



RESEARCH ARTICLE

Investigation of oleaginous plant-associated fungi from oil-producing plants: Molecular identification and gas chromatography-mass spectrometry (GC-MS) profiling

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Abstract

The study evaluated endophytic communities associated with five oil-bearing plants, including sesame, corn, sunflower, olives and castor, which were collected from Baghdad and Diyala (Iraq), evaluated their oil production capacity and identified metabolites from the lipid fraction. Out of 151 isolates were collected from 21 taxa. *Aspergillus niger* showed the highest frequency (6.62 %), while the genera *Aspergillus* and *Fusarium* were the most dominant endophytes. The highest oil yield was identified and recorded in *Aspergillus terreus* (24.12 %). While the lowest oil yield was observed in *Sclerotinia* spp. (3.96 %). Gas chromatography-mass spectrometry (GC-MS) analysis of *A. terreus* revealed a profile dominated by pentadecyl acrylate (21.0 %) and ethyl palmitate (20.01 %), with methyl stearate as the minor component (1.37 %). These results highlight biodiesel raw material and pharmacist-relevant metabolites, such as sources of metabolites.

Keywords: endophyte diversity; fungal metabolites; lipid accumulation; microbial lipids

Introduction

Endophytic fungi, which reside asymptotically within plant tissues, have gained considerable attention as a rich source of biologically active compounds with diverse applications in medicine, agriculture and industry. These microorganisms produce a wide range of primary and secondary metabolites, including enzymes, lipids and bioactive molecules with antimicrobial, antioxidant and anti-inflammatory properties. Their metabolic versatility and ecological adaptability make them promising candidates for sustainable biotechnological applications (1,2).

In recent years, increasing attention has been directed toward oleaginous fungi that accumulate substantial amounts of intracellular lipids, often exceeding 20 % of their dry biomass. Compared to conventional plant-based oils, microbial lipids offer advantages such as rapid growth, independence from agricultural land and the ability to utilise low-cost substrates (2,3)

Furthermore, there is limited information regarding the diversity and functional potential of oleaginous endophytic fungi associated with oil-bearing plants in arid and semi-arid regions, including Iraq. The integration of fungal diversity analysis with lipid quantification and chemical profiling techniques such as gas chromatography-mass spectrometry (GC-MS) remains insufficiently explored in this context (4).

Therefore, the present study aims to (i) isolate endophytic fungi from selected oil-producing plants, (ii) evaluate their lipid production potential, (iii) perform molecular identification of high-yielding isolates and (iv) characterise their chemical profiles using GC-MS analysis. This integrated approach is expected to provide insights into the biotechnological potential of oleaginous endophytic fungi as sustainable sources of microbial lipids and bioactive compounds.

Materials and Methods

Sample isolation

Fresh plant materials were collected between October and December 2024 from castor (*Ricinus communis* L.), maize (*Zea mays* L.) and sesame (*Sesamum indicum* L.) in Diyala Governorate and from sunflower (*Helianthus annuus* L.) and olive (*Olea europaea* L.) in Baghdad Governorate. Sampling sites included Al-Sha'la farms (Baghdad; 33.3128° N, 44.3615° E) and Mazid farms near Miqdadiyah (Diyala; 33.9664° N, 44.9161° E), as shown in Fig. 1. All samples were transported to the laboratory and processed within 24 hr. Plant segments were washed, surface-sterilised with 70 % ethanol (10 sec), rinsed with sterile distilled water, cut into 0.5–1 cm pieces and inoculated onto potato dextrose agar (PDA) medium supplemented with rose Bengal and antibiotics. Plates were incubated at 28 ± 2 °C for 7–10 days until fungal growth appeared, then sub-cultured.

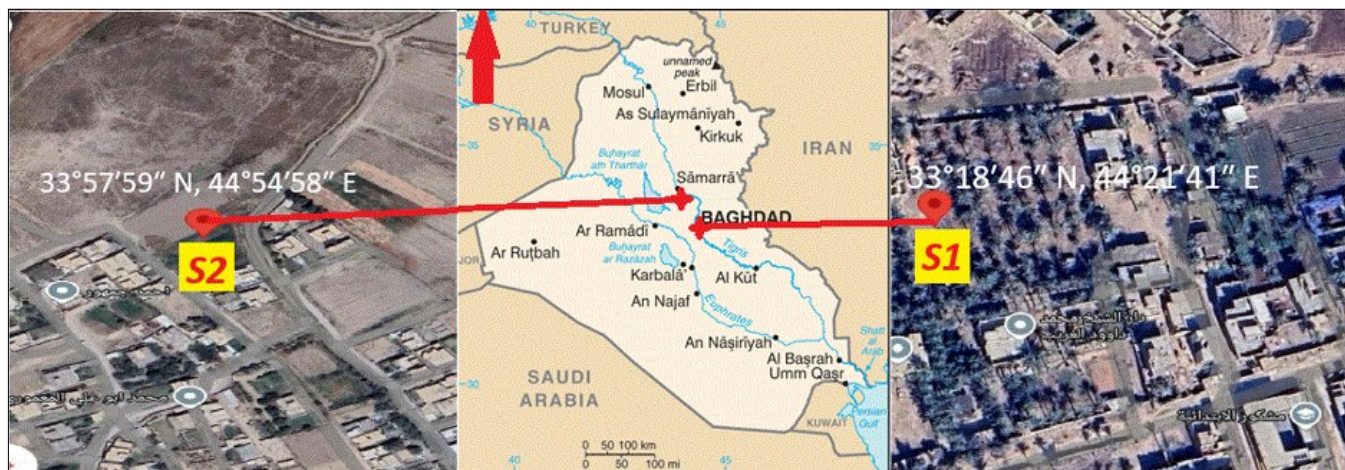


Fig. 1. Sampling sites.

S1 = Baghdad Governorate (33°18'46\" N, 44°21'41\")

S2 = Diyala Governorate (33°57'59\" N, 44°54'58\")

Fungal isolates were identified based on colony morphology and microscopic features (conidiophores, conidia and their arrangement) using standard taxonomic keys (5, 6). The frequency and percentage occurrence of each endophytic isolate were calculated using the formula below (7).

% occurrence of species =

$$\frac{\text{Colonies number of species}}{\text{Total number of species colonies}} \times 100 \quad (\text{Eqn. 1})$$

% frequency of species =

$$\frac{\text{Appearance in the sample}}{\text{Total number of species appearance}} \times 100 \quad (\text{Eqn. 2})$$

Determination of dry weight and extraction of lipids from endophytic fungi

Fungal isolates were first activated on PDA for 5–7 days, then cultivated in waste molasses dates medium (WMDM) as a fermentation medium. The medium was prepared by soaking 1 kg of palm dates in distilled water for 12 hr, then mashing and filtering. Subsequently, 500 g of the residue was mixed with 500 mL of distilled water, boiled for 30 min, filtered and the volume adjusted to 1 L. The medium was sterilised by autoclaving at 121 °C and 15 psi for 20 min and the pH was adjusted to 6.5 (8).

For fermentation, five mycelial plugs from each isolate were inoculated into 250 mL of medium in 500 mL Erlenmeyer flasks and incubated at 30 °C and 120 rpm for 8 days. Biomass was harvested by centrifugation (3000 rpm), filtered (Whatman No. 2), washed three times with distilled water and dried at 60 °C for 24 hr to determine dry weight (9, 10).

Molecular identification

The molecular identification of the highest oleaginous isolate was performed. Seven isolates of the fungus *Aspergillus* sp. (putatively *A. terreus*) that showed the highest lipid accumulation with staining of Sudan black B as seen in Fig. 2 were subjected to DNA extraction (11). Genomic DNA was amplified using universal primers ITS1 (5'-TCCGTAGGTGAACCTGCGG-3') and ITS4 (5'-TCCTCCGCTTATTGATATGC-3'), following the protocol (12). Polymerase chain reaction (PCR) conditions included an initial denaturation at 95 °C for 5 min, followed by 35 cycles of denaturation (95 °C, 30 sec), annealing (55 °C, 30 sec) and extension (72 °C, 1 min), with a final extension at 72 °C for 10 min. Polymerase chain reaction products were resolved on 1.5 % agarose gels stained with ethidium bromide (EtBr) and visualised under UV transillumination. A 100 bp DNA ladder was used as a molecular marker.

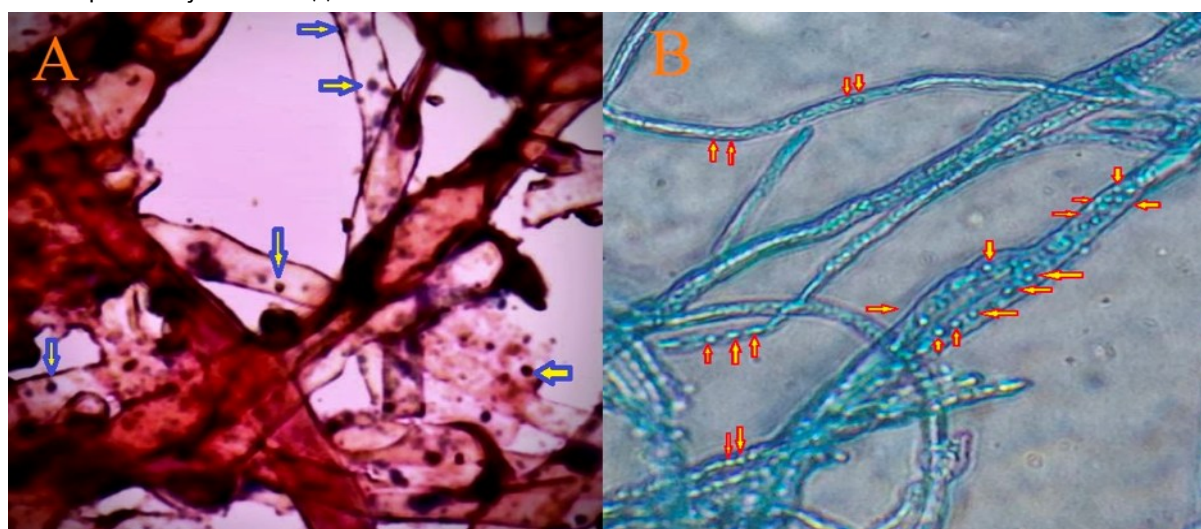


Fig. 2. The intracellular lipids for *Aspergillus terreus*. A: Stained with Sudan black B stain; B: Stained with cotton blue (X40).

Gas chromatography-mass spectrometry analysis

Using GC-MS, the lipid terrace was done to examine active chemicals in the extracts. To find bioactive chemicals performing on programs and data analysis (13). A Hewlett-Packard 5890 gas chromatograph was used to check samples planted with an HP 5972 MSD detector. Helium was used as a carrier gas and the sample was injected using an all-glass injector in split mode at a linear speed of 32 cm/s. A 30 m long, 25 μ m thick, 0.2 mm ID. The melted silica capillary column (HP-5) was used. The following temperature program was: 240–300 $^{\circ}$ C at 12 $^{\circ}$ C/min, with a grip of 24 min at 300 $^{\circ}$ C; 80–240 $^{\circ}$ C at 8 $^{\circ}$ C/min. When using computer findings, components were identified.

Statistical analysis

All experiments were conducted in triplicate ($n = 3$). Data were analysed using one way analysis of variance (ANOVA) to determine differences in oil yield among fungal isolates. Mean separation was performed using Fisher's least significant difference (LSD) test at $p < 0.05$. Results are expressed as mean $\pm$ standard deviation (SD) and means followed by different letters indicate significant differences. Statistical analyses were carried out using SPSS version 25.0 (IBM Corp., USA).

Results

A total of 151 fungal isolates were received from 225 samples of 5 host plant species: castor, maize, sesame, sunflower and olive; each represented by stem, root and leaf tissues, with 15 replicates in line with tissue. The result of the intersection map illustrates the

distribution and presence of endophytic fungi across five host plants (Fig. 3). A total of 21 fungal taxa were identified, with variable incidence among the hosts. Notably, *Fusarium* species (e.g., *F. Solani*, *F. oxysporum*, *F. Verticillioides*) have been among the most broadly disseminated fungi, being detected in more than one host (olive and sesame). *Aspergillus* spp., specifically *A. Flavus*, *A. terreus* and *A. niger*, also exhibited excessive prevalence across numerous hosts, highlighting their adaptability and ability to function as dominant endophytes. On the other hand, some fungi verified host specificity. For instance, *Penicillium citrinum* and *Mortierella alpina* have been constrained to sunflower and castor, respectively, at the same time as *Rhodosporidium* spp. (yeast-like) was detected in olive and sesame respectively. The dominance of *Fusarium* and *Aspergillus* spp. Throughout exclusive plant life, this finding aligns with previous research indicating their ecological versatility as each endophyte and opportunistic pathogens. Their ability to colonise multiple plant hosts show an extensive host range and an ability position in plant-microbe interactions, probably related to strain tolerance or the manufacturing of secondary metabolites.

As seen in Table 1, the results of isolation and laboratory identification revealed a notable variation in the distribution and occurrence rates of endophytic fungi across the target oleaginous plants. Regarding the overall frequency rates, the fungus *Aspergillus niger*, isolated from sesame, recorded the highest frequency in the study at 6.62 %, followed by *Aspergillus flavus* and *Fusarium solani*, which both recorded a frequency of 5.96 % in maize and olive, respectively. Conversely, the minimum frequency levels were recorded at 0.66 % for the fungi *Cladosporium* spp. and

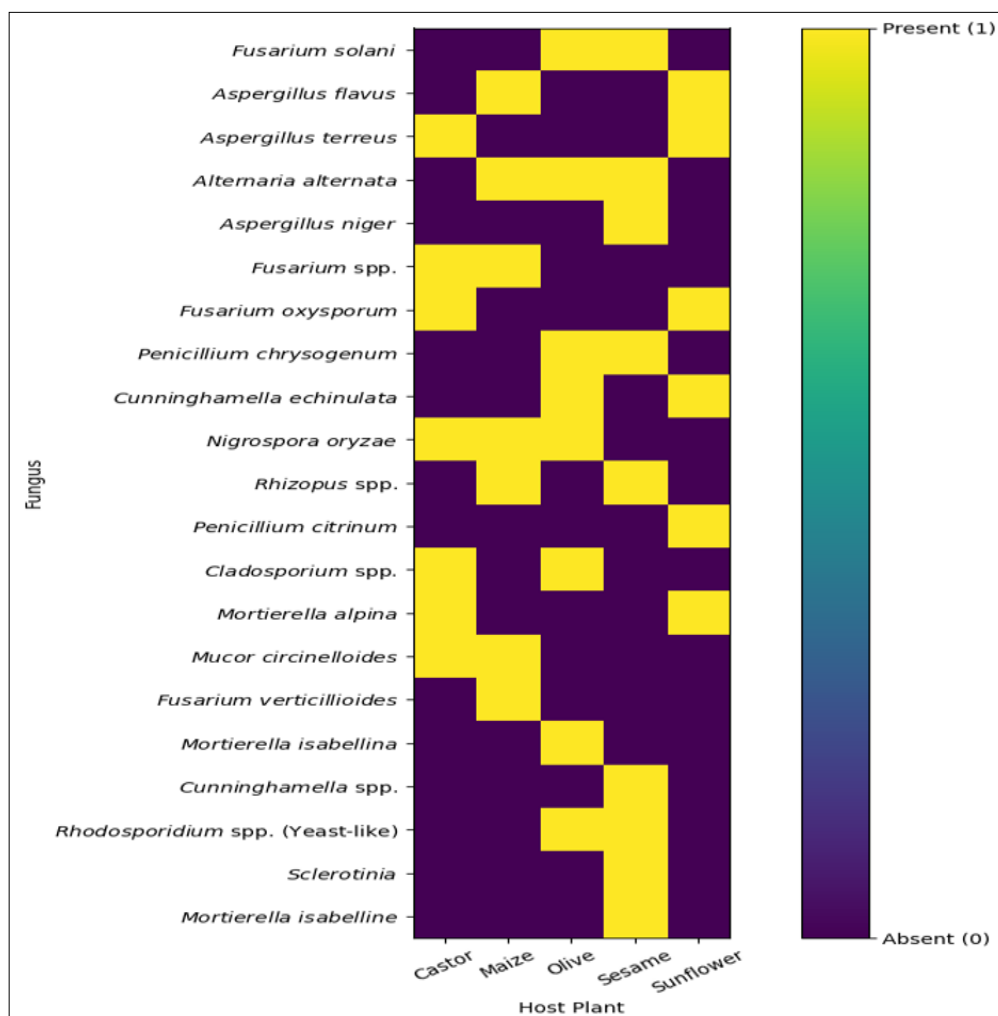


Fig. 3. Interaction map between endophytic fungi and oil-producing plants.

Table 1. The percentage of endophytic fungi isolated from different kinds of oleaginous plants

Plants	Endophytic fungi	Occurrence (%)	Frequency (%)
Castor	<i>Aspergillus terreus</i>	2.22	3.31
	<i>Cladosporium</i> spp.	0.44	0.66
	<i>Fusarium oxysporum</i>	0.88	1.32
	<i>Fusarium</i> spp.	1.77	2.64
	<i>Mortierella alpina</i>	0.44	0.66
	<i>Mucor circinelloides</i>	0.88	1.32
	<i>Nigrospora oryzae</i>	0.88	1.32
	<i>Alternaria alternata</i>	1.33	1.98
	<i>Aspergillus flavus</i>	4.0	5.96
Maize	<i>Fusarium</i> spp.	2.66	3.97
	<i>Fusarium verticillioides</i>	1.77	2.64
	<i>Mucor circinelloides</i>	1.33	1.98
	<i>Nigrospora oryzae</i>	0.88	1.32
	<i>Rhizopus</i> spp.	0.88	1.32
	<i>Alternaria alternata</i>	1.77	2.64
	<i>Aspergillus niger</i>	4.44	6.62
	<i>Cunninghamella</i> spp.	1.33	1.98
	<i>Fusarium solani</i>	3.55	5.29
Sesame	<i>Mortierella isabellina</i>	0.88	1.32
	<i>Penicillium chrysogenum</i>	2.66	3.97
	<i>Rhizopus</i> spp.	1.77	2.64
	<i>Rhodospiridium</i> spp. (Yeast-like)	0.88	1.32
	<i>Sclerotinia</i> spp.	1.33	1.98
	<i>Aspergillus flavus</i>	2.66	3.97
	<i>Aspergillus terreus</i>	3.11	4.63
	<i>Cunninghamella echinulate</i>	1.77	2.64
	<i>Fusarium oxysporum</i>	3.11	4.63
Sunflower	<i>Mortierella alpina</i>	1.77	2.64
	<i>Penicillium citrinum</i>	2.66	3.97
	<i>Alternaria alternata</i>	1.77	2.64
	<i>Cladosporium</i> spp.	1.77	2.64
	<i>Cunninghamella echinulate</i>	1.33	1.98
	<i>Fusarium solani</i>	4.0	5.96
	<i>Mortierella isabellina</i>	1.33	1.98
	<i>Nigrospora oryzae</i>	0.88	1.32
	<i>Penicillium chrysogenum</i>	1.33	1.98
Olive	<i>Rhodospiridium</i> spp. (Yeast-like)	0.44	0.66

Mortierella alpina in castor, as well as for *Rhodospiridium* spp. isolated from olive. Upon analysing the data for each plant host individually, it was found that castor was characterised by the prevalence of *A. terreus*, with an occurrence rate of 2.22 % and a frequency of 3.31 %. Other isolates, such as *Fusarium* spp. and *N. oryzae*, ranged between frequencies of 2.65 % and 1.32 %. In maize, *A. flavus* emerged as the most common species with an occurrence rate of 4.00 %, surpassing *Fusarium* spp. which recorded a frequency of 3.97 %, while other species like *Rhizopus* spp. recorded low frequency values not exceeding 1.32 %. Regarding sesame, the results demonstrated broad fungal diversity, where *A. niger* occupied the highest proportions with an occurrence of 4.44 %. Additionally, *F. solani* recorded a strong frequency of 5.30 %, while the least frequent isolates in this plant, such as *Rhodospiridium* spp., reached a value of 1.32 %. Moving to sunflower, both *A. terreus* and *F. oxysporum* shared the top occurrence rates at 3.11 % each, with a relative frequency reaching 4.64 %, while the isolates *C. echinulate* and *M. alpina* recorded equal frequencies of 2.65 %. Finally, the data for olive revealed a clear dominance of the fungus *F. solani*, with an occurrence rate of 4.00 % and a frequency of 5.96 %, followed by *A. alternata* and *Cladosporium* spp. at a frequency of 2.65 % each. In

comparison with other species in the same plant, *Rhodospiridium* spp. recorded the lowest presence with an occurrence rate of 0.44 % and a frequency not exceeding 0.66 %, reflecting a variation in biological affinity between endophytic fungi and the different types of oleaginous plant hosts.

According to the statistical analysis presented in Fig. 4, *A. terreus* (12.88 %), *F. solani* (10.23 %) and *Cunninghamella* spp. (8.55 %) were the highest oil-producing isolates. *Aspergillus niger* (6.95 %), *Cunninghamella echinulate* (5.59 %) and *Fusarium* spp. (7.12 %) showed moderate oil production. In contrast, lower oil yields were observed in *Rhizopus* spp. (5.05 %) and *Mortierella isabellina* (5.25 %), while the remaining isolates ranged from 1.69–4.41 %.

The oil yield of the investigated endophytic fungi ranged from 3.96–24.12 % (w/w) (Fig. 2, Table 2). The highest value was recorded in *A. terreus* (24.12 %), whereas the lowest value was observed in *Sclerotinia* spp. (3.96 %). Intermediate values were distributed among the remaining isolates, including *Cunninghamella* spp. (19.98 %), *F. solani* (17.73 %), *Fusarium* spp. (15.03 %), *Rhodospiridium* spp. (14.94 %), *Rhizopus* spp. (14.67 %) and *Mortierella isabellina* (14.40 %). Moderate values were recorded for *A. niger* (12.51 %), *C. echinulate* (12.15 %), *Mucor circinelloides* (9.90 %) and *N. oryzae* (9.00 %), while lower values were observed in *P. chrysogenum* (8.28 %), *P. citrinum* (8.10 %), *Cladosporium* spp. (8.01 %), *F. verticillioides* (7.92 %), *Colletotrichum* spp. (6.93 %) and *F. oxysporum* (6.75 %). The lowest group included *A. flavus* (5.22 %), *M. alpina* (4.23 %) and *A. alternata* (4.05 %). Statistical analysis indicated significant differences among isolates at $p \leq 0.05$.

This investigation efficiently proved the molecular identity of isolates of the fungus *Aspergillus* spp. (putatively *A. terreus*) through ITS-PCR, producing 600 bp amplicons, as shown in Fig. 5. The method gives the ability to use in scientific, commercial and ecological research and gives a strong foundation for unique fungal identity. Due to its fantastic sensitivity and specificity for species-level identity, the ITS area has been generally diagnosed as the usual DNA barcode for fungi. This study's consistent amplification of approximately 600 bp fragments confirms that each one tested isolate incorporates *Aspergillus* spp.

Table 2. Oil yield (% w/w) of endophytic fungal isolates

Endophytic fungus	(Mean $\pm$ SD) (n = 3)
<i>Alternaria alternata</i>	4.05 $\pm$ 0.27 ^f
<i>Aspergillus flavus</i>	5.22 $\pm$ 0.45 ^e
<i>Aspergillus niger</i>	12.51 $\pm$ 1.08 ^c
<i>Aspergillus terreus</i>	24.12 $\pm$ 1.35 ^a
<i>Cladosporium</i> spp.	8.01 $\pm$ 1.08 ^d
<i>Colletotrichum</i> spp.	6.93 $\pm$ 0.72 ^e
<i>Cunninghamella echinulate</i>	12.15 $\pm$ 1.62 ^c
<i>Cunninghamella</i> spp.	19.98 $\pm$ 0.81 ^b
<i>Fusarium oxysporum</i>	6.75 $\pm$ 0.72 ^e
<i>Fusarium solani</i>	17.73 $\pm$ 0.63 ^b
<i>Fusarium</i> spp.	15.03 $\pm$ 1.53 ^b
<i>Fusarium verticillioides</i>	7.92 $\pm$ 0.99 ^d
<i>Mortierella alpina</i>	4.23 $\pm$ 0.81 ^f
<i>Mortierella isabellina</i>	14.40 $\pm$ 0.72 ^b
<i>Mucor circinelloides</i>	9.90 $\pm$ 0.72 ^c
<i>Nigrospora oryzae</i>	9.00 $\pm$ 0.90 ^c
<i>Penicillium chrysogenum</i>	8.28 $\pm$ 1.08 ^d
<i>Penicillium citrinum</i>	8.10 $\pm$ 0.54 ^d
<i>Rhizopus</i> spp.	14.67 $\pm$ 1.26 ^b
<i>Rhodospiridium</i> spp.	14.94 $\pm$ 0.72 ^b
<i>Sclerotinia</i> spp.	3.96 $\pm$ 0.27 ^f

LSD ($P \leq 0.05$): 1.53

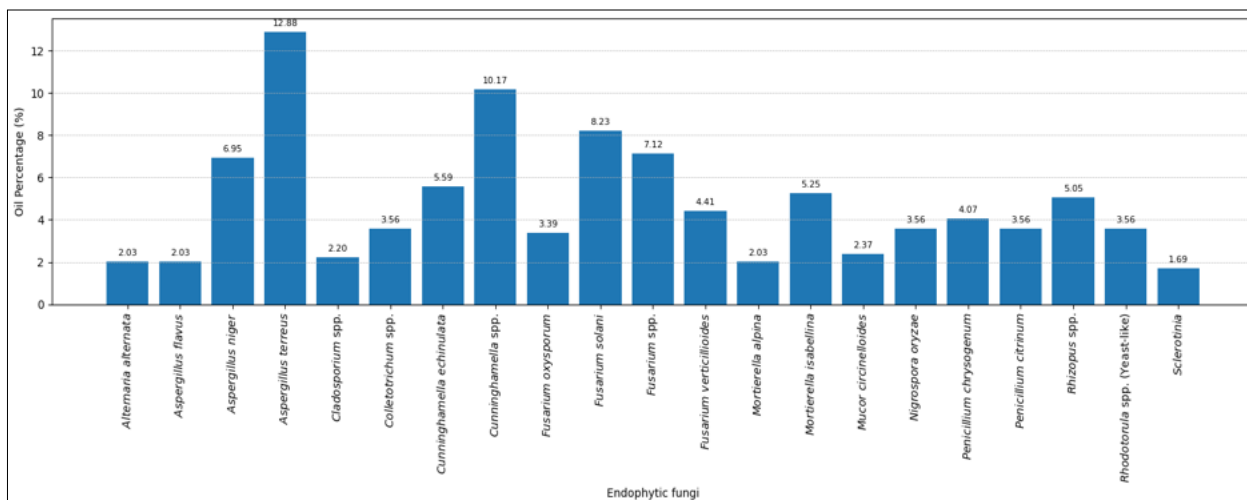


Fig. 4. Oil yield percentages of endophytic fungi.

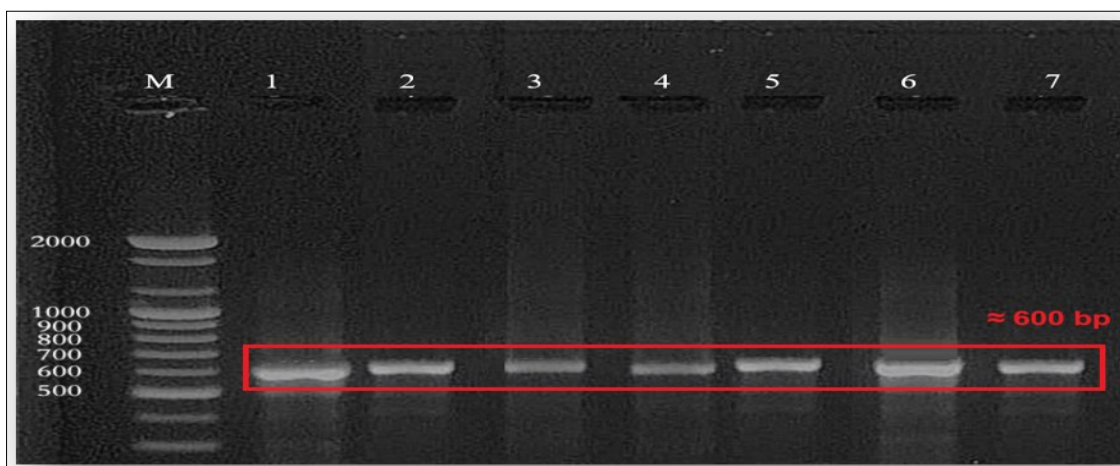


Fig. 5. Polymerase chain reaction (PCR) amplification of the ITS and ITS4 region in *Aspergillus terreus*. Lane M: DNA marker (100 bp ladder); Lanes 1–7: *Aspergillus terreus* isolates (approximately 600 bp amplicons).

The 7th peaks of the materials were shown in the GC-MS analysis (Fig. 6, Table 3). With a percent area of 5.05 % and a retention duration of 15.329 min, 1-hexacosanol was identified as the first peak. At a retention time of 26.188 mins, the remaining setup peak 2- propenoic acid, pentadecyl ester (pentadecyl acrylate) appears with a percentage area of 21.0 %, which is regarded as the maximum area percentage. Gas chromatography-mass spectrometry (GC-MS) examination of the dry ethyl acetate extract of *A. terreus* revealed the presence of 7 additives, which include phenol compounds, alcohols, hydrocarbons and fatty acid esters. There are further peaks in hexadecanoic acid and ethyl ester (ethyl palmitate) in the course of 19.561 mins of retention, with a complete area percentage of 20.01 %. The lower may be found at retention time 17.27 min in (methyl stearate), a total area percentage of (1.37 %). The results verify the oleaginous nature of the fungus. While a few phthalate contaminants were unnoticed, probable contamination from the lab device.

Discussion

The diversity of endophytic fungi recovered from the five oil-bearing hosts reflects strong ecological interactions influenced by host species and tissue type. The dominance of *Fusarium* and *Aspergillus* spp. corresponds with previous studies highlighting their metabolic flexibility and broad host range. Their capacity to colonise multiple plant species indicates high ecological adaptability, enabling them to persist as both beneficial endophytes and opportunistic pathogens (22, 23).

The occurrence of *Mortierella* and *Rhodospiridium* spp., although less frequent, is consistent with reports describing their lipid-accumulating capacity. Their association with oil-rich hosts such as sesame and olive may suggest a response to substrate availability or host-derived nutrients. Similarly, the detection of *P. citrinum* exclusively in sunflower may indicate a degree of host preference; however, this observation remains limited by sampling scope and requires further verification (15, 24, 25).

Aspergillus terreus is well documented for producing a range of secondary metabolites, including lovastatin and has also been reported in clinical contexts. In the present study, ITS-PCR analysis yielded single amplicons within the expected size range (550–650 bp), supporting species-level identification and confirming the suitability of ITS1/ITS4 primers for fungal barcoding (19–22) (19, 26–28).

The difference in oil output across isolates demonstrates the ability of endophytic fungi to redirect carbon flow towards lipid biosynthesis, which is frequently controlled by both genetic and environmental signals. Due to the antibacterial, anti-inflammatory and antioxidant qualities of their lipid metabolites, such as unsaturated fatty acids, oleaginous endophytes are especially attractive from a pharmacological standpoint (21, 29). Furthermore, their dual role in producing primary lipids and secondary metabolites underscores their potential applications in fungal biotechnology as efficient microbial cell factories. (1, 13). The relatively higher oil yield observed in *A. terreus* compared to other

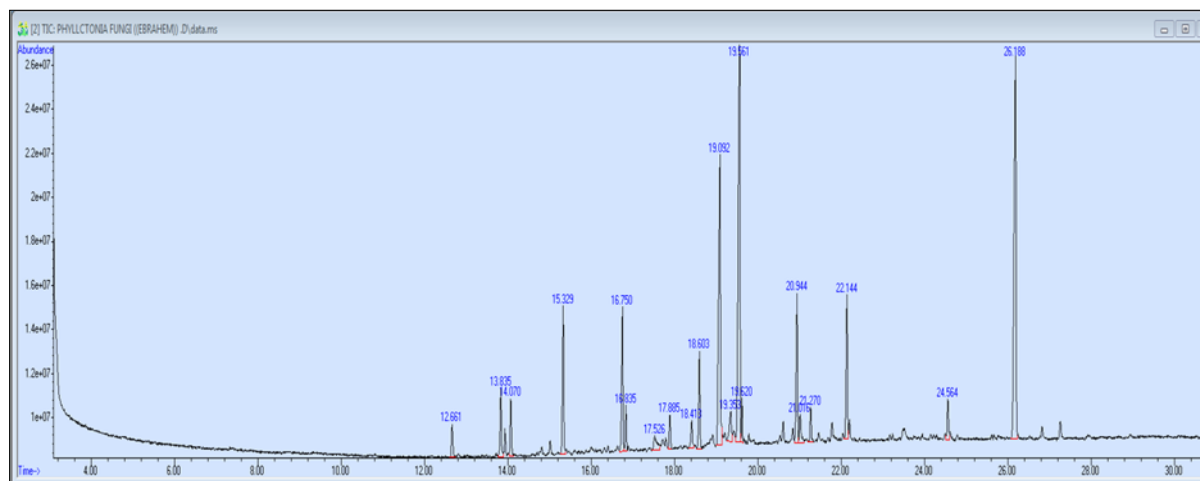


Fig. 6. Peaks of gas chromatography-mass spectrometry (GC-MS) analysis for *Aspergillus terreus* extract.

Table 3. Active compounds from *Aspergillus terreus* extract by gas chromatography-mass spectrometry (GC-MS) analysis

RT (min)	Compound	Area (%)	Molecular formula	Molecular weight (g/mol)	Chemical class	Concise structure	Biological activities	Reference
26.188	2-Propenoic acid, pentadecyl ester (Pentadecyl acrylate)	21.0	C ₁₈ H ₃₄ O ₂	282.47	Fatty acid acrylate ester	CH ₂ =CH-COO-(CH ₂) ₁₄ -CH ₃	antimicrobial/antibacterial/antifungal effects	(2, 14)
20.944	Methyl oleate	5.94	C ₁₉ H ₃₆ O ₂	296.49	Fatty acid methyl ester (C18:1, ω-9)	CH ₃ -(CH ₂) ₇ -CH=CH-(CH ₂) ₇ -COOCH ₃	antibacterial/antibiofilm and antioxidant activities.	(15, 16)
19.561	Hexadecanoic acid, ethyl ester (Ethyl palmitate)	20.01	C ₁₈ H ₃₆ O ₂	284.48	Fatty acid ethyl ester (C16:0)	CH ₃ -(CH ₂) ₁₄ -COOCH ₂ CH ₃	anti-inflammatory effect and antimicrobial potential	(17, 18)
19.092	Pentadecanoic acid (C15:0)	14.83	C ₁₅ H ₃₀ O ₂	242.4	Odd-chain saturated fatty acid	CH ₃ -(CH ₂) ₁₃ -COOH	anti-inflammatory, regulatory effects; antimicrobial	(15, 19)
17.27	Methyl stearate	1.37	C ₁₉ H ₃₈ O ₂	298.5	Fatty acid methyl ester (C18:0)	CH ₃ -(CH ₂) ₁₆ -COOCH ₃	anti-inflammatory, antioxidant	(17, 20)
16.75	1-Nonadecene / n-Nonadecanol-1 (trace isomers)	5.57	C ₁₉ H ₃₈ (1-Nonadecene); C ₁₉ H ₄₀ O (1-Nonadecanol)	Alkene: 266.50; Alcohol: 284.53	Long-chain alkene / fatty alcohol	Alkene: CH ₂ =CH-(CH ₂) ₁₇ -CH ₃ ; Alcohol: HO-(CH ₂) ₁₉ -CH ₃	antibacterial/ antifungal	(2, 3)
15.329	1-Heptacosanol	5.05	C ₂₇ H ₅₆ O	396.72	Very-long-chain fatty alcohol	HO-(CH ₂) ₂₆ -CH ₃	antibacterial, antioxidant and antifungal activities;	(21, 17)

isolates may be attributed to differences in metabolic efficiency under the tested conditions, particularly in carbon utilisation and lipid biosynthesis pathways. Intermediate yields recorded in *F. solani* and *Cunninghamella* spp. are within ranges reported in earlier studies, suggesting comparable metabolic performance (30, 31).

Variability in lipid production among isolates likely reflects the combined effects of genetic background and environmental conditions, both of which are known to influence lipid metabolism in fungi (32). In addition, several lipid-derived compounds identified in this study, particularly fatty acids, have been previously associated with biological activities such as antimicrobial and antioxidant effects, although their functional roles in this context were not directly assessed (23, 24).

Gas chromatography-mass spectrometry (GC-MS) analysis of *A. terreus* revealed a profile dominated by fatty acids and their methyl esters, including palmitic, oleic and linoleic acids. These compounds are commonly reported in microbial lipid studies and are frequently discussed in relation to biodiesel composition and bioactivity. The concurrent detection of lipid compounds and other metabolites, including polyketide-related compounds, indicates metabolic diversity within this isolate, although their specific contributions require further investigation (33–35).

Overall, the findings demonstrate variability in both fungal diversity and lipid production among endophytic isolates associated with oil-bearing plants. While *A. terreus* showed relatively higher lipid accumulation under the conditions tested, further studies are necessary to evaluate the reproducibility of these results, optimise cultivation parameters and assess potential applications at a larger scale.

Conclusion

The two most common endophytic genera identified among the five oil-bearing host plants were *Aspergillus* and *Fusarium*. The high oil yield of *Aspergillus terreus* may be attributed to its metabolic adaptability. Gas chromatography-mass spectrometry (GC-MS) profiling revealed the presence of fatty acids and their esters, which are commonly associated with biodiesel-related compounds and oleaginous characteristics. Detected compounds such as heptacosanol, pentadecanoic acid, nonadecene and palmitate have been previously associated with antibacterial, anti-inflammatory, or antioxidant properties. The relatively high lipid content observed in this isolate suggests its potential as a microbial source of lipid-derived compounds. However, additional studies are required to confirm their functional applications and scalability.

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Authors' contributions

All authors contributed equally. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflicts of interest to declare.

Ethical issues: None

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