6.4%

PlagScan by Turnitin Results of plagiarism analysis from 2022-12-21 07:50 UTC

Single cell oil of oleaginous marine microbes from Saudi Arabian mangroves as a potential feedstock for biodiesel pro.docx

Date: 2022-12-21 07:46 UTC

✱ All sources 65 | Internet sources 37

- [0] pubmed.ncbi.nlm.nih.gov/33424376/
  2.0% 18 matches
- [1] www.degruyter.com/document/doi/10.1515/bot-2021-0049/html
  0.2% 14 matches
- [2] www.degruyter.com/document/doi/10.1515/bot-2021-0061/html
  1.2% 13 matches
- [3] www.degruyter.com/document/doi/10.1515/bot-2016-0111/html?lang=de
  0.4% 13 matches
  ⊞ 1 documents with identical matches
- [5] www.ncbi.nlm.nih.gov/pmc/articles/PMC9029807/
  0.7% 10 matches
- [6] www.mdpi.com/1660-3397/19/10/571
  0.3% 10 matches
- [7] link.springer.com/chapter/10.1007/978-3-319-29137-6_22
  0.2% 7 matches
  ⊞ 1 documents with identical matches
- [9] sci.sohag-univ.edu.eg/main/wp-content/uploads/2022/05/2021-ملخصات-ابحاث-الكلية-.pdf
  0.8% 10 matches
- [10] www.ncbi.nlm.nih.gov/pmc/articles/PMC5994804/
  0.2% 9 matches
- [11] www.academia.edu/18181090/Modeling_of_single_cell_oil_production_under_nitrogen_limited_and_substrate_inhibition_conditions
  0.2% 8 matches
  ⊞ 1 documents with identical matches
- [13] link.springer.com/article/10.1007/s10811-017-1149-8
  0.2% 6 matches
- [14] www.ncbi.nlm.nih.gov/pmc/articles/PMC5628321/
  0.1% 7 matches
- [16] www.sciencedirect.com/science/article/pii/S1018364722004050
  0.5% 5 matches
- [17] www.sciencedirect.com/science/article/pii/S1319562X20305866
  0.6% 6 matches
- [19] www.semanticscholar.org/paper/Coupled-production-of-single-cell-oil-as-biodiesel-Kamat-Khot/50ee44174d5944ffa2614cac4b08e3e7544446
  0.2% 3 matches
- [20] www.academia.edu/25954595/Cultural_Optimization_of_Thraustochytrids_for_Biomass_and_Fatty_Acid_Production
  0.2% 6 matches
- [21] www.degruyter.com/journal/key/botm/64/6/html
  0.2% 3 matches
- [23] pubmed.ncbi.nlm.nih.gov/22646719/
  0.3% 4 matches
- [24] www.academia.edu/18056197/Biodiscovery_of_new_Australian_thraustochytrids_for_production_of_biodiesel_and_long_chain_omega_3_oil
  0.1% 5 matches
- [27] pubmed.ncbi.nlm.nih.gov/21478316/
  0.2% 4 matches
- [28] www.mdpi.com/1660-3397/13/12/7064
  0.1% 3 matches
- [30] docplayer.net/89630046-Vqvj-ss-fy-y-0v-plant-resources-of-south-east-asia-no-15-1-cryptogams-algae-w-f-prud-homme-van-reine-and-g-c-tro
  0.4% 5 matches
- [31] www.bertin-bioreagent.com/pr110929/13-wbr-docosenamide
  0.5% 2 matches
- [32] www.ncbi.nlm.nih.gov/pmc/articles/PMC8541261/
  0.1% 4 matches

☑ [33] www.researchgate.net/publication/225080053_Single_cell_oil_of_oleaginous_fungi_from_the_tropical_mangrove_wetlands_as_a_potential_f
0.2% 2 matches

☑ [34] www.mdpi.com/1660-3397/19/10/559/htm
0.1% 4 matches

☑ [35] www.semanticscholar.org/paper/Increase-of-Eicosapentaenoic-Acid-in-through-of-a-Kobayashi-Sakaguchi/b744814adad5a136215fcb7f46126
0.3% 4 matches

☑ [36] scholarworks.calstate.edu/downloads/n583xx705
0.3% 4 matches

☑ [38] www.fungaldiversity.org/fdp/sfdp/FD12-111-122.pdf
0.1% 4 matches

☑ [41] www.sciencedirect.com/science/article/abs/pii/S0960852418313464#!
0.1% 2 matches

☑ [45] journals.plos.org/plosone/article?id=10.1371/journal.pone.0125368
0.2% 3 matches

☑ [46] www.ncbi.nlm.nih.gov/pmc/articles/PMC2635718/
0.2% 1 matches

☑ [48] link.springer.com/article/10.1007/s00253-021-11425-5
0.1% 2 matches

☑ [50] www.sciencedirect.com/topics/agricultural-and-biological-sciences/labyrinthulomycetes
0.2% 2 matches

☑ [56] www.excli.de/vol19/excli2019-1672.pdf
0.1% 2 matches

☑ [62] link.springer.com/article/10.1007/s12010-020-03343-5
0.1% 1 matches

☑ [63] www.sciencedirect.com/science/article/abs/pii/S1341321X17300818
0.1% 1 matches

27 pages, 6534 words

PlagLevel: 6.4% selected / 15.4% overall

93 matches from 68 sources, of which 68 are online sources.

Settings

Data policy: *Compare with web sources, Check against my documents*

Sensitivity: *Medium*

Bibliography: *Consider text*

Citation detection: *Reduce PlagLevel*

Whitelist: --

[19]Single cell oil of oleaginous marine microbes from Saudi Arabian mangroves as a potential feedstock for biodiesel production

Mohamed A. Abdel-Wahab [a,b,*], Abdallah M. Elgorban [a,c,d], Ali H.[0] Bahkali [a]

[a] Botany and Microbiology Department, Faculty of Science, King Saud University, Riyadh, Saudi Arabia

[b] Department of Botany and Microbiology, Faculty of Science, Sohag University, Sohag 82524, Egypt

[c] Agricultural Research Center, Plant Pathology Research Institute, Giza, Egypt

[d] Center of Excellence in Biotechnology Research, King Saud University, Riyadh, Saudi Arabia

Corresponding author:

Mohamed A. Abdel-Wahab

https://orcid.[0]org/0000-0002-3176-8675

Professor of Marine Mycology

Department of Botany - Faculty of Science

Sohag University - Sohag 82524

EGYPT

E mail: mohamed.eisa@science.sohag.edu.eg

;;;;;;;;;;;;;mohamed700906@gmail.com

Mobile: 002-01016328938

Fax: 002-0934601159

Abstract

This study aims to explore microbes from mangrove in Saudi Arabia for their abilities to produce high level of lipids. Mangroves are seldom investigated for oleaginous microbes.[23] A total of 961 isolates of yeasts and filamentous fungi were isolated from 144 submerged marine samples include: 68 decaying leaves of Avicennia marina, 33 decaying thalli of Zostera marina, 14 decaying pneumatophores of Avicennia marina, 9 crab shells, 8 sediment, 7 decaying thalli of Turbinaria ornata and 5 decaying thalli of Cystoseira myrica.[9] Samples were collected from four mangrove sites:[9] Al-Leith, Jeddah and Yanbu at the Red Sea coast and the Syhat mangroves at the Arabian Gulf coast. Isolated fungi were grouped into 62 morphological types that include: 21 yeasts and 41 filamentous fungi. Fifty-four isolates of thraustochytrids were cultured from the four mangrove sites and were grouped into 22 strains. Two oleaginous yeasts: Hortaea werneckii (AL–19) and Rhodotorula mucilaginosa (AL–14) and four Aurantiochytrium strains: AL–22, AL–23, SY–78 and SY–85 produced high dry weight ranged between 32 and 49.3 g/L of which 35.2–62 % lipid and their fatty acid profile were determined using GC/MS.[11] Palmitic acid was the major fatty acid in the lipid of the four thraustochytrid isolates and ranged between 5.71 to 82% of the total fatty acids, while it was not recorded from the lipid of the two yeast isolates, 9-Octadecenamide, (Z)- was the major fatty acid amide in the lipid of the two yeast isolates and two thraustochytrid isolates and ranged between 26.94 and 56.63%, followed by 13-Docosenamide, (Z)- (20.44–34.99%) from the same four isolates. Other major lipid compounds were: Hexadecanamide (4.35–7.19 %), Cholestrol (7.24–15.07 %), Butylated Hydroxytoluene (3.46–15.76 %), Octadecanamide (3.95–7.9%), Phenol, 2-(1,1-dimethylethyl)-5-methyl- (1.78–10.33%) and Pentadecanoic acid (7.47%).

Keywords: Heterokonta; filamentous fungi; Labyrinthulomycetes, molecular phylogenetics; subtropics; red yeasts.

1. Introduction

Fungi as a source of oil has advantages over conventional plant and algal resources as they can be easily grown in bioreactors, have short life cycles, display rapid growth rates, are unaffected by space, light or climatic variations. Fungi are easier to scale up and can be grown on a wide range of inexpensive renewable carbon sources, e.g. lignocellulosic biomass and agro industrial residue (Khot et al., 2012). Major efforts have been made to replace fossil fuels that has had serious environmental issues especially the increased greenhouse effect through the emission of CO_2 and NOx gasses that consequently rise global temperature. Combustion of fossil fuels has contributed to the acidification of the oceans that significantly changes marine life.

[46] Biofuels are an attractive alternative as they can be used as transportation fuels with little change to the current technologies (Carere et al., 2008). Liquid transportation biofuels include: bioethanol and biodiesel (Demirbas, 2011). Most vehicles can use from 10% to 85 % ethanol blends for fuels. Bioethanol is produced by fermentation of corn glucose in the United States or sucrose in Brazil (Rosillo-Calle and Cortez, 1998). The International Energy Agency expects that biofuels will contribute 6% of total fuel use by 2030.

Recently lipids synthesis by oleaginous fungi from raw cheap materials has received great attention (Sergeeva et al., 2008; Zheng et al., 2012; Kyung et al., 2013; Venkata et al., 2014; Venkata Subhash and Venkata Mohan, 2014; Ranjan, 2015; Yang et al., 2014). [7] Those produced lipids can be used for biodiesel production (Economou et al., 2011; Papanikolaou et al., 2011). Fungal lipids have advantages over algal lipids because fungi are fast growing with short span, light independent and can degrade a wide range of carbon sources (Pant and Adholeya, 2010; Yousuf et al., 2010; Chen et al., 2012). Lipid production by oleaginous fungi using renewable carbon sources such as: glycerol, sewage water, whey and molasses were reported (Easterling et al., 2009; Chtzifragkou et al., 2010; Subramaniam et al., 2010; Bellou et al., 2012; Peng et al., 2013). Oleaginous microorganisms can convert a wide variety of carbon sources into stored lipids (Ratledge, 2004). Vegetable oils, animal fats and waste cooking oils

were traditionally used for biodiesel production (Venkata Subhash and Venkata Mohan, 2014). However, those traditional sources are unsustainable and expensive.

Thraustochytrids are oleaginous microorganisms that can utilize a wide range of substrates including: glucose, galactose, fructose, mannose, sucrose (Yokochi et al., 1998; Shene et al., 2010), complex organic matter (Bongiorni et al., 2005) and cellulosic biomass (Hong et al., 2012), for the production of polyunsaturated fatty acids (PUFAs). Thraustochytrids are lipid rich biomass that can be used for biodiesel and PUFA production (Johnson and Wen, 2009; Gupta, 2012; Abdel-Wahab et al., 2021a,b, 2022).

2. Materials and methods

2.1. Sampling sites and sample collection

One hundred and forty-four samples were collected from four mangrove sites along the Red Sea and the Arabian Gulf in Saudi Arabia namely: Al-Leith (20° 49′ 10″ N 39° 27′ 26″ E), Jeddah (22° 46′ 32″ N 39° 48′ 25″ E), Syhat (26° 29′ 32″ N 50° 02′ 46″ E) and Yanbu (24°02.55′ N 38°68.89′ E). Collected samples included: 68 decaying leaves of Avicennia marina, 33 decaying thalli of Zostera marina, 14 decaying pneumatophores of Avicennia marina, 9 crab shells, 8 sediment, 7 decaying thalli of Turbinaria ornata and 5 decaying thalli of Cystoseira myrica.

2.2. Isolation of filamentous fungi, yeasts and thraustochytrids

Decaying leaves and pneumatophores of Avicennia marina and decaying thalli of seaweeds were placed in clean plastic bags and brought to the laboratory on the same day. In the laboratory, samples were washed using sterile sea water, cut into small segments (ca 1 cm in length), surface sterilized using 5% sodium hypochlorite for 1 min, transferred into sterile sea water (1 min), surface dried using sterile filter paper and placed on the surface of GYPTA medium (1 g glucose, 1 g yeast extract, 1 g peptone, 10 g tomato juice, 2 g monosodium glutamate, 1 g tween 80, 0.2 g KH_2PO_4, 0.5 g chloramphenicol, 15 g agar in 1 l of half-strength natural seawater). Plates were incubated at 25 °C and examined every 24 h. Microbial growth were transferred to new plates and further purified until axenic cultures were obtained.

Pure cultures were maintained on GYP slants (30 g glucose, 5 g yeast extract, 10 g peptone in 1 L of 50% seawater) and re-subculture every two months. We also preserved them by cryopreservation at -80°C and re-subculture every 4 months.

2.3. Sudan Black B test of the isolated microbes

The 84 morphological strains isolated during the present study were tested for their abilities to produce high level of oil using Sudan Black B. Positive strains for oil production were further grown on a larger scale and the percentage of oil were determined using Sulfo-Phospho-Vanlin (SPV) method.

2.4. Quantification of microbial lipids using sulfo-phospho-vanillin (SPV) method

Phosphovanillin (PV) reagent was prepared by dissolving six milligrams of vanillin in 100 mL of hot water and further diluted to 500 mL with phosphoric acid. Oleic and palmitic acids were used as standard and diluted properly with concentrated sulfuric acid to reach 1 mg/mL. Reagents (oleic, palmitic, phosphoric and sulfuric acids and vanillin) were purchased from local company. Twenty-five mg of microbial cells were dissolved in one mL concentrated sulfuric acid, of which 20 µL of the samples were diluted in 180 µL of concentrated sulfuric acid, incubated at 100 ºC for 10 min. Samples were cooled to room temperature and 0.5 mL of phosphovanillin reagent was added, incubated at 37 ºC for 15 min, cooled to room temperature and stored for 45 min in a dark box for color development. The absorbance was measured at 530 nm in a spectrophotometer (Anschau et al., 2017, Abdel-Wahab et al. 2022).

2.5. Lipid extraction and analysis of fatty acids

Biomass and their dry weights were calculated and the lipid was extracted as previously described by Abdel-Wahab et al. (2022). Fatty acids profile of the extracted lipid was determined using methyl esters boron tri-fluoride method (Folch et al., 1957; AOAC, 2012; Abdel-Wahab et al., 2021a, 2022).

2.6. [32] DNA sequencing and phylogenetic analyses

Pure microbial strains were grown in liquid medium and DNA was extracted using MOBIO microbial DNA extraction kit according to the manufacturer's instructions. ITS region was amplified and sequenced using ITS1 and ITS4 primers. Partial SSU and LSU rDNA were amplified and sequenced using primers pairs NS1/NS4 and LROR/LR7 respectively (White et al., 1990; Bunyard et al., 1994).

PCR amplification and DNA sequencing were carried out by SolGent Inc., South Korea. The obtained sequences were deposited in GenBank (Figs. 2–3, 5). Sequences were aligned using ClustalX (Thompson et al., 1997). Phylogenetic analyses were carried out using MEGA X (Kumar et al., 2018). Bayesian phylogenetic analysis was performed using MrBayes 3.1.2 (Huelsenbeck and Ronquist, 2001; Ronquist and Huelsenbeck, 2003). MrModeltest 2.2 was used to determine the best-fit model for the sequences dataset (Nylander, 2004). The phylogenetic tree in Figure 2 was visualized using Njplot (Perrière and Gouy, 1996) and edited using Adobe Illustrator CS6.

3. Results and discussion

3.1. Diversity of oleaginous filamentous fungi and yeasts from Saudi mangroves

A total of 961 isolates (include 759 filamentous fungi and 202 yeasts) were isolated from 144 submerged marine samples that include: 68 decaying leaves of Avicennia marina, 33 decaying thalli of Zostera marina, 14 decaying pneumatophores of Avicennia marina, 9 crab shells, 8 sediment, 7 decaying thalli of Turbinaria ornata and 5 decaying thalli of Cystoseira myrica. Samples were collected from four mangrove sites: Al-Leith, Jeddah and Yanbu (Red Sea) and Syhat (Arabian Gulf). Isolated fungi were grouped into 62 morphological types that include: 21 yeasts and 41 filamentous fungi. Aspergillus and Penicillium species were the most common fungi and represented by 337 and 330 isolates respectively. Other recorded genera were: Cladosporium, Lasiodiplodia, Mortierella and Rhizopus. Forty-three isolates did not fruit in culture and were grouped into ten morphological types (Table 1).

The 202 isolates of yeasts were cultured from 48 samples of decaying leaves of Avicennia marina and seaweeds. The yeast isolates were grouped into 21 morphological types, of which four morphological types were identified using molecular phylogenetics of ribosomal genes.

3.2. Diversity of oleaginous thraustochytrids from the Saudi mangroves

Fifty-four isolates of thraustochytrids were cultured from the four mangrove sites namely: Al-Leith, Jeddah and Yanbu (Red Sea) and Syhat (Arabian Gulf). Isolated thraustochytrids were grouped into 22 strains. Isolated thraustochytrids belonged to two genera: Aurantiochytrium and Thraustochytrium

(Table 2). Thraustochytrids that produced high biomass and high levels of lipid were chosen for further study. Selected strains were grown on a larger volume of culture media and their lipid were extracted and the fatty acids and their derivatives were determined using GC/MS.

3.3. Molecular phylogenetics of yeasts and thraustochytrids

Four oleaginous yeast strains (AL–14, AL–15, AL–19 and AL–20) were selected and their taxonomical placements were determined based on LSU rDNA and ITS and were placed in Rhodotorula mucilaginosa and Hortaea werneckii (Table 1, Figures 1–3). DNA was extracted from the most promising thraustochytrid isolates (5 strains: AL–22, AL–23, SY–78, SY–85 and YB–39) and their taxonomical placements were determined based on ITS sequences. Thraustochytrids from the Arabian Gulf and the Red Sea formed a separate node basal to other known Aurantiochytrium species and might represent undescribed taxa (Figures 4-5).

3.4. Lipid profile of yeasts and thraustochytrid strains

Two oleaginous yeasts: Hortaea werneckii (Horta) Nishim. & Miyaji (AL–19) and Rhodotorula mucilaginosa (A. Jörg.) F.C. Harrison (AL–14) and four Aurantiochytrium strains: AL–22, AL–23, SY–78 and SY–85 produced high dry weight ranged between 32 and 49.3 g/L of which 35.2–62 % lipid. These promising results can be improved by changing the growth conditions using different combinations of different C/N ratio. Fatty acid profiles of the six strains on GC/MS were determined. Palmitic acid was the major fatty acid in the lipid of the four thraustochytrid isolates and ranged between 5.71 to 82% of the total fatty acids, while it was not recorded from the lipid of the two yeast isolates, 9-Octadecenamide, (Z)- was the major fatty acid amide in the lipid of the two isolates and two thraustochytid isolates and ranged between 26.94 and 56.63%, followed by 13-Docosenamide, (Z)- (20.44–34.99%) from the same four isolates. Other major lipid compounds were: Hexadecanamide (4.35–7.19 %), Cholestrol (7.24–15.07 %), Butylated Hydroxytoluene (3.46–15.76 %), Octadecanamide (3.95–7.9%), Phenol, 2-(1,1-dimethylethyl)-5-methyl- (1.78–10.33%) and Pentadecanoic acid (7.47%) (Tables 3).

4. Discussion

Palmitic acid was the major fatty acid in the four studied strains of thraustochytrids and ranged between 5.71 to 82.02% of the total fatty acids. The acid was previously reported in high levels from Aurantiochytrium species (Nagano et al., 2009; Ramos et al., 2009). Palmitic acid produced by thraustochytrids can be used to produce high quality biodiesel due to its high octane number, low iodine content and high oxidation stability. Genera of thraustochytrids were reported to accumulate commercially and biologically important fatty acids (Huang et al., 2003; Ward and Singh, 2005; Chang et al., 2014). The major fatty acids of thraustochytrids are palmitic acid C16, arachidonic acid C20:4, eicosapentaenoic acid C20:5, docosapentaenoic acid C22:5, and docosahexaenoic acid C22:6 (DHA) (Kobayashi et al., 2011). Among these fatty acids, palmitic acid has been reported to be potential alternative materials for microbial-derived biodiesel (Kobayashi et al., 2011). Velmurugan et al. (2021) studied the fatty acids composition of two strains of Aurantiochytrium cultured from Taiwan mangroves. Major fatty acids reported were the saturated acids: pentadecanoic (15:0), palmitic (C16:0), and unsaturated DHA (C22:6) which is consistent with previous results (Liu et al., 2014; Ludevese-Pascual et al., 2016; Jaritkhuan and Suanjit, 2018). Bai et al. (2022) isolated 58 thraustochytrid strains isolated from the coastal waters of Qingdao, China and studied their fatty acid profile. Isolated strains were phylogenetically affiliated with the genera: Botryochytrium, Oblongichytrium, Schizochytrium, Thraustochytrium, and Sicyoidochytrium. Palmitic acid was the most abundant fatty acid in the studied 58 strains and represented 7.90–37.12% of the total fatty acids.

Oleaginous yeast and thraustochytrid strains produced 9-Octadecenamide, (Z)- as the major fatty acid derivative (ranged between 26.94 and 56.63 % of the total fatty acids). 9-Octadecenamide, (Z)- (Oleamide) is the amid of Oleic acid and was first detected in human plasma and was shown to induce sleep in animals (Cravatt et al., 1995; Mckinney and Cravatt, 2005). Oleamide can be used for the treatment of mood and sleep disorders (Mechoulam et al., 1997). The third major fatty acid derivative was 13-Docosenamide, (Z)- (ranged between 20.44 and 34.99 % of the total fatty acids) and recorded from both yeasts and thraustochytrids. 13-Docosenamide is the amide of docosenoic acid (Erucic acid) and it was first identified from cerebrospinal fluid of sleep-deprived cats and from cerebrospinal fluid of rats

and humans.[31] 13-Docosenamide causes reduced mobility and slightly lessened awareness in rats (Cravatt et al., 1995; Li et al., 2017). Both 9-Octadecenamide, (Z)- and 13-Docosenamide, (Z)- have antimicrobial and anticancer activities (Tayung et al., 2011; Sharma et al., 2019).

5.[1] Conclusion

Microbes (filamentous fungi, yeasts and thraustochytrids) isolated from four mangrove sites along the coasts of the Arabian Gulf and the Red Sea in Saudi Arabia were screened for their abilities to produce high level of lipids. Isolated fungi were grouped into 62 morphological types that include: 21 yeasts and 41 filamentous fungi. Also, fifty-four isolates of thraustochytrids were cultured from the four mangrove sites and were grouped into 22 strains. The 84 morphological strains isolated during the present study were tested for their abilities to produce high level of oil using Sudan Black B. Positive strains for oil production were further grown on a larger scale and the percentage of oil were determined using Sulfo-Phospho-Vanlin (SPV) method. Two oleaginous yeasts: Hortaea werneckii and Rhodotorula mucilaginosa and four Aurantiochytrium strains produced high dry weight ranged between 32 and 49.3 g/L of which 35.2–62 % lipid and their fatty acid profile were determined using GC/MS. Palmitic acid was the major fatty acid in the lipid of the four thraustochytrid isolates and ranged between 5.71 to 82% of the total fatty acids, while it was not recorded from the lipid of the two yeast isolates, 9-Octadecenamide, (Z)- was the major fatty acid amide in the lipid of the two yeast isolates and two thraustochytid isolates and ranged between 26.94 and 56.63%, followed by 13-Docosenamide, (Z)- (20.44–34.99%) from the same four isolates. Other major lipid compounds were: Hexadecanamide, Cholestrol, Butylated Hydroxytoluene, Octadecanamide, Phenol, 2-(1,1-dimethylethyl)-5-methyl and Pentadecanoic acid.

[62] Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgements

This project was funded by the National Plan for Science, Technology and Innovation (MAARIFAH), King Abdulaziz City for Science and Technology, Kingdom of Saudi Arabia, Award No. 2-17-01-001-0049.

Fig. 1. a–f Hortaea werneckii (AL–19) isolated from decaying leaves of Avicennia marina, Al-Leith mangroves, Red Sea. Variously shaped vegetative cells with or without buds and pseudo-hyphae. g–i Rhodotorula mucilaginosa (AL–14) isolated from decaying leaves of Avicennia marina, Al-Leith mangroves, Red Sea. g–i Vegetative cells with or without buds. Bars: a–i = 5 µm.

Fig. 2. Phylogenetic relationship of Hortaea werneckii strains (AL–19 and AL–20) isolated during the current study . Phylogenetic analyses based on the nucleotide sequences of the LSU rDNA placed the two strains among the other strains of the species. The maximum likelihood (ML) tree (-ln likelihood = 3611.05) was constructed in MEGA X (Kumar et al., 2018). Phylogenetic trees obtained from ML, maximum parsimony (MP) and Bayesian inference posterior probabilities (BYPP) were similar in topology. Bootstrap support on the nodes represents ML and MP ≥50%. Branches with a BYPP of ≥95% are in bold. The two sequences of Hortaea werneckii generated in this study are in green, previous strains of the species from Red Sea are in red.

Fig. 3. Phylogenetic relationship of Rhodotorula mucilaginosa strains (AL–14 and AL–15) isolated during the current study. Phylogenetic analyses based on the nucleotide sequences of the LSU rDNA placed the two strains among the other strains of the species. The maximum likelihood (ML) tree (-ln likelihood = 2318.03) was constructed in MEGA X (Kumar et al., 2018). The maximum parsimonious data set consisted of 29 taxa include: 18 sequences of Rhodotorula mucilaginosa strains, 4 sequences of other Rhodotorula, 5 sequences of other taxa of Sporidiobolaceae and two taxa belong to Chrysozymaceae (outgroup). Phylogenetic trees obtained from ML, maximum parsimony (MP) and Bayesian inference posterior probabilities (BYPP) were similar in topology. Bootstrap support on the nodes represents ML and MP ≥50%. Branches with a BYPP of ≥95% are in bold. The two sequences of Rhodotorula mucilaginosa generated in this study are in red.

Fig. 4. Aurantiochytrium spp. isolated from decaying leaves of Avicennia marina from Syhat mangroves. a–c Aurantiochytrium sp. (SY–78) Variously shaped sporangia. d–g Aurantiochytrium sp. (SY–85). d–e Variously shaped sporangia. f–g Zoospores. Bars: a–g = 5 µm.

Fig. 5. Phylogenetic relationship of oleaginous thraustochytrid strains (AL–22, AL–23, SY–78, SY–85 and YB–39) isolated during the current study from Al-Leith, Syhat and Yanbu mangroves. Phylogenetic analyses based on the nucleotide sequences of the ITS region placed the five strains in a well-supported node basal to other strains of the genus Aurantiochytrium. The maximum likelihood (ML) tree (-ln likelihood =1185.76) was constructed in MEGA X (Kumar et al., 2018). Phylogenetic trees obtained from ML, maximum parsimony (MP) and Bayesian inference posterior probabilities (BYPP) were similar in topology. Bootstrap support on the nodes represents ML and MP ≥50%. Branches with a BYPP of ≥95% are in bold. The newly generated sequences in this study are in red.

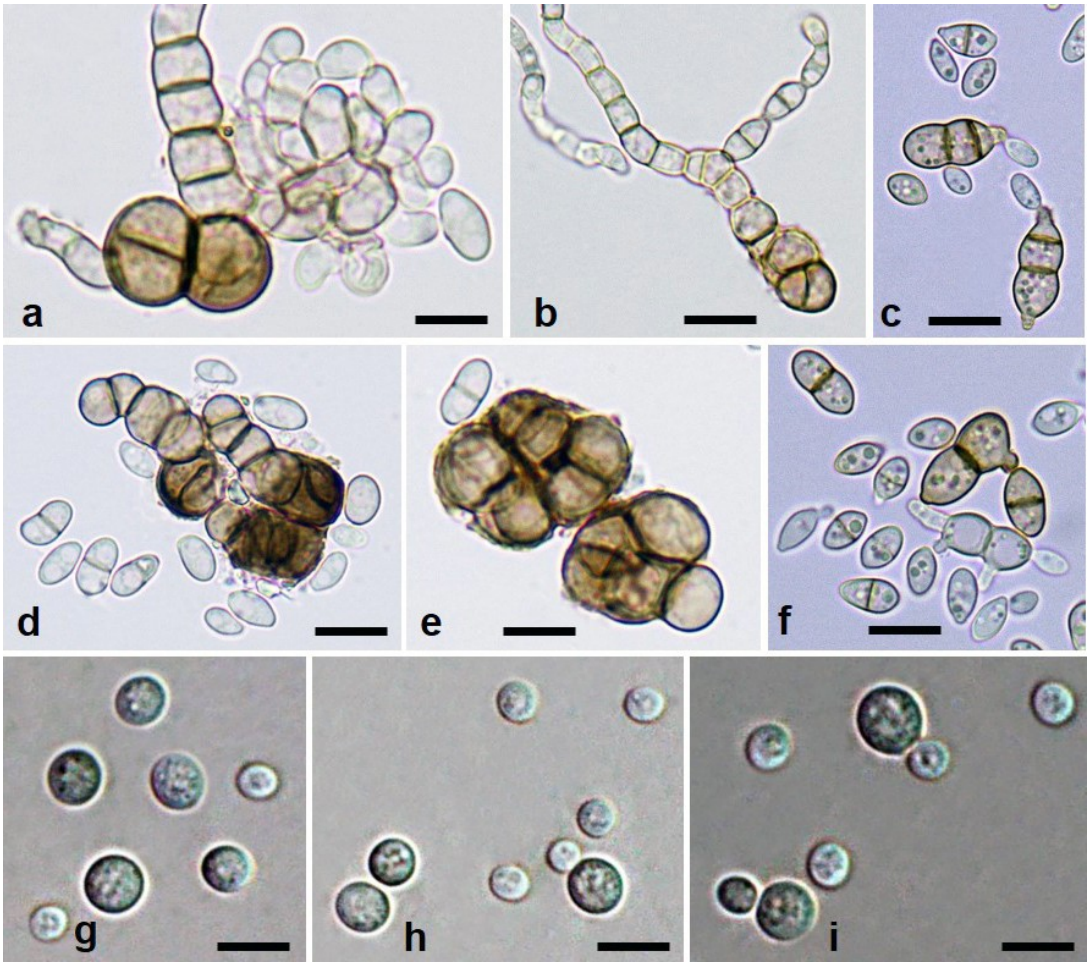

Fig. 1. a–f Hortaea werneckii (AL–19) isolated from decaying leaves of Avicennia marina, Al-Leith mangroves, Red Sea. Variously shaped vegetative cells with or without buds and pseudo-hyphae. g–i Rhodotorula mucilaginosa (AL–14) isolated from decaying leaves of Avicennia marina, Al-Leith mangroves, Red Sea. g–i Vegetative cells with or without buds. Bars: a–i = 5 µm.

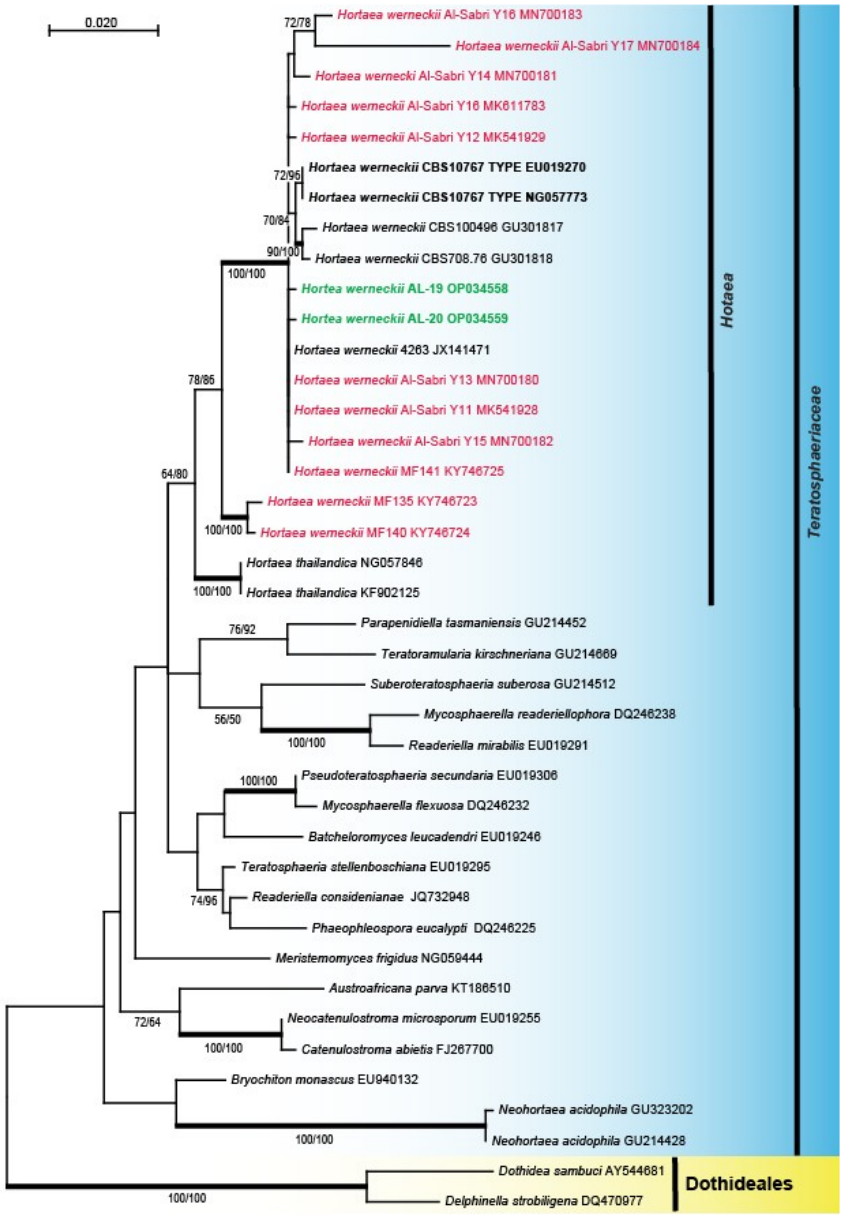

Fig. 2. Phylogenetic relationship of Hortaea werneckii strains (AL–19 and AL–20) isolated during the current study. Phylogenetic analyses based on the nucleotide sequences of the LSU rDNA placed the two strains among the other strains of the species. The maximum likelihood (ML) tree (-ln likelihood = 3611.05) was constructed in MEGA X (Kumar et al., 2018). Phylogenetic trees obtained from ML, maximum parsimony (MP) and Bayesian inference posterior probabilities (BYPP) were similar in topology. Bootstrap support on the nodes represents ML and MP ≥50%. Branches with a BYPP of ≥95% are in bold. The two sequences of Hortaea werneckii generated in this study are in green, previous strains of the species from Red Sea are in red.

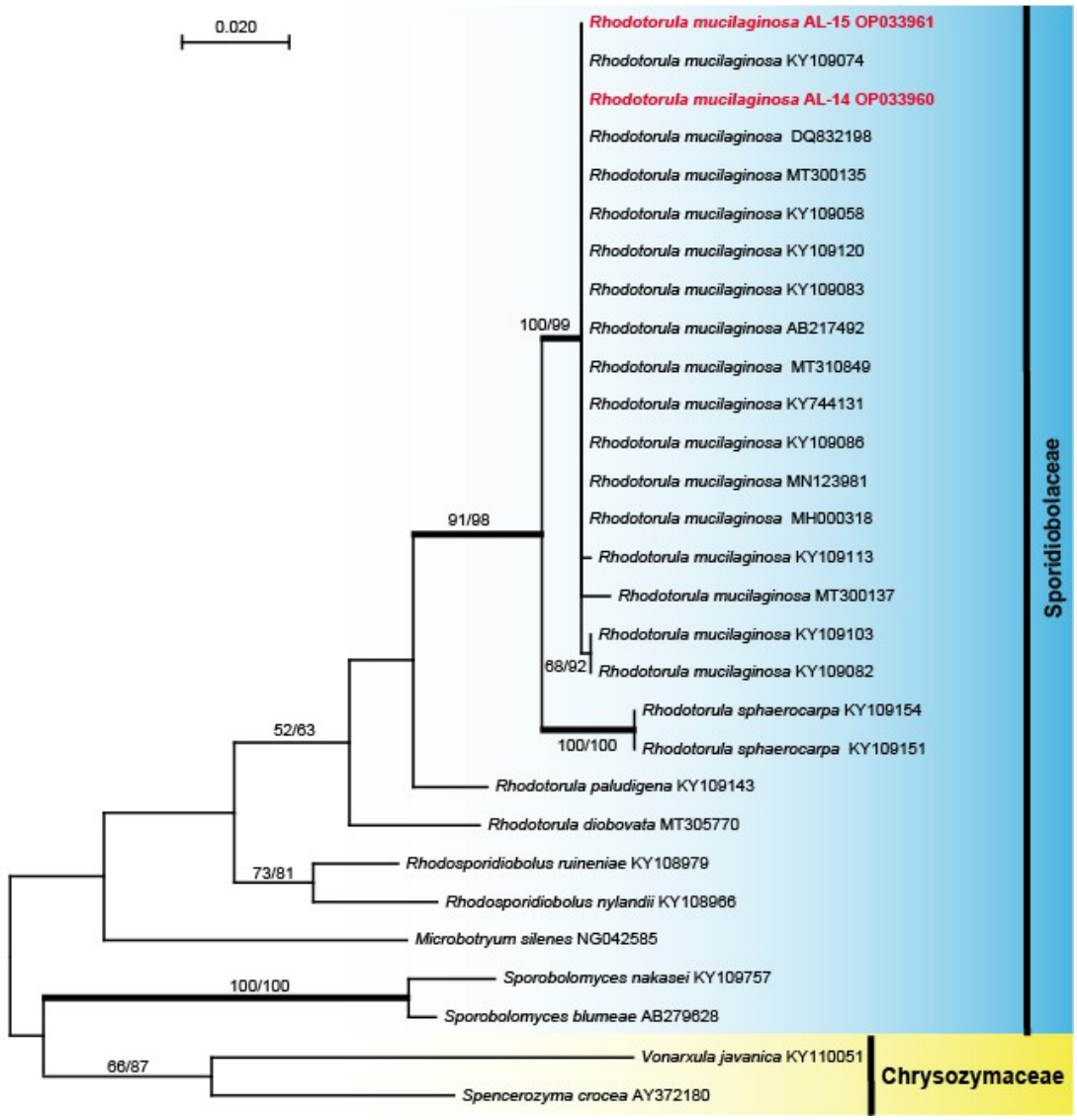

Fig. 3. Phylogenetic relationship of Rhodotorula mucilaginosa strains (AL–14 and AL–15) isolated during the current study. Phylogenetic analyses based on the nucleotide sequences of the LSU rDNA placed the two strains among the other strains of the species. The maximum likelihood (ML) tree (-ln likelihood = 2318.03) was constructed in MEGA X (Kumar et al., 2018). The maximum parsimonious data set consisted of 29 taxa include: 18 sequences of Rhodotorula mucilaginosa strains, 4 sequences of other Rhodotorula, 5 sequences of other taxa of Sporidiobolaceae and two taxa belong to Chrysozymaceae (outgroup). Phylogenetic trees obtained from ML, maximum parsimony (MP) and Bayesian inference posterior probabilities (BYPP) were similar in topology. Bootstrap support on the nodes represents ML and MP ≥50%. Branches with a BYPP of ≥95% are in bold. The two sequences of Rhodotorula mucilaginosa generated in this study are in red.

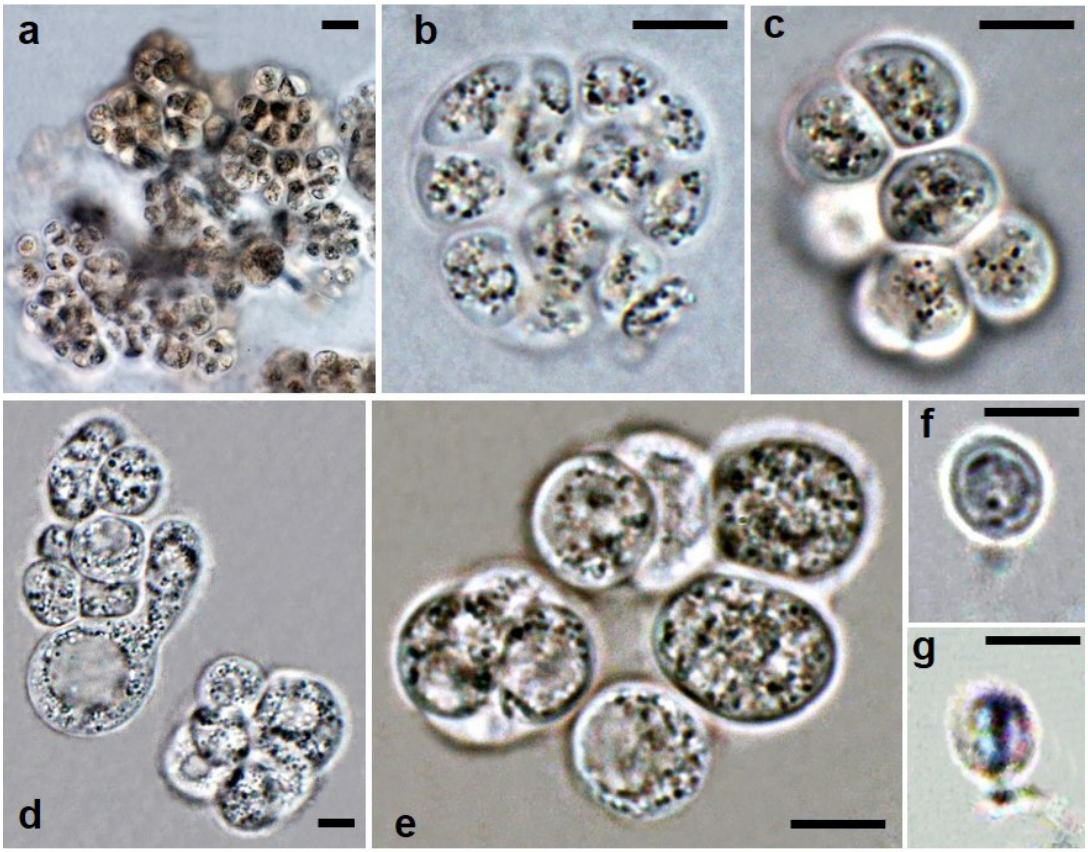

Fig. 4. Aurantiochytrium spp. isolated from decaying leaves of Avicennia marina from Syhat mangroves. a–c Aurantiochytrium sp. (SY–78) Variously shaped sporangia. d–g Aurantiochytrium sp. (SY–85). d–e Variously shaped sporangia. f–g Zoospores. Bars: a–g = 5 µm.

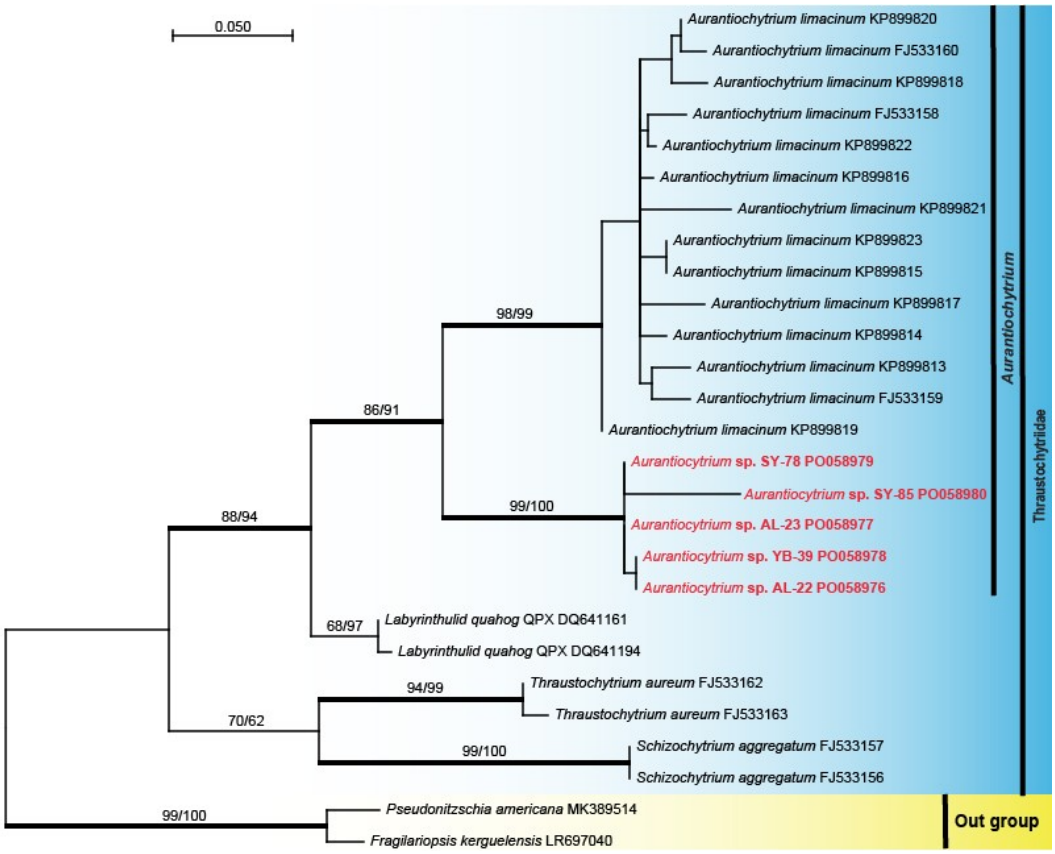

Fig. 5. Phylogenetic relationship of oleaginous thraustochytrid strains (AL–22, AL–23, SY–78, SY–85 and YB–39) isolated during the current study from Al-Leith, Syhat and Yanbu mangroves. Phylogenetic analyses based on the nucleotide sequences of the ITS region placed the five strains in a well-supported node basal to other strains of the genus Aurantiochytrium. The maximum likelihood (ML) tree (-ln likelihood =1185.76) was constructed in MEGA X (Kumar et al., 2018). Phylogenetic trees obtained from ML, maximum parsimony (MP) and Bayesian inference posterior probabilities (BYPP) were similar in topology. Bootstrap support on the nodes represents ML and MP ≥50%. Branches with a BYPP of ≥95% are in bold. The newly generated sequences in this study are in red.

Table 1 Filamentous fungi and yeasts isolated from Saudi mangroves: ;

Strain No.	Microorganism name	No. of isolates	Substrate	Dry weight (g/ L)	Lipid (% w/w)
#AL-14	Rhodotorula mucilaginosa (A. Jörg.) F.C. Harrison	4	Decaying thallus of Padina pavonica	36.2	35.2
#AL-15	R. mucilaginosa	4	Decaying thallus of Zostera marina	34.9	30.1
AL-16	Yeast	2	Decaying thallus of Sargassum		
AL-17	Yeast	2	Decaying thallus of Sargassum platycarpum		
AL-18	Yeast	1	Decaying thallus of Sargassum platycarpum		
#AL-19	Hortaea werneckii (Horta) Nishim. & Miyaji	10	Decaying leaves of Avicennia marina	42	46.2
#AL-20	H. werneckii	2	Decaying leaves of Avicennia marina	44.9	45
JD-11	Yeast	5	Decaying leaves of Avicennia marina		
JD-12	Yeast	5	Decaying leaves of Avicennia marina		
JD-13	Yeast	9	Decaying leaves of Avicennia marina		
JD-14	Sterile mycelium	7	Decaying leaves of Avicennia marina		
JD-15	Yeast	37	Decaying leaves of Avicennia marina		
JD-16	Aspergillus sp.	67	Decaying leaves of Avicennia marina		
JD-17	Yeast	5	Decaying thallus of Zostera marina		
JD-18	Aspergillus flavus Link	8	Decaying thallus of Zostera marina		
JD-19	Yeast	10	Decaying thallus of Zostera marina		
JD-20	Yeast	23	Decaying leaves of Avicennia marina		
JD-21	Penicillium citrinum Thom	15	Decaying leaves of Avicennia marina		
JD-22	Yeast	10	Decaying leaves of Avicennia marina		
JD-23	Yeast	12	Decaying leaves of Avicennia marina		
JD-24	Yeast	22	Decaying leaves of Avicennia marina		
JD-25	Sterile mycelium	9	Decaying leaves of Avicennia marina	42.7	19.25
JD-26	Yeast	11	Decaying leaves of Avicennia marina		
JD-27	Yeast	10	Decaying leaves of Avicennia marina		
JD-28	Sterile mycelium	8	Decaying leaves of Avicennia marina		
JD-29	Cladosporium sp.	12	Decaying thallus of Zostera marina		
JD-30	Yeast	11	Decaying leaves of Avicennia marina	;	;

Table 1 Cont.

JD-31	Penicillium sp.	6	Decaying leaves of Avicennia marina		
JD-32	Aspergillus terreus Thom	147	Sediment		
JD-33	Rhizopus sp.	2	Sediment	18.9	
JD-34	Mortierella sp.	6	Decaying leaves of Avicennia marina		
JD-35	Sterile mycelium	5	Decaying thallus of Sargassum platycarpum		
JD-36	Mortierella sp.	8	Sediment	23.1	
JD-37	Aspergillus sp.	21	Sediment		
JD-38	Aspergillus sp.	10	Decaying thallus of Sargassum platycarpum		
JD-39	Penicillium sp.	12	Decaying leaves of Avicennia marina		
#SY-69	Lasiodiplodia theobromae (Pat.) Griffon & Maubl.	3	Decaying leaves of Avicennia marina	48.2	34.1
#SY-70	Aspergillus sp.	7	Decaying leaves of Avicennia marina	43.1	48.23
SY-71	Rhizopus sp.	4	Decaying leaves of Avicennia marina	62.3	50.85
SY-72	Sterile mycelium	1	Decaying leaves of Avicennia marina		
SY-73	Sterile mycelium	1	Decaying wood of Avicennia marina		
SY-74	Penicillium sp.	3	Decaying leaves of Avicennia marina		
SY-75	Sterile mycelium	4	Decaying leaves of Zostera marina		
SY-76	Sterile mycelium	1	Decaying leaves of Avicennia marina		
YB-21	Yeast	7	Decaying leaves of Avicennia marina		
YB-22	Penicillium sp.	15	Decaying leaves of Avicennia marina		
YB-23	Sterile mycelium	2	Sediment		
YB-24	Penicillium sp.	15	Decaying thallus of Zostera marina		
YB-25	Penicillium sp.	21	Decaying thallus of Turbinaria ornata		
YB-26	Aspergillus sp.	6	Decaying thallus of Cystoseira myrica	21.6	
YB-27	Penicillium sp.	10	Decaying leaves of Avicennia marina		
YB-28	Penicillium sp.	9	Decaying leaves of Avicennia marina		
YB-29	Aspergillus sp.	13	Decaying thallus of Zostera marina		
YB-30	Aspergillus sp.	30	Sediment		
YB-31	Aspergillus sp.	25	Decaying pneumatophores of Avicennia marina	16.4	26.86
YB-32	Penicillium sp.	35	Decaying leaves of Avicennia marina	;	;

Table 1 Cont.

YB-33	Penicillium sp.	55	Crab shell	16.3	30.54
YB-34	Penicillium sp.	60	Sediment		
YB-35	Penicillium sp.	55	Sediment		
YB-36	Aspergillus niger Tiegh.	16	Decaying leaves of Avicennia marina		
YB-37	Sterile mycelium	5	Decaying leaves of Avicennia marina	7.1	
YB-38	Penicillium sp. 20	Decaying leaves of Avicennia marina		21.3	;

AL: Al-Leith mangroves, Al-Leith City, Re Sea, Saudi Arabia.

JD: Jeddah mangroves, Jeddah City, Red Sea, Saudi Arabia.

SY: Syhat mangroves, Dammam city, Arabian Gulf, Saudi Arabia.

YB: Yanbu mangroves, Yanbu City, Red Sea, Saudi Arabia.

#Supported by molecular data.

Studied strains in bold.

Table 2 Thraustochytrids isolated from Saudi mangroves:

Strain No.	Microorganism name	No. of isolates	Substrate	Dry weight (g/ L)	Lipid (% w/w)
AL-21	Aurantiochytrium sp.	3	Decaying leaves of A. marina		
#AL-22	Aurantiochytrium sp.	2	Decaying leaves of A. marina	46	62
#AL-23	Aurantiochytrium sp.	4	Decaying leaves of A. marina	32	44.8
AL-24	Thraustochytrium sp.	1	Decaying leaves of A. marina		
AL-25	Thraustochytrium sp.	2	Decaying leaves of A. marina		
AL-26	Aurantiochytrium sp.	2	Decaying leaves of A. marina	50.1	66.5
AL-27	Aurantiochytrium sp.	7	Decaying leaves of A. marina	43	52
AL-28	Aurantiochytrium sp.	1	Decaying leaves of A. marina	38	54.1
AL-29	Aurantiochytrium sp.	1	Decaying leaves of A. marina	43	57
AL-30	Aurantiochytrium sp.	4	Decaying leaves of A. marina		
JD-40	Aurantiochytrium sp.	6	Decaying leaves of A. marina	48.2	71.42
SY-77	Aurantiochytrium sp.	1	Decaying leaves of A. marina	16.1	38.3
#SY-78	Aurantiochytrium sp.	3	Decaying leaves of A. marina	32	44
SY-79	Aurantiochytrium sp.	1	Decaying leaves of A. marina	26.6	47.2
SY-80	Aurantiochytrium sp.	1	Decaying leaves of A. marina	21.8	39
SY-81	Aurantiochytrium sp.	3	Decaying leaves of A. marina	28	49
SY-82	Aurantiochytrium sp.	1	Decaying leaves of A. marina	13.4	36
SY-83	Aurantiochytrium sp.	4	Decaying leaves of A. marina		
SY-84	Aurantiochytrium sp.	2	Decaying leaves of A. marina	28.9	46.1
#SY-85	Aurantiochytrium sp.	1	Decaying thalli of Zostera marina	49.3	59.9
#YB-39	Aurantiochytrium sp.	3	Decaying leaves of A. marina	49.9	64.96
YB-40	Aurantiochytrium sp.	1	Decaying leaves of A. marina	52.8	60.39

AL: Al-Leith mangroves, Al-Leith City, Re Sea, Saudi Arabia.

JD: Jeddah mangroves, Jeddah City, Red Sea, Saudi Arabia.

SY: Syhat mangroves, Dammam city, Arabian Gulf, Saudi Arabia.

YB: Yanbu mangroves, Yanbu City, Red Sea, Saudi Arabia.

#Supported by molecular data.

Studied strains in bold.

Table 3 GC/MS analyses of fatty acids and their dervatives of promising strains:

Microbes/fatty acids (%)	Hortaea werneckii (AL-19)	Rhodotorula mucilaginosa (AL-14)	Aurantiochytrium sp. (AL-22)	Aurantiochytrium sp. (AL-23)	Aurantiochytrium sp. (SY-78)	Aurantiochytrium sp. (SY-85)
Palmitic acid ($C_{16}H_{32}O_2$)	-	-	5.71	7.52	71.92	82.02
9-Octadecenamide, (Z)- ($C_{18}H_{35}NO$)	49.68	56.63	37.73	26.94	-	-
13-Docosenamide, (Z)- ($C_{22}H_{43}NO$)	27.87	34.99	24.32	20.44	-	-
Hexadecanamide ($C_{16}H_{33}NO$)	7.06	7.19	6.51	4.35	-	-
Cholesterol ($C_{27}H_{46}O$)	-	-	7.24	15.07	-	-
Butylated Hydroxytoluene ($C_{15}H_{24}O$)	-	-	-	-	15.76	3.46
Octadecanamide ($C_{18}H_{37}NO$)	7.9	-	4.08	3.95	-	-
Phenol, 2-(1,1-dimethylethyl)-5-methyl- ($C_{11}H_{16}O$)	-	-	-	-	1.78	10.33
Pentadecanoic acid ($C_{15}H_{30}O_2$)	-	-	7.47	-	-	-
Stigmasterol ($C_{29}H_{48}O$)	-	-	2.23	4.36	-	-
1-Heptatriacotanol ($C_{37}H_{76}O$)	1.33	1.19	-	3.09	-	-
Methyl tetradecanoate ($C_{15}H_{30}O2$)	-	-	-	-	4.41	-

References

Abdel-Wahab, M.A., El-Samawaty, A.A.M., Elgorban, A.M., and Bahkali, A.H., 2021a. Fatty acid production of thraustochytrids from Saudi Arabian mangroves. Saudi J. Biol. Sci. 28, 855–864.

Abdel-Wahab, M.A., El-Samawaty, A.A.M., Elgorban, A.M., and Bahkali, A.H., 2021b. Thraustochytrids from the Red Sea mangroves in Saudi Arabia and their abilities to produce docosahexaenoic acid. Bot. Mar. 64, 489–501.

Abdel-Wahab, M.A., El-Samawaty, A.A.M., Elgorban, A.M., and Bahkali, A.H., 2022. Utilization of low-cost substrates for the production of high biomass, lipid and docosahexaenoic acid (DHA) using local native strain Aurantiochytrium sp. YB-05. J. King Saud Uni. Sci. 34, 102224.

Anschau, A., Caruso, C.S., Kuhn, R.C., Franco, T.T., 2017. Validation of the sulfo-phosphovanillin (spv) method for the determination of lipid content in oleaginous microorganisms. Braz. J. Chem. Eng. 34, 19–27.

AOAC, 2012. Official methods of analysis, Association of official analytical chemist. Washington D.C, USA.

Bai, M., Sen, B., Wen, S., Ye, H., He, Y., Zhang, X., Wang, G., 2022. Culturable diversity of thraustochytrids from coastal waters of Qingdao and their fatty acids. Mar. Drugs 20, 229.

Bellou, S., Moustogianni, A., Makri, A., Aggelis, S., 2012. Lipids containing polyunsaturated fatty acids synthesized by zygomycetes grown on glycerol. Appl. Biochem. Biotechnol. 166, 146–158.

Bongiorni, L., Pusceddu, A., Danovaro, R., 2005. Enzymatic activities of epiphytic and benthic thraustochytrids involved in organic matter degradation, Aquat. Microb. Ecol. 41, 299–305.

Bunyard, B.A., Nicholson, M.S., Royse, D.J., 1994. A systematic assessment of Morchella using RFLP analysis of the 28S rRNA gene. Mycologia 86, 762–772.

Carere, C.R., Sparling, R., Cicek, N., Levin, D.B., 2008. Third generation biofuels via direct cellulose fermentation. Int. J. Mol. Sci. 9, 1342–1360.

Chang, K.J.L., Nichols, C.M., Blackburn, S.I., Dunstan, G.A., Koutoulis, A., Nichols, P.D., 2014. Comparison of Thraustochytrids Aurantiochytrium sp., Schizochytrium sp., Thraustochytrids sp.,

and Ulkenia sp. for production of biodiesel, long-chain omega-3 oils, and exopolysaccharide. Mar. Biotechnol. 16, 396–411.

Chen, X.F., Huang, C., Xiong, L., Chen, X., Chen, Y., Maa, L.L., 2012. Oil production on wastewaters after butanol fermentation by oleaginous yeast Trichosporon coremiiforme. Bioresour. Technol. 118, 594–597.

Chtzifragkou, S., Fakas, M., Galiotou-Panayotou, M., Komaitis, G., Aggelis, G., Papanikolaou, S., 2010. Commercial sugars as substrates for lipid accumulation by Cunninghamella echinulata and Mortierella isabellina fungi. Eur. J. Lipid Sci. Technol. 112, 1048–1057.

Cravatt, B., Prospero-Garcia, O., Siuzdak, G., Gilula, N., Henriksen, S., Boger, D., Lerner, R. 1995. Chemical characterization of a family of brain lipids that induce sleep. Science 268, 1506–1509.

Demirbas, M.F., 2011. Biofuels from algae for sustainable development. Applied. Energy 88, 3473–3480.

Easterling, E.R., French, W.T., Hernandez, R., Licha, M., 2009. The effect of glycerol as a sole and secondary substrate on the growth and fatty acid composition of Rhodotorula glutinis. Bioresour. Technol. 100, 356–361.

Economou, C.N., Aggelis, G., Pavlou, S., Vayenas, D.V., 2011. Modelling of single-cell oil production under nitrogen limited and substrate inhibition conditions. Biotechnol. Bioeng. 108, 1049–1055.

Gupta, A., Barrow, C.J., Puri, M., 2012. Omega-3 biotechnology: thraustochytrids as a novel source of omega-3 oils, Biotechnol. Adv. 30, 1733–1745.

Folch, J., Lees, M., Stanley, G.H.S., 1957. A simple method for the isolation and purification of total lipids from animal tissues. J. Biol. Chem. 226, 497–509.

Hong, W.-K., Kim, C., Rairakhwada, D., Kim, S., Hur, B.-K., Kondo A, Seo, J.-W., 2012. Growth of the oleaginous microalga Aurantiochytrium sp. KRS101 on cellulosic biomass and the production of lipids containing high levels of docosahexaenoic acid, Bioprocess Biosyst. Eng. 35: 129–133.

Huang, J., Aki, Y., Yokochi, T., Nakahara, T., Honda, D., Kawamoto, S., Shigeta, S., Ono, K., Suzuki, O., 2003. Grouping newly isolated docosahexaenoic acid producing thraustochytrids based on

their polyunsaturated fatty acid profile and comparative analysis of 18S rRNA gene. Mar. Biotechnol. 5, 450–457.

Huelsenbeck, J.P., Ronquist, F., 2001. MRBAYES: Bayesian inference of phylogeny. Bioinformatics 17, 754–755.

Jaritkhuan, S., Suanjit, S., 2018. Species diversity and polyunsaturated fatty acid content of thraustochytrids from fallen mangrove leaves in Chon Buri Province, Thailand. Agric. Nat. Resour. 52, 24–32.

Johnson, M.B., Wen, Z., 2009. Production of biodiesel fuel from the microalga Schizochytrium limacinum by direct transesterification of algal biomass. Energy Fuels 23, 5179–5183.

Khot, M., Kamat, S., Zinjarde, S., Pant, A., Chopade, B., Ravikumar, A., 2012. Single cell oil of oleaginous fungi from the tropical mangrove wetlands as a potential feedstock for biodiesel. Microb. Cell Fact. 11, 71.

Kobayashi, T., Sakaguchi, K., Matsuda, T., Abe, E., Hama, Y., Hayashi, M., Honda, D., Okita, Y., Sugimoto, S., Okino, N., Ito, M., 2011. Increase of eicosapentaenoic acid in thraustochytrids through thraustochytrid ubiquitin promoter-driven expression of a fatty acid D5 desaturase gene. Appl. Environ. Microbiol. 77, 3870–3876.

Kumar, S., Stecher, G., Li, M., Knyaz, C., Tamura, K., 2018. MEGA X: Molecular Evolutionary Genetics Analysis across computing platforms. Mol. Biol. Evol. 35, 1547–1549.

Kyung, O.Y., Ju, J., Ahmad, B.R., Se, H.C., Seung, W.K., Chulhwan, P. 2013. Development of a Saccharomyces cerevisiae strain for increasing the accumulation of triacylglycerol as a microbial oil feedstock for biodiesel production using glycerol as a substrate. Biotechnol. Bioeng. 110, 343–347.

Li, M.-M., Zheng, J., Ling-Yun, S., Zhe-Shan, Q., Hai-Ling, Y., 2017. Antidepressant and anxiolytic-like behavioral effects of erucamide, a bioactive fatty acid amide, involving the hypothalamus–pituitary–adrenal axis in mice. Neurosci. Lett. 640, 6–12.

Liu, Y., Singh, P., Sun, Y., Luan, S., Wang, G., 2014. Culturable diversity and biochemical features of thraustochytrids from coastal waters of Southern China. Appl. Microbiol. Biotechnol. 98, 3241–3255.

Ludevese-Pascual, G., Pena, M.D., Tornalejo, J., 2016. Biomass production, proximate composition and fatty acid profile of the local marine thraustochytrid isolate, Schizochytrium sp. LEY7 using low-cost substrates at optimum culture conditions. Aquacult. Res. 47, 318–328.

McKinney, M. K., Cravatt, B. F. 2005. Structure and Function of Fatty Acid Amide Hydrolase. Annu. Rev. Biochem. 74, 411–432.

Mechoulam, R., Fride, E., Hanu, L., Sheskin, T., Bisogno, T., Di Marzo, V., Bayewitch, M., Vogel, Z., 1997. Anandamide may mediate sleep induction. Nature 389, 25–26.

Nagano, N., Taoka, Y., Honda, D., Hayashi, M., 2009. Optimization of culture conditions for growth and docosahexaenoic acid production by a marine thraustochytrid, Aurantiochytrium limacinum mh0186. JAOCS 58, 623–628.

Nylander, J.A.A., 2004. MrModeltest 2.2. Program distributed by the author. Evolutionary Biology Centre, Uppsala University.

Perrière, G., Gouy, M., 1996. WWW-query: an on-line retrieval system for biological sequence banks. Biochimie 78, 364–369.

Pant, D., Adholeya, A., 2010. Development of a novel fungal consortium for the treatment of molasses distillery wastewater. Environmentalist 30, 178–182.

Papanikolaou, S., Dimou, A., Fakas, S., Diamantopoulou, P., Philippoussis, A., Galiotou-Panayotou, M., 2011. Biotechnological conversion of waste cooking olive oil into lipid-rich biomass using Aspergillus and Penicillium strains. J. Appl. Mirobiol. 110, 1138–1150.

Peng, W., Huang, C., Chen, X., Xiong, L., Chen, X., Chen, Y.M. 2013. Microbial conversion of wastewater from butanol fermentation to microbial oil by oleaginous yeast Trichosporon dermatis. Ren. Energy 55, 31–34.

Ramos, M.J., Fernandez, C.M., Casas, A., Rodriguez, L., Perez, A. 2009. Influence of fatty acid composition of raw materials on biodiesel properties. Bioresour. Technol. 100, 261–268.

Ranjan, K.B. 2015. Endophytic fungi: prospects in biofuel production. Proc. Natl. Acad. Sci. India Sect. B. Biol. Sci. 85, 21–25.

Ratledge, C., 2004. Fatty acid biosynthesis in microorganisms being used for single cell oil production. Biochimie 86, 807–815.

Ronquist, F., Huelsenbeck, J.P., 2003. MRBAYES 3: Bayesian phylogenetic inference under mixed models. Bioinformatics 19, 1572–1574.

Rosillo-Calle, F., Cortez, L., 1998. Towards proalcohol II: a review of the Brazilian bioethanol programme. Biomass Bioenergy 14, 115–124.

Sergeeva, Y.E., Galanina, L.A., Andrianova, D.A., Feofilova, E.P., 2008. Lipids of filamentous fungi as a material for producing biodiesel fuel. Appl. Biochem. Microbiol. 44, 523–527.

Sharma, N., Sharma, V., Abrol, V., Panghal, A., Jaglan, S., 2019. An Update on Bioactive Natural Products from Endophytic Fungi of Medicinal Plants, in: Arora, D., Sharma, C., Jaglan S., Lichtfouse, E. (Eds.), Pharmaceuticals from Microbes. Springer, pp. 121–154.

Shene, C., Leyton, A., Esparza, Y., Flores, L., Quilodrán, B., Hinzpeter, I., Rubilar M (2010). Microbial oils and fatty acids: effect of carbon source on docosahexaenoic acid (c22:6 n-3, DHA) production by thraustochytrid strains. J. Soil Sci. Plant Nutr. 10, 207–216.

Subramaniam, R., Dufreche, S., Zappi, M., Bajpai, R., 2010. Microbial lipids from renewable resources: production and characterization. J. Ind. Microb. Biotechnol. 37, 1271–1287.

Tayung, K., Barik, B., Jha, D., Deka, D., 2011. Identification and characterization of antimicrobial metabolite from an endophytic fungus, Fusarium solani isolated from bark of Himalayan yew. Mycosphere 2, 203–213.

Thompson, J.D., Gibson, T.J., Plewniak, F., Jeanmougin, F., Higgins, D.G., 1997. The ClustalX windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucl. Acids Res. 25, 4876–4882.

Velmurugan, N., Sathishkumar, Y., Sonowal, S., Pang, K.L., Lee, Y.S., 2021. Characterization of cellular development and fatty acid accumulation in thraustochytrid Aurantiochytrium strains of Taiwan. Bot. Mar. 64, 477–487.

Venkata Subhash, G., Venkata Mohan, S., 2014. Lipid accumulation for biodiesel production by oleaginous fungus. Fuel 116, 509–515.

Venkata, M.S., Reddy, M.V., Chandra, R., Venkata Subhash, G., Devi, M.P., Srikanth, S., 2014. Bacteria for bioenergy: a sustainable approach towards renewability, biomass for sustainable applications. in: Gaspard, S., Ncibi, M.C. (Eds.), Pollution remediation and energy. RSC Publishers, Cambridge, pp. 251–289.

Ward, O.P., Singh, A., 2005. Omega-3/6 fatty acids: alternative sources of production. Process Biochem. 40, 3627–3652.

White, T.J., Bruns, T.D., Lee, S.B., Taylor, J.W., 1990. Analysis of phylogenetic relationships by amplification and direct sequencing of ribosomal DNA genes. in: Innis, M.A., Gelfand, D.H., Sninsky, J.J., White, T.J. (Eds.), PCR protocols: a guide to methods and applications. Academic, San Diego, pp. 315–322.

Yang, Y., Yan, M., Hu, B., 2014. Endophytic fungal strains of soybean for lipid production. Bioenerg. Res. 7, 353–361.

Yokochi, T., Honda, D., Higashihara, T., Nakahara, T., 1998. Optimization of docosahexaenoic acid production by Schizochytrium limacinum SR21, Appl. Microbiol. Biotechnol. 49: 72–76.

Yousuf, A., Sannino, F., Addorisio, V., Pirozzi, D., 2010. Microbial conversion of olive oil mill wastewaters into lipids suitable for biodiesel production. J. Agric. Food Chem. 58, 8630–8635.

Zheng, Y., Yu, X., Zeng, J., Chen, S., 2012. Feasibility of filamentous fungi for biofuel production using hydrolysate from dilute sulfuric acid pretreatment of wheat straw. Biotechnol. Biofuels. 50, 1–10.