide each year. Typhoid fever is caused by *Salmonella typhi* in humans (Mweu and English, 2008). *S. typhi* is a non-capsulated, Gram-negative, facultative anaerobic bacillus and a facultative intracellular human pathogen. Antibiotics are the primary treatment for typhoid; however, *S. typhi* has developed resistance to various antibiotics through changes in its characteristics, making typhoid fever increasingly difficult to treat (Dahiya et al., 2014; Kariuki et al., 2015). *Klebsiella pneumoniae* is an encapsulated, Gram-negative, rod-shaped, aerobic, and non-motile bacterium.

It can cause pneumonia in humans, and inadequate treatment may result in severe or chronic disease. *K. pneumoniae* commonly infects the respiratory system and can colonize the mucosal surfaces of the gastrointestinal tract and oropharynx. It may spread through respiratory droplets and contact with infected individuals. After entering the human body, it can exhibit high virulence and antimicrobial resistance (Jianget al., 2020). *K. pneumoniae* can acquire antibiotic-resistance elements responsible for the production of various β -lactamases and efflux pumps (Jiang et al., 2020). Multidrug-resistant *K. pneumoniae* may also exhibit resistance to colistin through mutational inactivation of the *mgrB* regulatory gene (Kidd et al., 2017). *Vibrio cholerae* is a Gram-negative, comma-shaped, motile, and facultatively anaerobic bacterium. *V. cholerae* causes cholera, which may lead to mild fever, vomiting, watery stools, and severe diarrhea. *V. cholerae* generally colonizes the small intestine and is a waterborne pathogen that can spread through inadequate sanitation and contaminated water. Oral rehydration therapy, intravenous fluid replacement, antibiotics, and improved hygiene are used in the management of cholera.

Poor sanitation and hygiene have historically contributed to the spread of cholera (Sharma et al., 2021). *V. cholerae* also exhibits antimicrobial resistance through mechanisms that include reduced permeability or increased active efflux of antibiotics, modification of antibiotic targets through post-transcriptional or post-translational mechanisms, and enzymatic hydrolysis or chemical modification of antibiotics (Das et al., 2020). *Escherichia coli* is a Gram-negative, rod-shaped, and facultatively anaerobic bacterium. Most *E. coli* strains are harmless; however, some pathogenic strains can cause serious disease in humans and warm-blooded animals. *E. coli* can be found in food, water, and the intestines of humans and animals. Pathogenic strains may cause dehydration, vomiting, severe diarrhea, and abdominal cramps. In the absence of appropriate treatment, severe infections may lead to complications such as anemia, severe dehydration, kidney failure, and, in some cases, death. Management may include oral or intravenous rehydration, appropriate antibiotic therapy, and the consumption of safe food and clean water.

Staphylococcus aureus is Gram-positive, round- shaped, beta-lactamase positive and facultative anaerobic bacterium. It can cause a wide variety of disease related to blood (sepsis), skin (staphylococcal scalded skin syndrome, cellulitis, impetigo, furuncles, and abscesses), respiratory system (pneumonia), heart (endocarditis), stomach (food poisoning) and bones (osteomyelitis)

(Ghalehnoo *et al.*, 2018). The emergence of MRSA (Methicillin-resistant *Staphylococcus aureus*) takes place when the native *S. aureus* strain gain MecA gene and becomes resistant to beta-lactam antibiotics. In the past years, there has been a significant use of drugs. That has led to significant evolution in bacteria.

That evolution has caused the resistance of *S. aureus* to increase drastically making its curability and deciding the line of treatment more difficult. About 180 filamentous fungal species make up the diverse genus *Aspergillus*, which is well known for producing a variety of secondary metabolites with therapeutic uses, such as anticancer and antimicrobial properties (Youssef and Singab, 2021). *Aspergillus flavus*, a saprophytic fungus, may produce metabolites with a wide range of biological activities, including antimicrobial activity against *Streptococcus gordonii*, *Bacillus subtilis*, *S. aureus*, *E. coli*, *Salmonella enteric*, *Pseudomonas aeruginosa*, *P. fluorescens* and *Candida albicans* (Dudeja *et al.*, 2021). Many antimicrobial compounds have already been reported from fungi belonging to *Aspergillus* species (Youssef and Singab, 2021). *Smilax zeylanica* L. (family Smilacaceae) is a perennial climbing plant widely distributed throughout tropical and subtropical regions of Asia and is traditionally used for the treatment of inflammatory disorders, skin ailments, fever, gastrointestinal disorders, and other diseases.

Different parts of the plant, particularly the roots and rhizomes, contain diverse secondary metabolites, including flavonoids, phenolics, saponins, tannins, alkaloids, terpenoids, steroids, and glycosides. These phytoconstituents have been associated with several pharmacological activities, including antioxidant, antimicrobial, anti-inflammatory, antidiabetic, hepatoprotective, analgesic, and wound-healing effects.

Extracts of *S. zeylanica* have demonstrated inhibitory activity against several clinically important microorganisms, including *Staphylococcus aureus*, *Escherichia coli*, *Pseudomonas aeruginosa*, and other bacterial and fungal pathogens. Its antimicrobial activity may be mediated through disruption of microbial cell membranes, alteration of cellular permeability, inhibition of essential metabolic enzymes, and interference with microbial growth and biofilm formation. The presence of multiple bioactive metabolites makes *S. zeylanica* a promising candidate for investigating novel antimicrobial agents, particularly against drug-resistant microorganisms. Further investigations are required to identify its active constituents and determine their mechanisms of action against multidrug-resistant pathogens (Hossain *et al.*, 2013).

2. MATERIALS AND METHODS

2.1 Collection and Authentication of Plant Materials

Fresh and healthy leaves of *Smilax zeylanica* L. and *Argemone mexicana* L. were collected from the local Garden. The collected plant materials were carefully examined to ensure that they were free from disease, fungal contamination, and physical damage. The leaves were separated from the plants and initially washed under running tap water to remove adhering soil and other extraneous materials, followed by rinsing with distilled water.

The cleaned leaves were blotted gently with absorbent paper and subjected to shade drying at room temperature under well-ventilated conditions, protected from direct sunlight to minimize degradation of thermolabile and photosensitive phytoconstituents. Similar shade-drying procedures have been reported for both *S. zeylanica* and *A. Mexicana* leaves (Dubey *et al.*, 2026). The identity of the collected plant materials was confirmed by a qualified taxonomist using relevant taxonomic and floristic characteristics. Representative voucher specimens of both plants were prepared, labelled, and deposited in the institutional herbarium for future reference. The authentication details were recorded as follows:

Table-1 Plant Authentication details

Plant	Family	Plant part	Authentication
<i>Smilax zeylanica</i> L.	Smilacaceae	Leaves	Authenticated by [Dr. Kunja Bihari Satapathy, Emeritus Professor, Department of Botany, Centurion University of Technology and Management, Bhubaneswar, Odisha], Voucher No. [UDPS-DT-1001]
<i>Argemone mexicana</i> L.	Papaveraceae	Leaves	Authenticated by [Dr. Kunja Bihari Satapathy, Emeritus Professor, Department of Botany, Centurion University of Technology and Management, Bhubaneswar, Odisha], Voucher No. [UDPS-DT-1002]

2.2 Preparation of Plant Material

The shade-dried leaves of *S. zeylanica* and *A. mexicana* were separately subjected to size reduction using a clean mechanical grinder. The resulting material was converted into a moderately coarse powder and passed through an appropriate sieve to obtain relatively uniform particle size. The powdered plant materials were separately collected in clean, dry, airtight containers and stored at room temperature until extraction. For the present study, 100 g of powdered leaves of each plant may be used for extraction. The quantity can be increased or decreased according to the requirements of subsequent antimicrobial and phytochemical investigations

2.3 Soxhlet Extraction with Petroleum Ether

2.3.1 *Smilax zeylanica* Leaf Extract

Approximately 100 g of powdered *Smilax zeylanica* and *Argemone Mexicana* leaves was accurately weighed and transferred into a Soxhlet extraction thimble. Approximately 500–750 mL of petroleum ether (40–60 °C or 60–80 °C, according to the grade used) was placed in the round-bottom flask of the Soxhlet apparatus. The extraction assembly was fitted securely, and continuous hot extraction was carried out under controlled heating. The solvent was allowed to evaporate, condense, and repeatedly pass through the powdered plant material. Extraction was continued until the siphoning solvent became almost colourless, indicating substantial exhaustion of extractable non-polar constituents. A Soxhlet procedure using petroleum ether for *S. zeylanica* leaves has been reported previously. After completion of extraction, the petroleum ether extract was allowed to cool and was filtered, if necessary, to remove any suspended plant particles. The solvent was subsequently removed under reduced pressure using a rotary evaporator at a controlled temperature not exceeding approximately 40–45 °C (Dubey *et al.*, 2025). The resulting concentrated extract was further dried to remove residual solvent and weighed. The dried petroleum ether extract was transferred to a clean, labelled amber-coloured container and stored at 4 °C until further phytochemical and antimicrobial investigations. The percentage yield of each petroleum ether extract was calculated using the following formula:

$$\text{Percentage yield (\%)} = \frac{\text{Weight of dried extract (g)}}{\text{Weight of powdered plant material (g)}} \times 100$$

2.4 GC-MS Analysis: The petroleum ether extract of both *S. zeylanica* and *A. mexicana* were analysed using GS-MS. The GC system (Perkin Elmer Clarus 600) accepts the Rtx-5MS capillary column with ease. Using 99.99 percent pure helium, a steady flow rate of 1.0 mL/min was attained and sustained. With an ionization energy of 70 eV (electron volt), a scan time of 0.2 seconds, a fragment spanning from 40 to 650 m/z, an injection quantity of 1 L (split ratio 10:1) and a temperature of 260 °C, the GC-MS spectral lines were found utilizing an ionization energy approach. In contrast, the column oven ran for three minutes. Retention times, peak areas, peak heights and spectral line patterns of the plant samples were compared to those of recognized chemicals in databases from the Wiley-8 library and the National Institute of Standards and Technology (NIST) library in order to identify the components (Dubey *et al.*, 2026).

3. RESULTS AND DISCUSSION

Identification of components: Identification was done using the calculated fragments, molecular mass and molecular structure. The NIST database and the Willy 8- library, which has more than 62,000 pattern entries, were used to interpret the GC-MS spectra. Together with their molecular weights and chemical structures, the components of the test materials were determined. The percentage amounts discovered in the sample were contrasted with component spectra from the Willy 8 collection and the NIST library. This was done in order to determine whether this plant species has any chemicals or a combination of them that could support its traditional and commercial therapeutic purposes. It also helps to determine the most effective methods for removing harmful compounds. The test materials' constituent parts were determined (Table 1, 2 and figures 3,4).

Table-1 Bioactive compound of *S. zeylanica*

Peak	Compound	RT (min)	Molecular formula	MW	Activity
1	D-Limonene	3.104	C ₁₀ H ₁₆	136.24	Antioxidant; antibacterial; antifungal; anti-inflammatory

2	Ascaridole	6.090	C ₁₀ H ₁₆ O ₂	168.23	Antimicrobial; anti-inflammatory
3	Citral	6.553	C ₁₀ H ₁₆ O	152.24	Antioxidant; antibacterial; antifungal; anti-inflammatory
4	Carotol	8.634	C ₁₅ H ₂₆ O	222.37	Antioxidant; antifungal; anti-inflammatory
5	Longifolene	8.914	C ₁₅ H ₂₄	204.36	Antioxidant; antimicrobial
6	Caryophyllene	9.071	C ₁₅ H ₂₄	204.36	Antioxidant; anti-inflammatory; antibacterial; antifungal
7	2,4-Di-tert-butylphenol	10.201	C ₁₄ H ₂₂ O	206.33	Antioxidant; antibacterial; antifungal
8	trans-Geranylgeraniol	10.438	C ₂₀ H ₃₄ O	290.49	Antioxidant; antimicrobial; anti-inflammatory
9	Dodecanoic acid	10.777	C ₁₂ H ₂₄ O ₂	200.32	Antibacterial; antifungal; anti-inflammatory
10	Ar-Turmerone	12.294	C ₁₅ H ₂₀ O	216.32	Antioxidant; antibacterial; antifungal; anti-inflammatory
11	Tetradecanoic acid	13.306	C ₁₄ H ₂₈ O ₂	228.37	Antibacterial; antifungal; anti-inflammatory
12	Phytol	14.330	C ₂₀ H ₄₀ O	296.54	Antioxidant; antimicrobial; anti-inflammatory
13	n-Hexadecanoic acid	15.975	C ₁₆ H ₃₂ O ₂	256.43	Antioxidant; anti-inflammatory; antibacterial
14	Octadecanoic acid	18.867	C ₁₈ H ₃₆ O ₂	284.48	Antibacterial; antifungal; anti-inflammatory
15	Squalene	28.776	C ₃₀ H ₅₀	410.73	Antioxidant; antimicrobial; anti-inflammatory

Table-2 Bioactive compound of *A. mexicana*

No.	Chemical compound	RT (min)	Molecular formula	MW (g/mol)	Activity
1	Phthalan	5.13	C ₈ H ₈ O	120	Antioxidant, antibacterial, antifungal, anti-inflammatory
2	4H-Pyran-4-one, 2,3-dihydro-3,5-dihydroxy-6-methyl-	6.39	C ₆ H ₈ O ₄	144	Antioxidant, antibacterial
3	Benzene, 1,3-bis(1,1-dimethylethyl)-	6.18	C ₁₄ H ₂₂	190	Antibacterial, antifungal
4	Pentanoic acid, 5-hydroxy-, 2,4-di-tert-butylphenyl ester	11.20	C ₁₉ H ₃₀ O ₃	306	Antifungal
5	3,7,11,15-Tetramethyl-2-hexadecen-1-ol	14.17	C ₂₀ H ₄₀ O	296	Antibacterial, antifungal
6	7,9-Di-tert-butyl-1-oxaspiro(4,5)deca-6,9-diene-2,8-dione	19.11	C ₁₇ H ₂₄ O ₃	276	Antibacterial, antifungal
7	Phenol, 2,2'-methylenebis[6-(1,1-dimethylethyl)-4-ethyl-	27.94	C ₂₅ H ₃₆ O ₂	368	Antioxidant
8	10-Nonadecanol	29.48	C ₁₉ H ₄₀ O	284	Antioxidant

9	n-Hexadecanoic acid (Palmitic acid)	12.78*	C ₁₆ H ₃₂ O ₂	256.42	Antibacterial, anti-inflammatory
10	Phytol	14.99*	C ₂₀ H ₄₀ O	296.54	Antioxidant, anti-inflammatory, antibacterial, antimicrobial
11	9,12,15-Octadecatrienoic acid (α -linolenic acid)	15.35*	C ₁₈ H ₃₀ O ₂	278.43	Antioxidant, anti-inflammatory
12	9,12-Octadecadienoic acid (linoleic acid)	15.18†	C ₁₈ H ₃₂ O ₂	280.45	Antioxidant, anti-inflammatory, antimicrobial
13	Hexadecanoic acid, methyl ester (methyl palmitate)	13.836†	C ₁₇ H ₃₄ O ₂	270.46	Antioxidant, antibacterial, anti-inflammatory
14	9-Octadecenoic acid, methyl ester (methyl oleate)	15.112†	C ₁₉ H ₃₆ O ₂	296.49	Antibacterial, anti-inflammatory
15	Stearic acid, methyl ester (methyl stearate)	15.145†	C ₁₉ H ₃₈ O ₂	298.51	Antimicrobial
16	Tetradecanoic acid, methyl ester (methyl myristate)	12.405†	C ₁₅ H ₃₀ O ₂	242.40	Antibacterial, antifungal
17	9,12,15-Octadecatrienoic acid methyl ester	14.70*	C ₁₉ H ₃₂ O ₂	292.46	Antioxidant, anti-inflammatory
18	9,12,15-Octadecatrienoic acid ethyl ester	15.39*	C ₂₀ H ₃₄ O ₂	306.49	Antioxidant, anti-inflammatory
19	Arachidonic acid, TMS derivative	8.645‡	C ₂₃ H ₄₀ O ₂ Si	376.65	Anti-inflammatory-related lipid activity
20	Dodecanoic acid, TMS derivative	9.890‡	C ₁₅ H ₃₂ O ₂ Si	272.50	Antibacterial, antifungal
21	Palmitic acid, TMS derivative	15.189‡	C ₁₉ H ₄₀ O ₂ Si	328.61	Antibacterial, anti-inflammatory
22	10-Undecenoic acid, TMS derivative	9.000‡	C ₁₄ H ₂₈ O ₂ Si	256.46	Antifungal, antibacterial
23	Longifolene	8.915§	C ₁₅ H ₂₄	204.36	Antioxidant, antimicrobial
24	2,4-Di-tert-butylphenol	10.202§	C ₁₄ H ₂₂ O	206.33	Antioxidant, antibacterial, antifungal
25	2,5-Di-tert-butyl-1,4-benzoquinone	9.671§	C ₁₄ H ₂₂ O ₂	222.33	Antioxidant, antimicrobial
26	Dodecanoic acid (Lauric acid)	10.779§	C ₁₂ H ₂₄ O ₂	200.32	Antibacterial, antifungal, anti-inflammatory
27	Tetradecanoic acid (Myristic acid)	13.317§	C ₁₄ H ₂₈ O ₂	228.37	Antibacterial, antifungal
28	Pentadecanoic acid	14.579§	C ₁₅ H ₃₀ O ₂	242.40	Anti-inflammatory, antibacterial
29	Octadecanoic acid (Stearic acid)	18.868§	C ₁₈ H ₃₆ O ₂	284.48	Antibacterial, anti-inflammatory
30	Squalene	28.779§	C ₃₀ H ₅₀	410.73	Antioxidant, anti-inflammatory

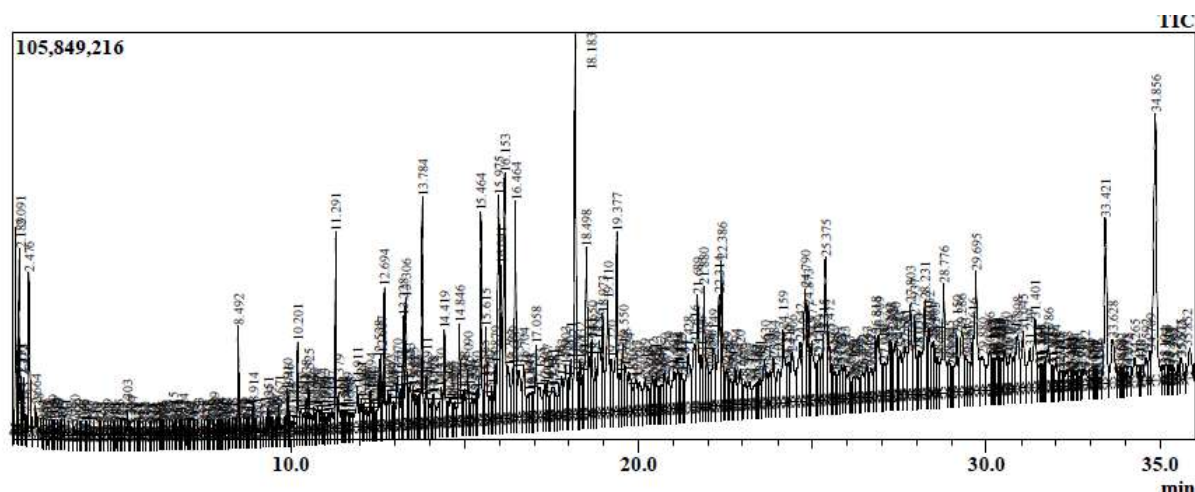


Figure 1- GC MS-Chromatogram of *Smilax zeylanica*

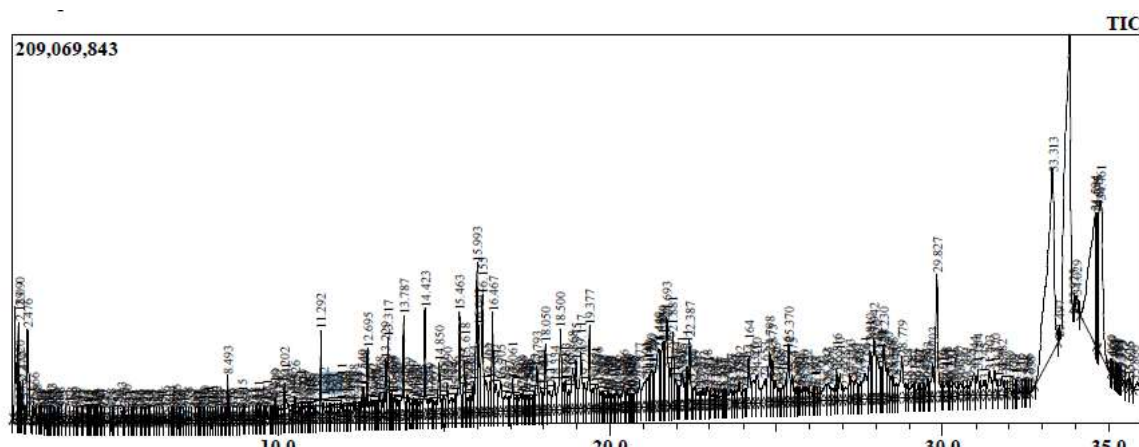


FIGURE 2- Gc Ms-Chromatogram of *Argemone Mexicana*

3.4 Discussion

The GC–MS profiling demonstrated that petroleum-ether extracts of *Smilax zeylanica* and *Argemone mexicana* contain chemically diverse terpenoids, fatty acids, esters and phenolic derivatives, supporting their potential as sources of antimicrobial phytoconstituents. In *S. zeylanica*, limonene, citral, caryophyllene, phytol, dodecanoic acid, tetradecanoic acid, n-hexadecanoic acid, octadecanoic acid and squalene were detected. *A. mexicana* showed a broader profile, including phytol, palmitic acid, linoleic acid, α -linolenic acid, methylated fatty acids, longifolene and squalene. These findings agree with the reported pharmacological potential of *S. zeylanica* and *A. mexicana* and with previous reports of antibacterial constituents from *A. mexicana* (Hossain et al., 2013; Bhattacharjee et al., 2010; More et al., 2017). The antimicrobial relevance of the present compounds is also supported by independent experimental studies. Citral has been shown to damage bacterial membranes, alter membrane potential and reduce intracellular ATP, including activity against resistant *Enterobacter* and *Staphylococcus* strains. Phytol has demonstrated antibacterial and antifungal activity and can induce oxidative stress and DNA damage in *Pseudomonas aeruginosa*. Therefore, the co-occurrence of these metabolites may contribute to the biological activity of both plants in resistant pathogens. However, GC–MS identification alone does not establish antimicrobial efficacy; purified compounds, MIC/MBC assays, synergy studies and mechanistic validation are required.

4. CONCLUSION

The present GC–MS investigation provides evidence that *S. zeylanica* and *A. mexicana* leaves contain several metabolites with reported antimicrobial, antioxidant and anti-inflammatory properties. *S. zeylanica* was characterized by monoterpenes and sesquiterpenes such as D-limonene, citral, caryophyllene and longifolene, together with fatty acids, phytol and squalene, whereas *A. mexicana* contained phytol, palmitic acid, linoleic acid, α -linolenic acid, longifolene, squalene and several fatty-acid

esters. The presence of these compounds is consistent with earlier phytochemical and pharmacological observations on both medicinal plants and strengthens the rationale for investigating them as sources of antimicrobial leads. Mechanistically, published studies indicate that compounds detected in the present extracts can act through complementary pathways, including membrane disruption, alteration of membrane potential, ATP depletion and oxidative stress. Citral, for example, has demonstrated membrane-damaging and antibiofilm effects, while phytol has shown antibacterial activity associated with oxidative stress and DNA damage. These observations support a possible multi-component effect of the extracts, although this remains a hypothesis until experimentally tested. Future work should therefore combine MIC/MBC determination, antifungal assays, biofilm testing, compound isolation, cytotoxicity evaluation and molecular studies. Such validation would clarify whether these GC–MS-identified constituents can be developed into safe and effective antimicrobial agents for antimicrobial therapy.

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AUTHOR CONTRIBUTIONS

Debashis Tripathy: Conceptualization, Investigation, Methodology, Laboratory Analysis

Sagar Kumar Mishra: Data Curation, Formal Analysis, Supervision, Writing—Review & Editing.

CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

ETHICS STATEMENT

Ethical approval was not required for this study.

DATA AVAILABILITY STATEMENT

Data supporting the findings of this study are available from the corresponding author upon reasonable request.

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