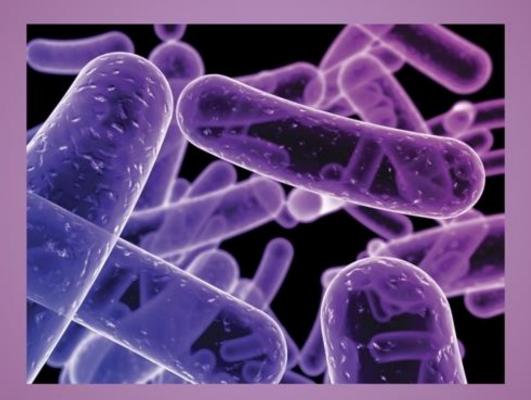


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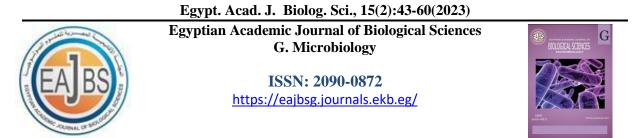


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GC-MS Analysis, Antifungal, and Antioxidant Activity of Rice Straw-Based Extract Produced by *Aspergillus tubingensis* AUMC 15759 in Solid State Fermentation

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ABSTRACT

Black aspergilli are excellent candidates for a variety of secondary metabolites. In this investigation, Aspergillus tubingensis AUMC 15759 produced certain bioactive compounds in solid-state fermentation (SSF) utilizing some agricultural wastes, namely bagasse, barley bran, bean hay, date palm leaves, flax seeds, orange peels, rice straw, soybean, and wheat bran. Rice straw extract yielded the highest inhibition zones of 14.1±0.2, 13.6±0.85, 12.0±0.9, and 15.0±0.9 mm, against Candida albicans, Candida glabrata, Candida krusei, and Saccharomyces cerevisiae. The rice straw extract demonstrated impressive antioxidant activity (%DPPH) that was nearly similar to that of ascorbic acid exhibiting IC₅₀ of 1.2±0.2 mg/ml. The liquid/liquid fractionation approach of the rice straw crude extract's liquid yielded five fractions, with the dichloromethane fraction being the most effective. GC-MS analysis disclosed the identification of nine substances linked to phenolic chemicals (3,4,5-trimethoxy phenol, 4-((1E)-3-Hydroxy-1-propenyl)-2-methoxyphenol, Phi. -Aspidinol, m-Aminophenylacetylene, and 1-Phenyl-2-propene), fatty acids (Palamitic acid and cis,cis-Linoleic acid), quinone derivative (2,6-Dimethyl-3-(methoxymethyl)-p-benzoquinone), and alkaloid (N-Didehydrohexacarboxyl-2,4,5-trimethylpiperazine). The dichloromethane fraction displayed potent antifungal activity. The MIC was 6.25 mg/ml, with inhibition zones of 14.0±0.4, 15.5±0.7, 14.0±0.4, and 14.2±0.2 mm against the investigated fungi, respectively. It also had the lowest IC_{50} (1.4±0.2) when compared to the remaining fractions of *n*- butanol (1.8 \pm 0.4), ethyl acetate (1.5 \pm 0.6), *n*-hexane (11.5 \pm 0.2), and water (13.5 \pm 1.1), or ascorbic acid (10.64 \pm 0.84) mg/ml. Finally, this fungus displayed antifungal and antioxidant activities when grown on agricultural wastes. It can be concluded that the tested strain of A. tubingensis displayed antifungal and antioxidant activities when grown on agricultural wastes, particularly rice straw.

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INTRODUCTION

Fungi are a diverse group of microorganisms that play a number of roles in human life. Antibiotics, antimicrobials, antioxidants, antiviral, anti-inflammatory, enzyme inhibitors, cytotoxic. hypercholesteremic, immunomodulators, and immunosuppressive medicines have primarily been examined in fungi (Naher et al., 2021; Conrado et al., 2022). Secondary metabolites, such as aromatic compounds, alkaloids, amino acids, fatty acids, phenolic compounds, and quinone derivatives have been recorded to be produced by fungi in several kinds of literature (Brambilla et al., 1988; Nishina et al., 1991; Cole et al., 2003; Leyden et al., 2007; Dhahir et al., 2012; Adedoyin et al., 2013; Zabka and Pavela, 2013; Evidente et al., 2014; Li et al., 2014; Dheeb, 2015; Kareem et al., 2015; Chandra and Arora, 2016; Gao et al., 2016; Mollavali et al., 2016; He et al., 2017; Pathak et al., 2018; Chen et al., 2021; Widjajanti et al., 2022).

Species of Alternaria, Aspergillus, Claviceps, Fusarium, and Penicillium are the most active fungi producing approximately 15,600 fungal metabolites (Sulvok et al., 2020). Black aspergilli are excellent candidates for various secondary metabolite aflatoxins, production, including N-Ps, fumonisins, cyclopiazonic acid, ophiobolins, and others. Many of these active compounds have remarkable biological properties, such as antibacterial, antioxidant, anticancer, antianti-HIV, and antitubercular hyperuric. properties (Choque et al., 2015; Siddiquee, 2018).

Each year, agriculture produces five billion metric tons of lignocellulosic biomass, which includes barley bran, barley hay, bean straw, date palm leaves, rice bran, rice husk, sugarcane bagasse, wheat bran, wheat straw, leftover fruits and vegetable wastes, corn cobs, cassava stems, peanut shells, coconut shells, leaves, and leftover cotton leaf scraps (Abou Hussein and Sawan, 2010; Khanh and Thanh, 2010; Ismail *et al.*, 2018; AL-Kolaibe *et al.*, 2021). Rice straw has a high potential as a biomass source since it is high in cellulose (39%), hemicellulose (22%), lignin (16%), and ash (18%) (Sarnklong *et al.*, 2010; Minu *et al.*, 2012), as well as high silica content (El Safty, 2020).

Consequently, this research was put forward in order to use some agricultural sustainable sources for the wastes as production of secondary metabolites. Therefore, the ability of Aspergillus tubingensis AUMC 15759 to create certain active metabolites that have antifungal and/or antioxidant activity, using the rice straw waste in solid-state fermentation was assessed.

MATERIALS AND METHODS 1. Strain Isolation and Identification:

The Aspergillus isolate used in this study was recovered from a soil sample close to the Sohag-Qena Road, Sohag Governorate, Egypt, using the dilution plate method (Harris and Sommers, 1968). Appropriate dilution of the soil suspension was transferred to Petri plates containing Czapek's-Dox agar (CzA). The plates were then incubated at 25°C for 10 days. The developed culture was then purified on CzA using the single spore isolation technique (Choi et al., 1999), and preserved in Assiut University, Mycological Centre's culture collection as AUMC 15759. This isolate was selected for evaluation of its ability to utilize some agricultural wastes to produce bio-active metabolites that may be beneficial as antifungal and/or antioxidant compounds.

2. Morphological Identification of the *Aspergillus* Isolate:

The Aspergillus isolate used in this study was morphologically identified based macroscopic its and microscopic on characteristics using some relevant references (Raper and Fennell, 1965; Moubasher, 1993). Growth rates of the new species were studied on Czapek's agar (CZ; (Raper and Fennell, 1965), malt extract agar (MEA; (Samson et al., 2010), Czapek's yeast Autolysate agar (CYA; (Pitt, 1979). Inoculations were made from spore suspensions prepared in a 0.2% agar and 0.05% Tween 80 solution (Samson et al., 2014). Plates were inoculated in a three-point

pattern using a micropipette and inoculum size of $1.0 \ \mu$ L/spot, and the plates were then incubated in the dark at 25°C for 7 days. The microscopic characteristics were examined from the MEA culture.

2.1. Molecular Identification of the *Aspergillus* Isolate:

For molecular identification of such isolate, DNA was extracted at the Molecular Biology Unit, Assiut University, Assiut, Egypt following CTAB method described by Moubasher *et al.* (2019). PCR was conducted at SolGent Co., Ltd. (Yuseong-Gu, 34014, Daejeon, South Korea), using SolGent EF (Al-Bedak and Moubasher, 2020), and the universal primer pair Bt2a and Bt2b were used for amplification of the *beta-tubulin* gene (Glass and Donaldson, 1995).

3. Phylogenetic Analysis:

Using the DNASTAR (version 5.05), a contiguous sequence of the Aspergillus isolate AUMC 15759 was produced. Sequences that were most similar to the Aspergillus isolate AUMC 15759's Betatubulin sequence, were all downloaded from the GenBank database. All sequences in this analysis were aligned by MAFFT (version 6.861b) (Katoh and Toh, 2010). The alignment gaps and weak uninformative characters were optimized by **BMGE** (Criscuolo and Gribaldo, 2010). MEGA X (version 10.2.6) was used to conduct the maximum-likelihood (ML) and maximumparsimony (MP) phylogenetic analyses (Kumar et al., 2018), and the robustness of the most parsimonious trees was evaluated by (Felsenstein, 1000 replications 1985). Utilizing Modeltest 3.7's Akaike information criterion (AIC), the optimum nucleotide substitution model for ML analysis was identified (Posada and Crandall, 1998). The resulting tree was edited and saved in TIF format (Al-Bedak et al., 2020).

4. Agricultural Wastes:

Nine agricultural wastes, namely bagasse (B), barley bran (BB), bean hay (BH), date palm leaves (DPL), flax seeds (FS), orange peels (OP), rice straw (RS), soybean (SB), and wheat bran (WB), were used in this study. All substrates were acquired from local markets in Assiut Governorate, Egypt. Prior to use, the wastes were prepared following Ramadan *et al.* (2023).

5. Solid-state Fermentation (SSF):

The agricultural wastes under test were separated into 10 gm portions and placed into 500 ml Erlenmeyer conical flasks individually. After that, citrate buffer (pH 5.0) was used to further wet the leftovers until they contained 80% moisture. A 5.0 ml spore suspension of *Aspergillus* sp. AUMC 15759, grown for seven days, was produced and added to each flask at a concentration of 1.5×10^8 spores/ml. The incubation period was seven days at a static temperature of 30°C.

6. Harvesting of the Crude Extracts:

Following the incubation time, the flask contents underwent a 48 h oven drying process at 60°C. The mycelial mat and solid substrate were homogenized and stirred in 50 ml of methanol for 2 h at 180 rpm in each flask. The clear supernatant was obtained after centrifugation (10,000 rpm at 4°C for 10 min). The methanol extract was evaporated (Heidolph: Model reddot winner 2020; Germany). The sample was lyophilized using a freeze drier (VirTis: Model 6 KBTES-55, NY; USA).

7. Determination of the Antifungal Activity:

Candida albicans AUMC 13415, Candida glabrata AUMC 13412, Candida krusei AUMC 13420, and Saccharomyces cerevisiae AUMC 13515 were obtained from Assiut University Mycological Centre (AUMC)'s culture collection for use in this assay. The antifungal activities of crude extracts, derived from Aspergillus sp. AUMC 15759's fermentation of nine agricultural wastes were evaluated using the well diffusion method (Magaldi et al., 2004; Valgas et al., 2007). The tested fungi were grown in Sabouraud's dextrose broth for 24 h before being used to inoculate 9-cm-diameter Petri plates with a spore suspension containing 1.5×10^8 spore/ml (= 0.5 McFarland standard solution). Dimethyl sulfoxide (DMSO) was utilized to make 20 mg/ml solutions of the nine extracts. A 50 µl of each extract solution (20 mg/ml) was separately transferred to a 5-mm well in the Sabouraud's dextrose agar (SDA). As positive antifungal reference drug, fluconazole (15 mg/ml) was used.

8. Antioxidant Activity:

The crude extracts were employed at concentrations of 20, 10, 5, 2.5, 1.25, 0.62, 0.31, and 0.15 mg/ml in methanol solution. A 40 µl aliquot of the sample-containing methanol solution was mixed with 3 ml of 0.004% freshly-prepared 2,2-diphenyl-1picrylhydrazyl (DPPH) radical (Yen and Duh, 1994). The mixture was then kept in the dark for 15 min. At 515 nm, the absorbance was determined (Model: Spectronic 1201, Milton Roy; Canada). Until the absorbance stabilized, the decline in absorbance was constantly observed, and data was gathered for 16 min at 1-minute intervals. Ascorbic acid was used as a standard. The 50% inhibitory concentration (IC_{50}) , the concentration required to inhibit DPPH radical by 50%, was estimated from graphic plots of the dose-response curve. The experiment was conducted in triplicates. The percentage inhibition (PI) of the DPPH radical was estimated using equation (1):

 $PI = (AC - AT) \times 100$ (1)

Where AC = control absorbance at zero time; AT = sample absorbance + DPPH at 16 min. 9. Liquid/liquid Fractionation of the Crude

9. Liquid/liquid Fractionation of the Crude Extracts:

Using the liquid-liquid fractionation technique (Colgrove and Svec, 1981), the crude extract powder (18 g) was suspended in

200 ml of distilled water in a separating funnel. 200 ml of each of n-hexane, dichloromethane, ethyl acetate, and *n*-butanol, were sequentially added to the extract. The mixture was vigorously shacked for 10 min, and the process was repeated three times. Each solvent fraction was then collected, pooled and dried under reduced pressure, yielding five fractions, namely *n*-hexane, dichloromethane, ethyl acetate, n-butanol, and aqueous fractions. The antifungal activity of the five fractions produced was tested at concentrations of 25, 12.5, 6.25, 3.75, 1.85, and 0.9 mg/ml. Nystatin (50 mcg/disc) was used as a positive control. Antioxidant activity was carried out as stated previously. The most active portion was analyzed using Chromatography-Mass Gas Spectroscopy (GC-MS).

10. GC-MS Analysis:

The Analytical Chemistry Unit Faculty of Science, (ACAL), Assiut University, Egypt, conducted this analysis to determine the active components of the dichloromethane fraction. A 0.5 gm of the tested fraction's residue was dissolved in 5 ml methanol and then centrifuged for 15 min (10,000 rpm at 5°C). A 10 μ l of the tested fraction was submitted to a GC-MS instrument (7890A-5975B: Thermo-Scientific GC/MS; type ISQ; USA). The following GC-MS conditions were used in this study (Table 1).

Table 1. Parameters and process conditions employed for the GC-MS analysis of the dichloromethane fraction produced by *Aspergillus* isolate AUMC 15759 utilizing rice straw in SSF.

Parameter	Specifications and process conditions				
Column type	HP-5MS Capillary Standard non-polar				
Column dimensions	$30 \text{ mm} \times 0.25 \text{ mm} \times 0.25 \mu\text{m}$ film				
Equilibration time	0.5 min				
Max temperature	280°C				
Oven program	at 120°C for 5 min, 30°C/min rose to				
	265°C for 25 min; then 50°C/min rose to				
	280°C for 5 min				
Run time	48 min				
Post run	260°C for 2 min				
Flow program	0.5 ml min for 10.9 min and then 1 ml min				
	for 30 min				
MS source	230–250°C				
MS Quad	150–200°C				

RESULTS 1. Morphological identification of the *Aspergillus* isolate AUMC 15759:

Aspergillus isolate AUMC 15759 showed identical morphological characteristics to Aspergillus tubingensis. The fungus has moderate growth and sporulation on MEA after 7 days at 25°C. Conidiophore pale brown, brown, smooth. Vesicle biseriate, spherical, 40-80 μ m. conidia globose to subglobose, 3-5 μ m. Sclerotia is absent (Fig. 1).

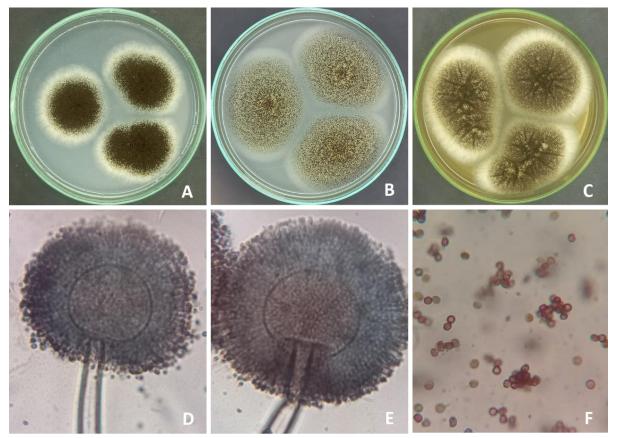


Fig. 1. *Aspergillus tubingensis* AUMC 15759. (A–C), Seven-day-old colonies on Cz, MEA, and CYA at 25°C (D–E), Conidiophore and biseriate conidial heads (F), Conidia.

2. Molecular Studies and Phylogenetic Analysis:

Based on a megablast search on NCBIs database using the β -tubulin gene sequence of the Aspergillus isolate AUMC 15759 in this study, the closest hits are Aspergillus tubingensis QF 05 [(GenBank accession number KY608858; identities = 542/543 (99.82%); Gaps = 1/543 (0%)], Aspergillus tubingensis NBRC 31125 and NBRC 4407 [(GenBank accession numbers LC573675 and LC573673; identities = 541/542 (99.82%); Gaps = 1/542 (0%)].

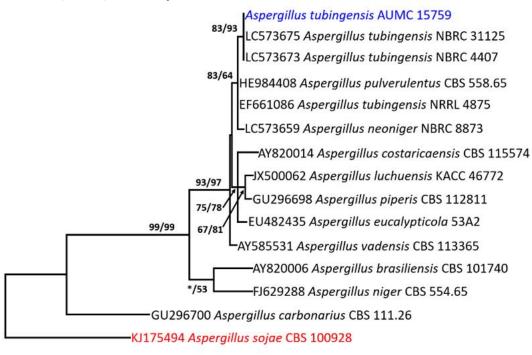
>Aspergillus tubingensis AUMC 15759's Beta-tubulin sequence:

CGGTGCTGCTTTCTGGTACGTA TTCACTGCCACTGGATTGGGGATGGA ACATCATCTCTCAAGCTATCTTAGCTT GAGTTCAGATGTTATCCATCGGGGAT ATAGCTACGGTTAAGAACACGTCTAA CAACTCAACAGGCAGACCATCTCTGG CGAGCACGGCCTTGACGGCTCCGGTG TGTAAGTACAACATTTTCACACCTCTC AATTGGTCAACAATGTGGAAAGGATT GGGTTTCCTGACGCGCAGGATAGTTA CAATGGCACCTCCGACCTCCAGCTGG AGCGCATGAACGTCTACTTCAACGAG GTTAGATCACACCGTCCCTGAGTTTTT TCACGACAATATCATCAATGTCCTGA

GTATGTCCCCCGTGCCGTCCTCGTCGA TCTCGAGCCCGGTACCATGGACGCCG TCCGTGCCGGTCCCTTCGGCCAGCTCT TCCGCCCCGACAACTTCGTCTTCGGCC AGTCCGGTGCTGGTAACAACTGGGCC AAGGGTCACTAACTGAGGGT

For molecular identification of the *Aspergillus* isolate AUMC 15759 in this study, β -tubulin-based phylogenetic analysis was conducted. The final dataset, which contained 15 sequences, produced 522 characters, of which 338 characters could align unambiguously, 101 were counted as variable (29.9% of complete), and 34 as informative characters (10.1%). Kimura 2-parameter modeled by using a discrete Gamma distribution (K2+G) was the perfect model to

represent the relationship between taxa. Maximum parsimony analysis produced 9 trees, the most parsimonious of which with a tree length of 211 steps, - log-likelihood of 1684.58, consistency index of 0.746667, retention index of 0.762500, and composite index of 0.569333, is presented to depict the evolutionary history of the *Aspergillus* isolate in this study (Fig. 2). In the phylogenetic analysis, the isolate in this study was grouped with two Aspergillus tubingensis strains, A. tubingensis NBRC 31125 and A. tubingensis NBRC 4407, endorsing a very strong support value of 83% ML/93% MP. As a result, the isolate in this study was identified as Aspergillus tubingensis.



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Fig. 2. The most parsimonious phylogenetic tree using a heuristic search (1000 replications) of *A. tubingensis* AUMC 15759 β -tubulin sequence (blue) compared to most similar β -tubulin sequences of *Aspergillus*: section Nigri. ML/MP \geq 50% are indicated close to respective nodes. The tree is rooted to *Aspergillus sojae* CBS 100928 as out-group (red).

3. Production of Secondary Metabolites by *Aspergillus tubingensis* AUMC 15759 Utilizing Agricultural Wastes:

Rice straw's crude extract was the most effective compared to the remaining

extracts exhibiting the highest inhibition zones of 14.1 ± 0.2 , 13.6 ± 0.85 , 12.0 ± 0.9 , and 15.0 ± 0.9 mm against the four tested fungi, *C. albicans, C. glabrata, C. krusei* and *S. cerevisiae*, respectively (Table 2 and Fig. 3).

 Table 2. Antifungal activity (mean±SD; n=3), represented in mm of inhibition zones, of the crude extracts of different agricultural wastes fermented by *A. tubingensis* AUMC 15759 in SSF. The antifungal drug nystatin was used as a positive control.

	Inhibition zone (mm)							
Produced extracts	C. albicans	C. glabrata	C. krusei	S. cerevisiae				
Bagasse	13.0±0.6	-	-	12.5 ± 0.4				
Barley bran	-	-	-	-				
Bean hay	-	-	-	14.0±0.7				
Date palm leaves	143±0.4	-	-	-				
Flaxseeds	-	-	-	-				
Orange peels	-	-	-	-				
Rice straw	14.1±0.2	13.6±0.8	12.0±0.9	15.0±0.9				
Soybean	-	9.5 ± 0.7	9.6±0.4	-				
Wheat bran	13.5±0.7	12.6±0.5	11.9±0.1	-				
Antifungal (Nystatin)	40.0±1.1	27.0±0.9	17.5±0.7	37.5±0.6				
A		B						
E		F	G	H				
			K	O O O				
		N		P				

Fig. 3. Antifungal activity of the crude extracts of different agricultural wastes fermented by *A. tubingensis* AUMC 15759 in SSF. (A–D), *C. albicans*; (E–H), *C. glabrata*; (I–L), *C. krusei*; and (M–P), *S. cerevisiae*.

4. Antioxidant Activity of Agricultural Wastes' Crude Extracts Produced by *A. tubingensis* AUMC 15759 in SSF:

used in this study, were examined. Rice straw produced the most powerful antioxidant activity exhibiting IC_{50} of 1.2 ± 0.4 mg/ml (Figs. 4-5).

The antioxidant potential of different extracts derived from the agricultural wastes,

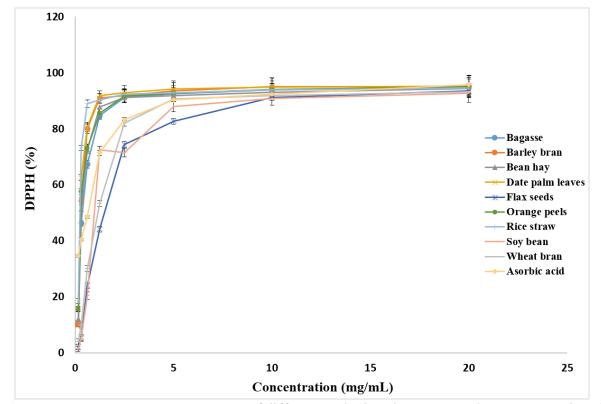


Fig. 4. Antioxidant activity (% DPPH) of different agricultural wastes' crude extracts produced by *A. tubingensis* AUMC 15759 in SSF compared to ascorbic acid as standard.

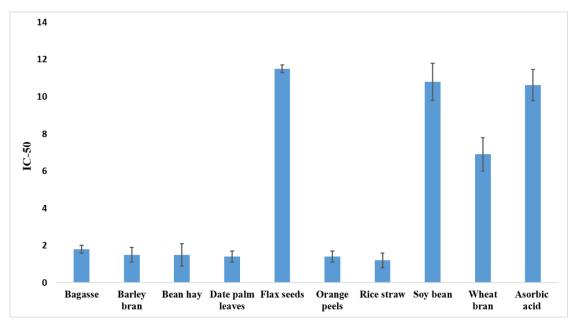


Fig. 5. IC₅₀ of different agricultural wastes' crude extracts produced by *A. tubingensis* AUMC 15759 in SSF compared to ascorbic acid as standard.

5. Fractionation of the Rice Straw Crude Extract:

It was determined whether the fractions obtained using *n*-hexane, dichloromethane, ethyl acetate, *n*-butanol and water had any antifungal properties. The four examined fungi—*C. albicans*, *C. glabrata*, *C. krusei*, and *S. cerevisiae*—were all unaffected

by aqueous fraction, whereas the fraction obtained by dichloromethane was the strongest one in terms of antifungal activity. The concentration of 6.25 mg/ml was the MIC exhibiting 14.0 ± 0.4 , 15.5 ± 0.7 , 14.0 ± 0.4 , and 14.2 ± 0.2 mm inhibition zone against the tested fungi, respectively (Fig. 6 and Table 3).

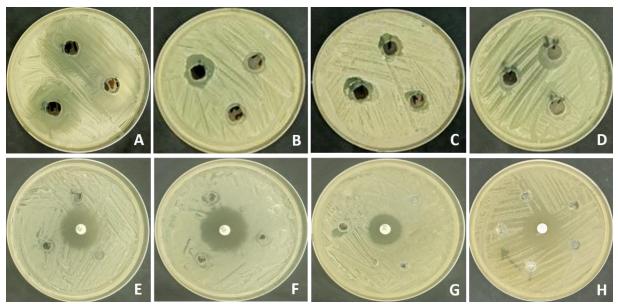


Fig. 6. The antifungal potential of the dichloromethane fractions obtained by liquid-liquid fractionation technique on Rice straw extract (A–D), *C. albicans, C. glabrata, C. krusei*, and *S. cerevisiae*, respectively. (E–H), Effect of nystatin on the tested fungi *C. albicans, C. glabrata, C. krusei* and *S. cerevisiae*, respectively.

Table 3. The antifungal activity of the fractions harvested from rice straw extract produced byA. tubingensis AUMC 15759 in SSF compared to nystatin as a positive control.

	C. albicans				C. glabrata				C. krusei				S. cerevisiae			
Fractions	25	12.5	6.25	3.75	25	12.5	6.25	3.75	25	12.5	6.25	3.75	25	12.5	6.25	3.75
	mg/mL	mg/mL	mg/mL	mg/mL	mg/mL	mg/mL	mg/mL	mg/mL	mg/mL	mg/mL	mg/mL	mg/mL	mg/mL	mg/mL	mg/mL	mg/mL
Hexane	-	-	-	-	15.0±0.7	14.0±0.3	13.0±0.3	-	14.0±0.7	13.5±0.2	13.0±0.1	-	14.1±0.7	13.2±0.8	13.1±0.3	-
Dichloromethane	30.0±0.3	28.0±0.2	14.0±0.4	-	16.5±0.5	16.0±0.6	15.5±0.7	-	16.0±0.2	15.0±0.1	14.0 ± 0.4	-	15.2±0.2	14.9±0.1	14.2±0.2	-
Butanol	-	-	-	-	15.0±0.5	14.0±0.9	13.5±0.4	-	15.5±0.3	15.0±0.1	14.5±0.4	-	21.0±0.2	16.0±0.1	15.0±0.3	-
Ethyl acetate	10.0±0.1	-	-	-	13.5±0.4	13.1±0.7	13.0±0.4	-	13.0±0.1	12.9±0.2	12.5±0.4	-	18.5	18.0±0.3	16.9±0.4	-
Aqueous	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Nystatin	27.0±0.3			25.0±0.7			30.2±0.5			33.2±0.9						

6. Antioxidant Activity:

The dichloromethane fraction showed remarkable antioxidant activity of 95.0% of DPPH activity, which is almost similar to that of ascorbic acid (95.6%). The fractions of nbutanol, ethyl acetate, n-hexane and aqueous showed a narrower spectrum of DPPH activity ranging from 90% to 93% (Fig. 7). Dichloromethane fractions exhibited the lowest IC₅₀ (1.4±0.2) compared to the remaining fractions of *n*- butanol (1.8±0.4), ethyl acetate (1.5±0.6), *n*-hexane (11.5±0.2), aqueous (13.5±1.1), and ascorbic acid (10.64±0.84) mg/ml (Fig. 8).

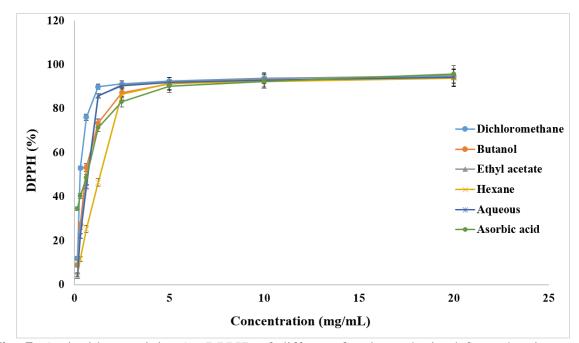


Fig. 7. Antioxidant activity (% DPPH) of different fractions obtained from the rice straw extract produced by *A. tubingensis* AUMC 15759 in SSF compared to ascorbic acid as standard.

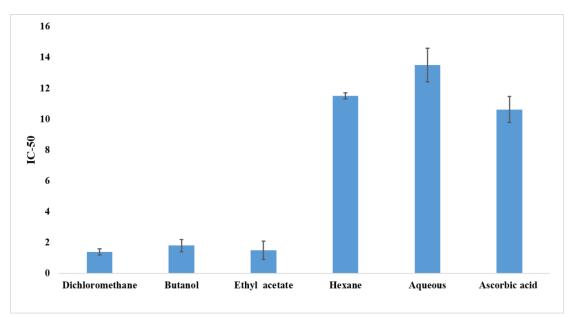


Fig. 8. IC_{50} of different fractions obtained from the rice straw extract produced by *A*. *tubingensis* AUMC 15759 in SSF compared to ascorbic acid as standard.

7. GC-MS Analysis:

The GC-MS analysis of the dichloromethane fraction (the most active fraction) was carried out for the detection of its components that have antifungal and/or antioxidant activities. The current results revealed the identification of nine peaks (Fig. 9), based on retention time, molecular weight, and fragmentation pattern of the most

prominent chemicals. The most prevalent compounds were five phenolic compounds (3,4,5-trimethoxy phenol, 4-((1E)-3-Hydroxy-1-propenyl)-2-methoxyphenol, Phi. -Aspidinol, m-Aminophenylacetylene, and 1-Phenyl-2-propene) which comprised 50% of the total and two fatty acids (Palamitic acid and cis,cis-Linoleic acid) constituted 20%. Quinone derivatives (2,6-Dimethyl-3(methoxymethyl)-p-benzoquinone), and alkaloids (N-Di-dehydrohexacarboxyl-2,4,5trimethylpiperazine) were also detected comprising 10% each. The detected compounds were found to have antioxidants, antibacterial, cytotoxic, antitubercular, antifungal, anti-acne, and anti-inflammatory activities (Table 4).

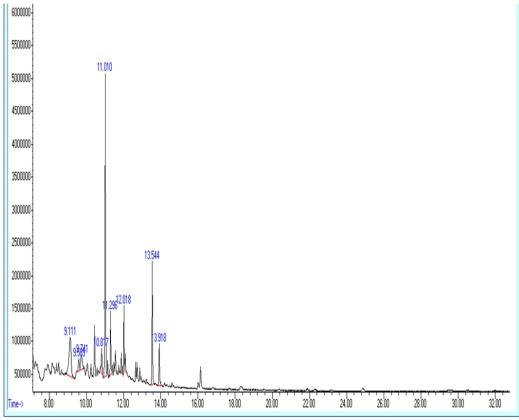


Fig. 9. GC-MS chromatogram of the dichloromethane fraction produced by *Aspergillus tubingensis* AUMC 15759 in SSF.

Table 4. GC–MS spectral analysis of the chemical compounds detected in the dichloromethanefraction derived from the rice straw extract produced by Aspergillus tubingensis AUMC15759 in SSF.

RT (min)	Compound name	und name Compound Biological activity		Molecular weight	Molecular formula
9.596	2,6-Dimethyl-3-(methoxymethyl)-	Quinone	Antioxidants, antibacterial,	180	$C_{10}H_{12}O_3$
	p-benzoquinone	derivatives	cytotoxic, antitubercular, antifungal		
9.743	3,4,5-trimethoxy phenol	Phenolic compound	Antioxidants, antifungal	184	$C_9H_{12}O_4$
10.438	4-((1E)-3-Hydroxy-1-propenyl)- 2- methoxyphenol	Phenolic compound	Antioxidants, antifungal	180	$C_{10}H_{12}O_3$
10.819	PhiAspidinol	Phenolic compound	Antibacterial, anti-acne, anti- inflammatory	224	$C_{12}H_{16}O_4$
11.016	N-Di-dehydrohexacarboxyl-2,4,5- trimethylpiperazine	Alkaloids	Antioxidants, antifungal	294	$C_{15}H_{22}N_2O_4$
11.299	Palamitic acid	Fatty acid	Cytotoxicity, antioxidant, antimicrobial	256	C16H32O2
12.018	cis,cis-Linoleic acid	Fatty acid	Cytotoxicity, antioxidant, antimicrobial	280	C ₁₇ H ₃₀ O ₂
13.549	m-Aminophenylacetylene	Phenolic compound	Antioxidants, antifungal	117	C ₈ H ₇ N
13.918	1-Phenyl-2-propene	Phenolic compound	Antioxidants, antifungal	150	C ₉ H ₁₀ S

DISCUSSION

Five billion metric tons of agricultural wastes, including wheat bran, cotton leaf scraps, sugarcane bagasse, rice bran, rice straw, and fruit and vegetable waste, are produced from annually agriculture worldwide. About half of the plant matter consists of lignocellulose, which is the most abundant green organic matter on earth (Singh et al., 2012). It is made up of noncovalent and covalent connections holding cellulose (35–50%), hemicellulose (20–35%), and lignin (15-25%) in close proximity to one another (Limayem and Ricke, 2012). Therefore, it is crucial to transform these wastes into beneficial products with industrial and commercial value while also minimizing their detrimental impact on the environment (Wang et al., 2016; AL-Kolaibe et al., 2021). The most effective use of agricultural output requires an integrated and sustainable strategy. Rice straw contains significant amounts of cellulose (39%), hemicellulose (22%), lignin (16%), and ash (18%), and it has a high potential as a biomass source (Sarnklong et al., 2010; Minu et al., 2012; El Safty, 2020).

Fungi have been extensively studied for the production of several extracellular metabolites such as antibiotics, antimicrobials, antioxidants, antiviral, anti-inflammatory, enzyme inhibitors, cytotoxic, hypercholesteremic, immunomodulators, and immunosuppressive medications (Choque et al., 2015; Siddiquee, 2018; Naher et al., 2021; Conrado et al., 2022; Ramadan et al., 2023). Thus, in this study, A. tubingensis AUMC 15759 was used to ferment nine agricultural under solid-state fermentation wastes conditions to identify which of them is deemed a valuable substrate for the synthesis of bioactive metabolites. The crude methanol extract of rice straw was shown to be the most effective in terms of antifungal and antioxidant properties. It showed a significant positive impact on the tested fungi, C. albicans, C. glabrata, C. krusei, and S. cerevisiae, over the remaining crude extracts.

The liquid/liquid fractionation of rice straw's crude extract resulted in five different

fractions, the most effective of which was the dichloromethane fraction in terms of antifungal activity, and it showed remarkable antioxidant activity of 95.0%, which was almost identical to that of ascorbic acid (95.6%). Based on the retention time, molecular weight, and fragmentation pattern of the most significant compounds, the current results revealed the identification of five phenolic chemicals (3,4,5-trimethoxy 4-((1E)-3-Hydroxy-1-propenyl)-2phenol, methoxyphenol, Phi.-Aspidinol, m-Aminophenylacetylene, and 1-Phenyl-2propene), which accounted for 50%, and two fatty acids (Palamitic acid and cis,cis-Linoleic acid) accounted for 20%, were detected. Ouinone derivative (2,6-Dimethyl-3-(methoxymethyl)-p-benzoquinone), and alkaloid (N-Di-dehydrohexacarboxyl-2,4,5trimethylpiperazine) were also found comprising 10% each. Fungi have been found to create secondary metabolites such as aromatic chemicals, alkaloids, amino acids, fatty acids, phenolic compounds, and quinone derivatives (Brambilla et al., 1988; Nishina et al., 1991; Cole et al., 2003; Leyden et al., 2007; Dhahir et al., 2012; Adedoyin et al., 2013: Zabka and Pavela, 2013: Evidente et al., 2014; Li et al., 2014; Dheeb, 2015; Kareem et al., 2015; Chandra and Arora, 2016; Gao et al., 2016; Mollavali et al., 2016; He et al., 2017; Pathak et al., 2018; Chen et al., 2021; Widjajanti et al., 2022). Species of Alternaria, Aspergillus, Claviceps, Fusarium, and Penicillium are the most active fungi producing approximately 15,600 fungal metabolites (Sulyok et al., 2020).

The components of the dichloromethane fraction obtained in this study were found to have an effect on the examined fungi, C. albicans, C. glabrata, C. krusei, and S. cerevisiae. Regarding the active metabolites produced by A. tubingensis, the active metabolite biosynthesized by A. AHS4, anofinic acid (2,2tubingensis dimethyl-2H-1-benzopyran-6-carboxylic acid), was isolated from ethyl acetate fraction. It had potent antibacterial activity against Pseudomonas aeruginosa, Staphylococcus aureus, Escherichia coli, Candida albicans, and Bacillus subtilis, which are all human pathogenic microorganisms. A. tubingensis has been also documented to excrete asperazine, funalenone, malformins, naphthoaurasperone γ-pyrones (including B), pyranonigrin A, tensidol A & B, (nigragillin) (Samson et al., 2007). The liquid culture of Chaetomium globosum showed potent in vitro antibacterial activity against Bacillus subtilis, Escherichia coli and Pseudomonas fluorescens. It also recorded significant antifungal activity against Candida albicans, Fusarium solani, F. oxysporum, Rhizoctonia solani and Pythium ultimum (Awad et al., 2014).

On the other hand, the fungus has also been reported to transform deoxynivalenol (He *et al.*, 2008), cause keratitis in humans (Kredics *et al.*, 2009), degrade the polyurethane polyester (Khan *et al.*, 2017), produce ochratoxin A and zearalenone on sorghum grains (Lahouar *et al.*, 2017), cause primary skin infection (Frías-De-León *et al.*, 2018), and pomegranate fruit rot in China (Guo *et al.*, 2021).

The dichloromethane fraction showed 95.0% of DPPH activity, which almost similar to that of ascorbic acid (95.6%), and it exhibited the lowest IC₅₀ (1.4±0.2) compared to the remaining fractions of *n*- butanol (1.8±0.4), ethyl acetate (1.5±0.6), *n*-hexane (11.5±0.2), aqueous (13.5±1.1), and ascorbic acid (10.64±0.84) mg/ml. The petroleum ether and ethyl acetate extracts of the liquid culture of *Chaetomium globosum* showed potent *in vitro* antioxidant activity, and the ethyl acetate extract showed the presence of prenisatin, chrysophanol, chrysazin, **DEFEDENCIES**

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chaetoviridin A and B (Awad *et al.*, 2014). Finally, utilizing agricultural wastes by this fungus demonstrated antifungal and antioxidant activity. More research is required before it can be applied in agriculture and/or medicine.

Conclusion

Aspergillus tubingensis AUMC 15759 utilizes agricultural wastes to produce some bioactive metabolites in SSF. Rice straw produced the most active crude extract in terms of antifungal and antioxidant activity. The liquid/liquid fractionation technique resulted in five fractions, the most effective of which was the dichloromethane fraction. GC-MS analysis revealed the identification of nine compounds related to phenolic chemicals (5 compounds), fatty acids (2), quinone derivatives, and alkaloid (one compound each). The dichloromethane fraction displayed the highest antifungal against C. albicans, C. glabrata, C. krusei, and S. cerevisiae. It also showed remarkable antioxidant activity which was almost identical to that of ascorbic acid.

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