AGROTECH
ISSN: 2773-4870 **eISSN:** 2821-3106
DOI: https://doi.org/10.53797/agrotech.v7i2.2.2026

In Vitro Antifungal Evaluation and Chemical Composition of *Acacia mangium* Extracts Against Anthracnose Disease

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Received 10 June 2026; Accepted 06 July 2026; Available online 21 July 2026

Abstract: Anthracnose, caused by *Colletotrichum truncatum*, is a major disease of chilli that results in substantial yield and quality losses. This study evaluated the antifungal activity and chemical composition of *Acacia mangium* leaf and stem extracts against *C. truncatum* under *in vitro* conditions. The pathogen was isolated from symptomatic chilli fruits and identified as *C. truncatum* based on internal transcribed spacer (ITS) sequencing and phylogenetic analysis, showing 99.82% similarity to reference sequences deposited in GenBank. Ethanol extracts of *A. mangium* leaves (AMLE) and stems (AMSE) were evaluated for antifungal activities using the poisoned food technique at concentrations ranging from 50 to 500 mg/mL. Both extracts exhibited strong concentration-dependent antifungal activity, with significant differences among treatment concentrations ($p < 0.05$). Complete inhibition of pathogen mycelial growth was achieved at concentrations of 200 mg/mL and above for both extracts. At lower concentrations, AMSE exhibited slightly greater antifungal activity than AMLE, producing 76.5% and 81.0% fungal growth inhibition at 50 and 100 mg/mL, respectively, while AMLE inhibited fungal growth by 73.0% at 50 mg/mL. In contrast, benomyl (positive control) produced only 30.0% fungal growth inhibition under the experimental conditions tested. Gas chromatography-mass spectrometry (GC-MS) analysis identified 25 compounds in AMLE and 35 compounds in AMSE. AMLE was dominated by squalene, α-tocopherol and lupenone, whereas AMSE was characterized primarily by oleic acid, linoleic acid, butyl linolenate and glycidyl oleate. The distinct phytochemical profiles of the two extracts suggest that different classes of bioactive metabolites may contribute to their antifungal activity. Overall, the results demonstrate that *A. mangium* possesses promising potential as a source of natural antifungal compounds and provide a scientific basis for the development of plant-based biofungicides as environmentally friendly alternatives for the sustainable management of chilli anthracnose.

Keywords: *Acacia mangium*, *Colletotrichum truncatum*, antifungal activity, crude extracts, GC–MS

1. Introduction

Chilli (*Capsicum annuum* L.) is one of the most widely cultivated vegetable crops worldwide and is valued for its economic, nutritional, and culinary significance. Global chilli production exceeded 36 million tonnes in 2023, with Asia accounting for the largest share, particularly in countries such as China, India, Indonesia, and Thailand (Food and Agriculture Organization of the United Nations., 2024). In Malaysia, chilli is an economically important crop; however, domestic production remains insufficient to meet consumer demand, resulting in substantial annual imports. Despite its economic value, chilli cultivation is severely constrained by anthracnose disease, one of the most destructive fungal diseases affecting both field-grown and postharvest fruits. Under favourable environmental conditions, anthracnose can cause substantial yield and postharvest losses, severely reducing fruit quality, marketability, and shelf life, particularly in tropical and subtropical regions where disease development is favoured (Dowling et al., 2020). The disease is primarily caused by species of the genus *Colletotrichum*, including *Colletotrichum truncatum*, which produces characteristic sunken necrotic lesions on infected fruits and contributes significantly to economic losses throughout the chilli production chain (Saxena et al., 2016).

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Anthracnose management is particularly challenging because *Colletotrichum* species can infect chilli fruits at different developmental stages and may remain latent until fruit ripening, making early detection and effective control difficult (Saxena et al., 2016; Dowling et al., 2020). In addition, the pathogen exhibits considerable genetic diversity and adaptability, which can influence its virulence, host range, and response to disease management strategies (Talhinhas & Baroncelli, 2023). The warm and humid conditions prevalent in many chilli-growing regions further favour disease development and dissemination, increasing the risk of severe outbreaks (Dowling et al., 2020). Consequently, there is growing interest in the development of integrated and environmentally sustainable disease management approaches. Among these, plant-derived bioactive compounds have attracted considerable attention due to their biodegradability, low environmental impact, and potential to reduce dependency on synthetic fungicides while providing effective protection against phytopathogenic fungi (Usman et al., 2026).

Plant extracts contain diverse secondary metabolites, including terpenoids, phenolics, flavonoids, alkaloids, and fatty acids, which have demonstrated antimicrobial activity against a wide range of phytopathogenic fungi (Jiang et al., 2023). These compounds may inhibit fungal growth through disruption of cell membrane integrity, interference with cellular metabolism, and suppression of spore germination and mycelial development (Leiva-Mora et al., 2025). As a result, botanical extracts are increasingly being investigated as sustainable tools for crop protection and disease management (Isman, 2020).

Acacia mangium Willd. (Fabaceae) is a fast-growing tropical tree species widely cultivated for timber production, reforestation, and land rehabilitation programmes throughout Southeast Asia. Despite its economic importance, *A. mangium* has exhibited invasive characteristics in certain ecosystems due to its rapid growth, adaptability to poor soils, and ability to establish dense stands that suppress native vegetation. As invasive alien species pose ecological and economic challenges, sustainable utilization strategies have been proposed to transform invasive biomass into value-added products while contributing to their management (IPBES, 2023). Previous studies have reported that *A. mangium* and *A. mangium*-derived products contain phenolic compounds, flavonoids, terpenoids, and fatty acids associated with antioxidant and antibacterial activities, highlighting their potential as sources of natural bioactive compounds (Maroof et al., 2023; Pereira et al., 2022). Therefore, the valorization of *A. mangium* biomass as a source of bioactive compounds may simultaneously support invasive species management and the development of environmentally friendly disease control alternatives. Nevertheless, information regarding the antifungal activity and chemical composition of *A. mangium* leaf extracts against *C. truncatum* remains limited.

Identification of antifungal constituents is important for elucidating their potential role in plant disease management. Phytochemical profiling provides valuable information on the compounds present in plant extracts and their possible biological functions. Gas chromatography–mass spectrometry (GC–MS) is commonly employed for the separation, detection, and characterization of volatile and semi-volatile compounds in complex plant matrices. Accordingly, this study was undertaken to assess the *in vitro* antifungal effects of ethanol extracts obtained from *A. mangium* against *C. truncatum* and to characterise their chemical constituents using GC–MS. The information generated may support the development of plant-based fungicidal products as environmentally sustainable alternatives for the control of chilli anthracnose.

2. Material and methods

2.1 Isolation and Identification of *Colletotrichum truncatum*

Diseased chilli fruits exhibiting characteristic anthracnose lesions were used as the source of fungal isolates. Tissue fragments measuring approximately 5 × 5 mm were excised from the advancing margin of symptomatic and asymptomatic tissues. Surface disinfection was carried out by sequential treatment with 70% ethanol for 30 s and 1% sodium hypochlorite for 1 min, followed by three rinses with sterile distilled water. The disinfected tissues were dried under aseptic conditions on sterile filter paper before being transferred onto potato dextrose agar (PDA) plate. Cultures were incubated at 25 ± 2°C for 5–7 days to allow fungal growth. Hyphal tips from emerging colonies were subsequently subcultured onto fresh PDA plates to establish pure cultures for further characterization.

Fungal pathogen species identification was confirmed using molecular techniques targeting the internal transcribed spacer (ITS) region of ribosomal DNA. PCR amplification was performed with universal fungal ITS primers, and the resulting amplicons (approximately 550 bp) were visualized on 1% agarose gel to verify successful amplification. Purified PCR products were submitted for commercial sequencing, after which forward and reverse reads were assembled to generate a consensus sequence. Species identity was determined by comparing the consensus sequence with reference sequences deposited in the National Center for Biotechnology Information (NCBI) database using the BLASTn algorithm.

2.2 Collection and Authentication of Plant Material

Fresh leaves and stems of *Acacia mangium* Willd. were collected from Selangor, Malaysia. Plant identification and authentication were carried out by a qualified taxonomist at Universiti Putra Malaysia (UPM). A voucher specimen (MFI 0104/19) was deposited in the Herbarium, Institute of Bioscience, Universiti Putra Malaysia, for future reference.

2.3 Preparation of *Acacia mangium* Crude Extracts

Leaves and stems of *A. mangium* were thoroughly cleaned with running tap water followed by distilled water to eliminate surface impurities. The plant materials were then air-dried at ambient temperature until a constant weight was obtained before being separately pulverized into fine powder using a laboratory grinder. For extraction, 100 g of each powdered sample was immersed in ethanol at a plant material-to-solvent ratio of 1:10 (w/v) and left at room temperature for 48 h with intermittent shaking. Following extraction, the mixtures were filtered through Whatman No. 1 filter paper, and the resulting filtrates were concentrated under reduced pressure using an EYELA N-1300 rotary evaporator (Tokyo Rikakikai Co., Ltd., Japan) maintained at 40–45°C. The concentrated extracts were further dried to obtain crude extracts and stored at 4°C until required for subsequent analyses. The crude extracts derived from leaves and stems were designated as *A. mangium* leaf extract (AMLE) and *A. mangium* stem extract (AMSE), respectively.

2.4 *In Vitro* Antifungal Assay

The antifungal efficacy of *A. mangium* leaf extract (AMLE) and stem extract (AMSE) against *C. truncatum* was assessed using the poisoned food method. Different concentrations of each crude extract were prepared by incorporating the appropriate amount of extract into molten potato dextrose agar (PDA) to achieve final concentrations of 50, 100, 200, 300, 400, and 500 mg mL^{-1}. PDA without extract was included as the negative control, whereas benomyl served as the positive control. Approximately 15 mL of the amended medium was dispensed into sterile 9-cm Petri dishes and allowed to solidify. A mycelial disc (5 mm in diameter) excised from the actively growing edge of a pure *C. truncatum* culture was then placed at the centre of each plate. The inoculated plates were maintained at room temperature, and colony growth was monitored by measuring the radial expansion of the fungus until the control colonies completely covered the Petri dishes. Each treatment was arranged with four replicates, comprising six plates per replicate. Antifungal activity was expressed as the percentage inhibition of radial growth (PIRG), calculated according to the following equation:

$$\text{PIRG (\%)} = [(C - T) / C] \times 100$$

where C is the radial growth of the fungal colony in the untreated control, and T is the radial growth recorded in the extract-amended medium.

2.5 Gas Chromatography–Mass Spectrometry (GC–MS) Analysis

Chemical profiling of *Acacia mangium* leaf extract (AMLE) and stem extract (AMSE) was performed using a Shimadzu GCMS-QP2010 Ultra (Shimadzu Corporation, Kyoto, Japan). Separation of analytes was achieved on an SLB-5ms fused silica capillary column (30.0 m × 0.25 mm i.d.; film thickness 0.25 μm), with helium serving as the carrier gas at a constant flow rate of 0.80 mL min^{-1}. Aliquots of the extracts were injected using a split ratio of 10:1, while the injector temperature was maintained at 250°C. The chromatographic run commenced at 50°C and the oven temperature was subsequently increased to 300°C at a programmed rate of 3°C min^{-1}. Upon reaching the final temperature, the system was held isothermally for 10 min. The interface and ion source temperatures were fixed at 250°C and 200°C, respectively. Mass spectra were recorded over a scanning range of m/z 40–700 with an event time of 0.10 s and a scan speed of 1000. Putative identification of the detected compounds was accomplished by matching the acquired spectra with entries contained in the National Institute of Standards and Technology (NIST) library available within the instrument software. The abundance of each compound was estimated from its chromatographic peak area and reported as a percentage of the total ion chromatogram.

2.6 Statistical Analysis

A completely randomized design (CRD) was employed, with each treatment represented by four independent replicates consisting of six petri dishes each. The percentage inhibition of radial growth (PIRG) data were subjected to analysis of variance (ANOVA) to assess the effects of the treatments. Differences among treatment means were further examined using the Least Significant Difference (LSD) procedure when the ANOVA indicated statistical significance. Statistical significance was declared at $P < 0.05$. All analyses were performed using SAS statistical software version 9.4 (SAS Institute Inc., Cary, NC, USA).

3. Results

3.1 Molecular identification of the anthracnose disease pathogen

ITS-based molecular identification confirmed the anthracnose disease pathogen isolate as *Colletotrichum truncatum* (Figure 1). Amplification of the ITS region successfully produced a PCR amplicon of approximately 553 bp. BLASTn analysis of the ITS sequence revealed 99.82% similarity with *C. truncatum* sequences deposited in GenBank. Phylogenetic analysis further supported this identification, as the isolate clustered together with reference *C. truncatum* strains. These results confirmed that the anthracnose pathogen used in this study was *C. truncatum*.

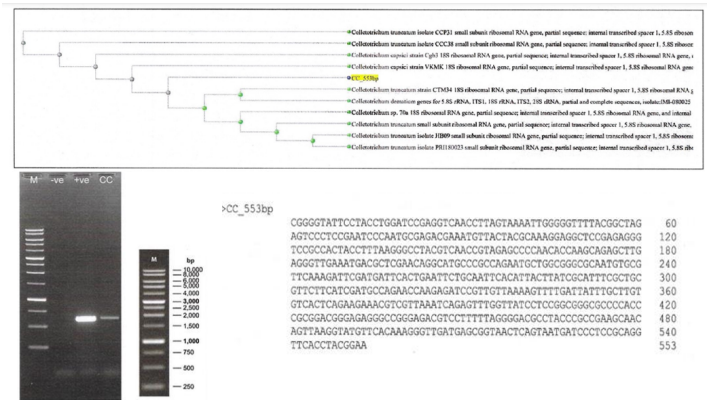

Fig. 1: Molecular identification of the anthracnose pathogen as *Colletotrichum truncatum* based on ITS sequencing, PCR amplification, and phylogenetic analysis.

3.2 Antifungal activity of *Acacia mangium* extracts

The antifungal activity of *Acacia mangium* leaf extract (AMLE) and stem extract (AMSE) against *Colletotrichum truncatum* was evaluated using the poisoned food technique at concentrations ranging from 50 to 500 mg/mL. Both extracts exhibited concentration-dependent antifungal activity, whereby higher extract concentrations resulted in greater inhibition of fungal mycelial growth. Complete inhibition of mycelial growth was observed for both AMLE and AMSE at concentrations of 200, 300, 400, and 500 mg/mL, with 100% percentage inhibition of radial growth (PIRG) (Figure 2). At the lowest concentration tested, AMLE and AMSE inhibited mycelial growth by 73.0% and 76.5%, respectively. AMSE showed slightly higher antifungal activity than AMLE at lower concentrations, with 76.5% inhibition at 50 mg/mL and 81.0% inhibition at 100 mg/mL. In comparison, the positive control, benomyl, exhibited only 30.0% inhibition, while no inhibition was observed in the negative control. These findings indicate that both leaf and stem extracts of *A. mangium* possess strong antifungal activity against *C. truncatum*. The complete inhibition observed at concentrations of 200 mg/mL and above suggests that the extracts contain bioactive constituents capable of suppressing the growth of the anthracnose pathogen, as shown by the absence of visible mycelial growth in treated plates (Figure 3).

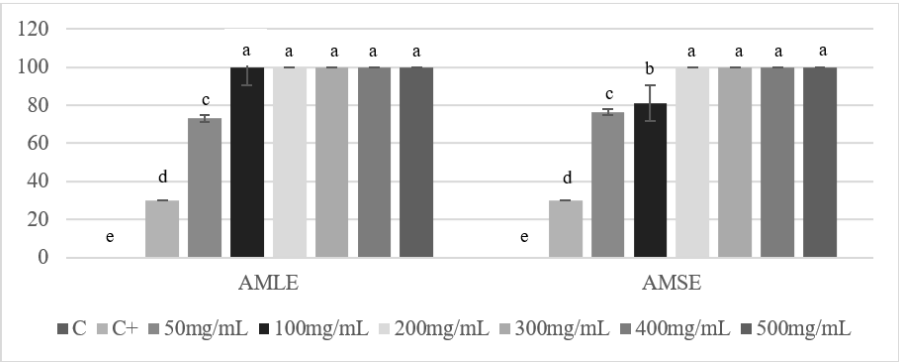

Fig. 2: Antifungal activity of *Acacia mangium* leaf extract (AMLE) and stem extract (AMSE) against *Colletotrichum truncatum*, expressed as percentage inhibition of radial growth (PIRG) after 8 days of incubation. Means followed by the same letter are not significantly different according to the LSD test at $P < 0.05$.

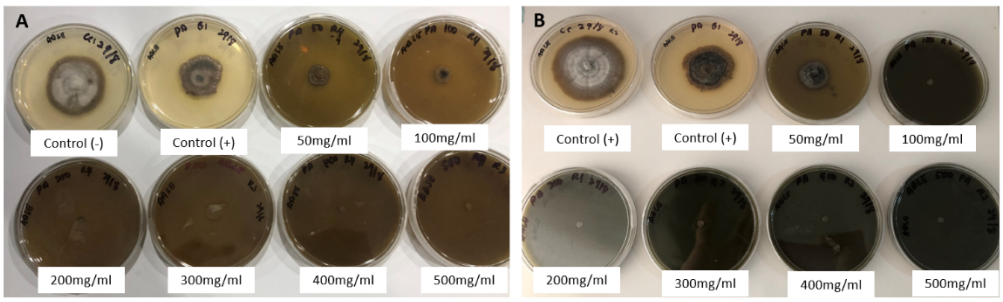

Fig. 3: Effect of *Acacia mangium* stem extract (AMSE) (A) and leaf extract (AMLE) (B) on the mycelial growth of *Colletotrichum truncatum* in poisoned PDA medium after 8 days of incubation.

3.3 GC-MS analysis of *Acacia mangium* leaf and stem extracts

GC-MS chromatograms of the ethanol leaf and stem extracts of *A. mangium* are presented in Figure 4, while the identified compounds and their relative abundances are summarised in Tables 1 and 2. GC-MS analysis of the ethanol leaf extract of *A. mangium* detected 25 compounds with varying relative peak areas (Table 1). Squalene was the most abundant compound, accounting for 28.16% of the total peak area, followed by α-tocopherol (20.08%), lupenone (12.22%), resorcinol (5.41%), octadecadienol (3.75%), tetratriacontane (3.16%), lupeol (2.32%), γ-tocopherol (2.30%), stigmasterol (2.29%), phytol (2.09%), and diacetone alcohol (2.09%). The extract was mainly composed of terpenoids, tocopherols, sterols, fatty alcohols, and hydrocarbon derivatives.

GC-MS analysis of the ethanol stem extract of *A. mangium* identified 35 compounds (Table 2). The major constituents were octadec-9-enoic acid (oleic acid) (28.79%) and octadecadienoic acid (linoleic acid) (24.30%), followed by butyl linolenate (6.11%), cis-9-hexadecenal (6.01%), glycidyl oleate (5.55%), and inositol (4.51%). Other compounds detected at lower concentrations included methyl 6,9-octadecadienoate (2.99%), ethanol, 2-(9,12-octadecadienyloxy)- (2.37%), oleoyl chloride (2.19%), ergosta-7,22-dien-3-ol (1.69%), glycidyl palmitate (1.68%), diepoxy tricyclotriacontane (1.40%), cholest-7-en-3-ol (1.03%), lupenone (1.03%), and palmitoyl chloride (1.05%). Overall, the stem extract was predominantly composed of fatty acids and their derivatives, together with sterol and triterpenoid compounds.

The GC–MS profiles revealed distinct chemical compositions between the leaf and stem extracts. While the leaf extract was characterized by high levels of terpenoids, tocopherols and sterols, the stem extract was dominated by fatty acids and fatty acid derivatives, particularly oleic acid and linoleic acid.

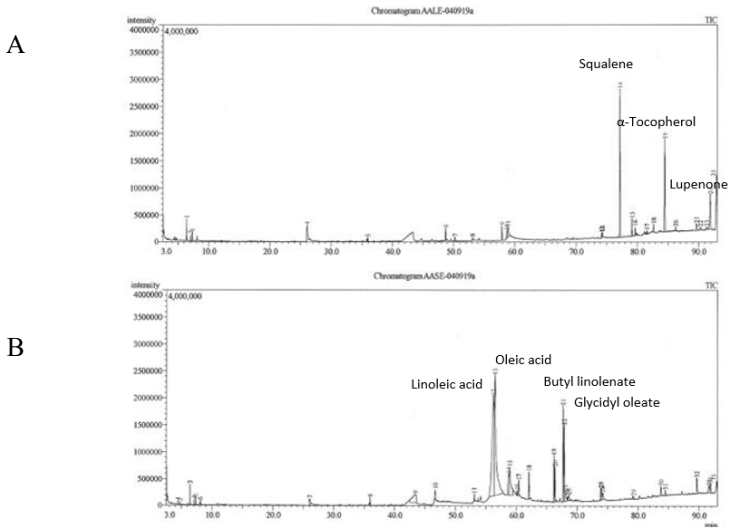

Fig. 4: GC–MS chromatograms of ethanol extracts of Acacia mangium: (A) leaf extract (AMLE) and (B) stem extract (AMSE). Major phytochemical constituents identified in each extract are indicated at their corresponding retention times.

Table 1: Chemical composition of ethanol leaf extract of *Acacia mangium* (AMLE) by GC–MS analysis.

Peak No.	Retention Time (min)	Compound Identified	Peak Area (%)
1	6.38	Diacetone alcohol	2.09
2	7.04	Ethylbenzene	0.65
3	7.32	1,4-Dimethylbenzene	1.21
4	26.04	Resorcinol	5.41
5	35.95	Phenol	0.71
6	48.69	Phytol	2.09
7	50.21	Neophytadiene	0.66
8	53.06	n-Hexadecanoic acid	0.63
9	57.88	Phytol	2.44
10	58.69	9,12-Octadecadien-1-ol	2.12
11	58.85	Octadecadienol	3.75
12	74.19	*not identified*	0.79
13	74.31	9-Octadecenoic acid	1.64
14	77.16	Squalene	28.16
15	79.12	Tetrapentacontane	3.16
16	79.63	Solanesol	1.58
17	81.62	Diepoxy tricyclotriacontane	1.00
18	82.70	γ-Tocopherol	2.30
19	84.49	α-Tocopherol	20.08
20	86.26	Octacosyl acetate	0.91
21	89.66	Stigmasterol	2.29
22	90.28	Methyl commate	0.89
23	91.28	α-Amyrin	0.87
24	91.89	Lupenone	12.22
25	92.92	Lupeol	2.32

Table 2: Chemical composition of ethanol stem extract of *Acacia mangium* (AMSE) by GC–MS analysis.

Peak No.	Retention Time (min)	Compound Identified	Peak Area (%)
1	4.4263	Methoxymethyl trimethyl dioxolane	0.08
2	4.7602	Toluene	0.06
3	6.4018	Diacetone alcohol	0.62
4	7.0522	Ethylbenzene	0.18
5	7.3230	1,4-Dimethylbenzene	0.34
6	8.0798	1,4-Dimethylbenzene	0.15
7	26.0260	Resorcinol	0.69
8	35.9492	Phenol	0.40
9	43.3950	Inositol	4.51
10	46.6672	Hexadecenoic acid	0.66
11	53.0968	Hexadecenoic acid	0.39
12	56.2397	Octadecadienoic acid (Linoleic acid)	24.30
13	56.5135	Octadec-9-enoic acid (Oleic acid)	28.79
14	58.7342	Ethanol, 2-(9,12-octadecadienyloxy)-	2.37
15	58.8907	cis-9-Hexadecenal	6.01
16	60.1050	Linoleoyl chloride	0.37
17	60.3855	Palmitoyl chloride	1.05
18	62.0768	Glycidyl palmitate	1.68
19	66.1860	Methyl 6,9-octadecadienoate	2.99
20	66.3695	Oleoyl chloride	2.19
21	67.6937	Butyl linolenate	6.11
22	67.8625	Glycidyl oleate	5.55
23	68.0917	Diepoxy tricyclotriacontane	1.40
24	68.4125	7,10-Hexadecadienal	0.29
25	68.6368	Glycidyl palmitate	0.51
26	73.8640	α-Glyceryl linoleate	0.84
27	73.9732	Oleic anhydride	0.85
28	74.1775	Butyl 9,12-octadecadienoate	0.99
29	79.2227	1-Heptacosanol	0.32
30	83.7702	Stigmast-5-en-3-ol	0.77
31	84.4787	α-Tocopherol	0.36
32	89.6560	Ergosta-7,22-dien-3-ol	1.69
33	91.6160	Cholest-7-en-3-ol	1.03
34	91.8818	Lupenone	1.03
35	92.8870	Lupeol acetate	0.43

4.0 Discussion

The present study demonstrated that ethanol extracts of *A. mangium* leaves and stems possess strong antifungal activity against *C. truncatum*, the causal agent of chilli anthracnose. Accurate identification of the pathogen is essential for evaluating the efficacy of potential antifungal agents, as different *Colletotrichum* species may vary in their pathogenicity, host range and responses to antifungal compounds. In this study, ITS sequencing and phylogenetic analysis confirmed the identity of the fungal isolate as *C. truncatum*, providing a reliable basis for subsequent antifungal evaluation. Molecular approaches have become important tools for species-level identification of anthracnose pathogens, particularly within the *Colletotrichum* species complex where morphological characteristics alone are often insufficient for accurate discrimination (Damm et al., 2012; Talhinhas & Baroncelli, 2021).

Both *A. mangium* leaf extract (AMLE) and stem extract (AMSE) significantly inhibited the mycelial growth of *C. truncatum* in a concentration-dependent manner, with complete inhibition observed at concentrations of 200 mg/mL and above. Similar dose-dependent antifungal responses have been reported for various plant-derived extracts, where increasing extract concentrations generally enhance fungal growth suppression due to the greater availability of bioactive compounds (Jiang et al., 2023). The complete inhibition observed in the present study indicates that the extracts contained sufficient concentrations of antifungal metabolites capable of effectively suppressing fungal growth.

Although both extracts exhibited strong antifungal activity, AMSE showed slightly greater inhibition than AMLE at lower concentrations. Such differences are likely associated with variations in phytochemical composition between plant organs. Secondary metabolites are often distributed unevenly within plant tissues, reflecting their distinct physiological and ecological functions (Wink, 2010). Consequently, differences in the abundance and composition of bioactive compounds between leaves and stems may influence their antifungal efficacy.

GC-MS analysis revealed distinct phytochemical profiles between the leaf and stem extracts. The leaf extract was characterized primarily by terpenoids, tocopherols and triterpenoids, whereas the stem extract was dominated by fatty acids and their derivatives. These compositional differences suggest that different groups of metabolites may contribute to the antifungal activity observed in each extract, despite producing comparable levels of fungal growth inhibition. The antifungal activity observed in this study may be attributed to the combined effects of several bioactive compounds identified in the extracts. Major constituents of the leaf extract included squalene, α-tocopherol, lupenone and lupeol, while oleic acid, linoleic acid and butyl linolenate were among the predominant compounds detected in the stem extract. Fatty acids such as oleic and linoleic acids have been reported to inhibit fungal growth through disruption of cell membrane integrity and permeability, leading to leakage of intracellular components and impairment of essential cellular processes (Desbois & Smith, 2010). Similarly, terpenoids and triterpenoids, including squalene, lupeol and lupenone, have been associated with antimicrobial activities through membrane disruption and interference with metabolic pathways (Dzubak et al., 2006). Phenolic compounds such as resorcinol may further contribute to antifungal activity through inhibition of fungal enzymes and induction of oxidative stress (Borges et al., 2015). The strong inhibitory activity observed in both AMLE and AMSE is therefore likely the result of synergistic interactions among multiple phytochemical constituents rather than the action of a single compound.

Plant-derived secondary metabolites have received considerable attention as environmentally friendly alternatives to synthetic fungicides because of their broad-spectrum antimicrobial activities and lower environmental impact (Isman, 2020; Jiang et al., 2023). Interestingly, despite being dominated by different classes of compounds, both *A. mangium* extracts achieved complete inhibition of *C. truncatum* at concentrations of 200 mg/mL and above. The slightly superior performance of AMSE at lower concentrations may indicate an important contribution of fatty acid-rich constituents to the observed antifungal activity. Nevertheless, further studies involving bioassay-guided fractionation, compound isolation and mechanistic investigations are required to identify the specific metabolites responsible for fungal growth inhibition.

In addition to its bioactive potential, *A. mangium* is a fast-growing plantation species widely cultivated throughout tropical regions for timber production, pulp and paper industries, land rehabilitation and agroforestry systems (Krisnawati et al., 2011; Hegde et al., 2013; Koutika & Richardson, 2019). The present findings suggest that, beyond its established economic importance, *A. mangium* may represent a valuable source of natural antifungal compounds for sustainable disease management. Under the experimental conditions employed in this study, both extracts exhibited greater inhibition of *C. truncatum* than benomyl, highlighting their potential as alternative or complementary biofungicidal agents. Further greenhouse and field evaluations are required to validate their practical application for chilli anthracnose management.

5. Conclusion

The present findings indicate that *A. mangium* possesses considerable potential as a source of natural antifungal compounds against *C. truncatum*, a major pathogen responsible for chilli anthracnose. Identification of the fungal isolate through ITS sequence analysis and phylogenetic assessment verified its taxonomic placement as *C. truncatum*. Both leaf and stem ethanol extracts effectively suppressed mycelial development, with complete growth inhibition achieved at concentrations of 200 mg mL^{-1} and higher. Although both extracts displayed strong antifungal properties, the stem extract exhibited slightly greater inhibitory activity at lower concentrations. Chemical profiling by GC–MS demonstrated marked differences in the composition of the two extracts. The leaf extract contained predominantly terpenoid-, tocopherol-, and triterpenoid-related compounds, whereas fatty acids and their derivatives were the principal constituents of the stem extract. The antifungal effects observed are likely associated with the collective action of these phytochemical constituents. Taken together, the results suggest that *A. mangium* extracts may serve as a sustainable alternative for the development of plant-based antifungal products. Additional investigations focusing on the isolation of active compounds, elucidation of their modes of action, and validation under greenhouse and field conditions are necessary to support their practical application in anthracnose management.

Acknowledgement

The authors would like to express their sincere gratitude to the Malaysian Agricultural Research and Development Institute (MARDI) and Universiti Pendidikan Sultan Idris (UPSI) for providing the facilities, technical support, and research resources that made this study possible. The authors also thank all individuals who contributed directly or indirectly to the successful completion of this research.

Conflict of Interest
The authors declare no conflicts of interest.

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