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A *Talaromyces* Fungal Species with Strong Antimicrobial Activity from Deception Island, Antarctica

(Spesies Kulat *Talaromyces* dengan Aktiviti Antimikrob Kuat dari Pulau Deception, Antartika)

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ABSTRACT

Deception Island is well-known for harboring highly diverse microbial communities due to its unique volcanic environment in Antarctica. Most studies focused on bacteria, and relatively little was known about the fungal species on this island. The present study was aimed to determine the antimicrobial production and nutrient utilization profiles of a soil fungus from Deception Island, designated as Im33. Our findings showed that the strain had maximum mycelial growth and sporulation on malt-extract agar (MEA) medium, but it demonstrated the strongest antimicrobial activity in yeast extract-malt extract broth (YMB) medium. Phylogenetic analysis of the internal transcribed spacer 1 and 2 regions showed that it is a species belonging to the genus *Talaromyces*. It was resistant to cycloheximide concentrations up to 1,000 mg/L and exhibited broad-spectrum antimicrobial activity against Gram-positive and Gram-negative test pathogens, as well as being able to utilize a variety of carbon sources. This is the first report of a *Talaromyces* species from Deception Island. The capability of the strain to produce broad-spectrum antimicrobial compounds and various enzymes indicated that Antarctic fungi, like their bacterial counterparts, have adopted various adaptation strategies to compete and survive in the extreme environment.

Keywords: Antarctic; antimicrobial resistance; enzymes; fungus; South Shetland Islands

ABSTRAK

Pulau Deception terkenal dengan kepelbagaian komuniti mikrob kerana persekitaran gunung berapinya yang unik di Antartika. Kebanyakan kajian tertumpu kepada bakteria dan spesies kulat di pulau ini tidak begitu diketahui. Kajian ini bertujuan untuk menentukan profil pengeluaran antimikrob dan penggunaan nutrien kulat tanah dari Pulau Deception, iaitu Im33. Penemuan kami menunjukkan bahawa strain ini mempunyai pertumbuhan miselia dan spora maksimum pada media agar-ekstrak malt (MEA), tetapi menunjukkan aktiviti antimikrob yang paling kuat dalam media ekstrak malt ekstrak yis (YMB). Analisis filogenetik bagi kawasan *spacer* 1 dan 2 yang tertranskripsi secara dalaman menunjukkan bahawa kulat ini tergolong dalam genus *Talaromyces*. Kulat ini tahan terhadap kepekatan sikloheksimida sehingga 1,000 mg/L dan menunjukkan aktiviti antimikrob spektrum luas terhadap patogen Gram-positif dan Gram-negatif, di samping dapat menggunakan pelbagai punca karbon. Ini merupakan laporan pertama spesies *Talaromyces* dari Pulau Deception. Keupayaan strain ini untuk menghasilkan sebatian antimikrob spektrum luas dan pelbagai enzim menunjukkan bahawa kulat Antartika, seperti bakteria lain, telah menggunakan pelbagai strategi penyesuaian untuk bersaing dan bertahan dalam persekitaran yang ekstrem.

Kata kunci: Antartika; enzim; kulat; Pulau Shetland Selatan; rintang antimikrob

INTRODUCTION

Terrestrial bacteria and fungi are the major sources of antimicrobial compounds and antibiotics that have medical applications. Antibiotics have been an effective antibacterial therapy to treat various diseases. However, in recent years, there has been an increase in multidrug-

resistant pathogens to the existing antibiotics (Davies & Davies 2010; Karaiskos et al. 2019). The matter has become worse due to the lack of new classes of antibiotics being discovered, and this has become a public health problem (Karaiskos et al. 2019). Hence, efforts have been made to look for novel antibiotics in recent years in pristine environments, including Antarctica (Lo Guidice, Bruni & Michaud 2007; Lo Giudice et al. 2007; Tomova et al. 2015; Wong et al. 2011).

Antarctic bacteria are known to produce antimicrobial compounds as a strategy to compete with other microbes for space and nutrients to survive in the harsh environment (Lo Guidice, Bruni & Michaud 2007; Lo Giudice et al. 2007; Wong et al. 2011). In Deception Island, numerous bacteria isolated from sediment and soil samples were detected to exhibit inhibitory effects against other bacteria and yeast (Cheah et al. 2015; Tomova et al. 2015). Deception Island is a member of the South Shetland Islands in Antarctica. Active volcanic eruptions on Deception Island have altered the landscape and created environments that are remarkably different from those found elsewhere in Antarctica, resulting in the development of highly diverse microbial communities (Ibáñez et al. 2003). Many bacteria and fungi have been isolated from Deception Island (Blanco et al. 2012; Cheah et al. 2015; Gesheva 2012). However, unlike bacteria, relatively little research attention has been paid to fungi in this habitat.

Fungi are well known for their ability to thrive at extremes of temperature, pH, nutrients, and ultraviolet radiation, as well as to survive in environments contaminated with heavy metals and pharmaceutical products (Svahn et al. 2015). Although they are abundantly found in the soils, wooden structures, and macroalgae on Deception Island (Furbino et al. 2014; Gesheva 2012; Held, Arenz & Blanchette 2011), information on their antimicrobial activities is scarce. Hence, this study was conducted to determine the antimicrobial production and to profile the nutrient utilization profiles of a soil fungus from Deception Island.

Materials and Methods

Strain isolation and maintenance

The fungal strain was isolated from a soil sample collected under rotten grass at Deception Island, Antarctica. The purified strain was maintained on yeast extract-malt extract agar (YMA) slant media at 28 °C and as glycerol suspensions (20%, v/v) at -80 °C.

Morphological characterization

Colony morphology of the strain was observed on Czapek yeast extract agar (CYA), lignocellulose agar (LCA), YMA, malt-extract agar (MEA), potato dextrose agar (PDA), and Sabouraud dextrose agar (SDA) (Sharma & Pandey 2010). Using a sterile cork borer, 6 mm plugs were removed from a 7-day old lawn culture, transferred in triplicates onto each agar, and incubated at 28 °C for 4 days. The conidiophore branching and conidial size, shape, and ornamentation were observed under a Hitachi S-3400N variable pressure scanning electron microscope (SEM) (Hitachi High-Technologies Co., Japan). A small amount of mycelium was mounted on an aluminum stub and directly viewed in VP mode. The microscope chamber was supplied with elevated gas pressure and the observation was carried out at low values of electron beam intensity (5.00 kV).

Molecular characterization

The DNA extraction protocol was according to Balmas et al. (2005) with minor modifications. A total of 0.5 g of lyophilized cells was crushed using a sterile glass rod. Subsequently, 1.5 mL of extraction buffer [50 mM Tris-hydrochloride (Tris-HCl), pH 8; 50 mM EDTA; and 2% sodium dodecyl sulphate (SDS)] was added and mixed several times. The sample was incubated with shaking at 68 °C for 30 min and centrifuged at maximum speed for 15 min. The supernatant was transferred to a new tube. An equal volume of phenol-chloroform was added, mixed, and centrifuged at maximum speed for 15 min. The aqueous layer was transferred to a new tube. An equal volume of chloroform: isoamyl alcohol was added and centrifuged at maximum speed for 15 min. The aqueous layer was transferred to a new tube and an equal volume of isopropanol was added. The sample was mixed by inverting several times and centrifuged at maximum speed for 15 min. After discarding the isopropanol, the pellet was air-dried at room temperature and resuspended in 80 µL of sterile MilliQ water.

The DNA sample was treated with 1 µL ribonuclease A (RNase A) (10 mg/mL) before being incubated at 37 °C for 30 min. Then, 0.1 volume of 3M sodium acetate (NaOAc) (pH 5.2) and 2.5 volumes of ice-cold 95% ethanol were added. The sample was incubated at -20 °C overnight and centrifuged at maximum speed for 10 min. The supernatant was discarded, and the pellet was washed twice with 70% ethanol, air-dried at room temperature, and resuspended in 80 µL of sterile MilliQ water. The DNA yield was assessed using 1% (w/v) agarose gel

electrophoresis followed by DNA quantification using the Nanovue™ Plus spectrophotometer (GE Healthcare, United Kingdom). The DNA samples were kept at -20 °C for further analysis.

ITS AMPLIFICATION

The internal transcribed spacer 1 and 2 (ITS1-5.8S-ITS2) regions were amplified using primers ITS1 and ITS4 as described by White et al. (1990) with slight modifications. The PCR reaction mixture consisted of 10 ng of genomic DNA, 1X PCR buffer, 1.5 mM $MgCl_2$, 200 µM dNTPs, 1.25 unit Taq polymerase (Promega, USA), 0.4 µM of each primer and sterile MilliQ water was added to a final volume of 25 µL. PCR was performed with an initial denaturation step at 95 °C for 5 min, followed by 30 cycles of 30 s at 95 °C, 30 s at 55 °C, 1 min at 72 °C for extension, and a final extension at 72 °C for 10 min in an Eppendorf C1000 Thermal Cycler (Eppendorf, Germany). The amplified PCR products were separated on 1 % (w/v) agarose gels stained with ethidium bromide (0.5 µg/mL) and using the Alpha Image gel documentation system (Alpha Innotech, USA). The band of interest was excised, purified using a QIAquick Gel Extraction kit (Qiagen, Germany), and sequenced using an automated sequencer (First BASE Laboratories, Malaysia).

SPECIES IDENTIFICATION AND PHYLOGENETIC ANALYSIS

The sequence was analyzed using BLASTn (Altschul et al. 1990) and the phylogenetic analysis was performed using the Molecular Evolutionary Genetics Analysis version 6.0 (MEGA6) software (Tamura et al. 2013). The Multiple Sequence Comparison by Log-Expectation (MUSCLE) algorithm of the MEGA package was used to align the ITS1-5.8S-ITS2 rDNA sequences obtained from the GenBank database (http://www.ncbi.nlm.nih.gov /genbank/). For the construction of a phylogenetic tree, a substitution model was generated using MEGA 6 (Tamura et al. 2013). All non-informative positions were eliminated. The analysis involved 97 nucleotide sequences with a total of 454 positions in the final dataset. The consensus phylogenetic tree was obtained by maximum likelihood (ML) analysis based on the Kimura 2-parameter model (Kimura 1980). The initial tree(s) for the heuristic search were automatically obtained by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with a superior log-likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.3477)). The rate variation model allowed for some sites to be evolutionarily invariable ([+I], 32.6128% sites). The tree topography was evaluated using bootstrap analysis of 1000 repetitions. The evolutionary history was also inferred using the Maximum Parsimony (MP) method. The most parsimonious tree with a length of 877 was used. The consistency index is 0.305455, the retention index is 0.758126, and the composite index is 0.262794 (0.231573) for all sites and parsimony-informative sites. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the common topology branches with the ML tree (Felsenstein 1985). The MP tree was obtained using the Subtree-Pruning-Regrafting (SPR) algorithm (Nei & Kumar 2000).

CYCLOHEXIMIDE SENSITIVITY TEST

The strain was spread in triplicates on YMA supplemented with different concentrations of cycloheximide (25 mg/L, 50 mg/L, 100 mg/L, 150 mg/L, 200 mg/L, and 1,000 mg/L). A cycloheximide-susceptible fungal strain was used as a positive control. The same procedure was repeated by spreading the strain on YMA without cycloheximide as a negative control. The plates were incubated at 28 °C for 5 days and the presence of any growth was observed.

PRODUCTION OF ANTIMICROBIAL COMPOUNDS IN DIFFERENT MEDIA

Strain Im33 was grown in 20 mL of CYA, LCA, YMA, MEA, PDA, and SDA liquid media with shaking at 28 °C for 7 days. Several colonies of *Escherichia coli* TOP10 were transferred to a tube of sterile saline until a 0.5 McFarland turbidity standard was achieved (OD_{625nm} = 0.08-0.13). The suspension was swabbed onto fresh Mueller-Hinton agar (MHA) and several wells were made on each agar using a sterile cork borer (7 mm in diameter). The 7-day old broth cultures were centrifuged at 10,000 rpm for 10 min. One hundred microliters of each supernatant were aliquoted in triplicates into the wells. The concentration of 100 mg/mL of ampicillin was used as a positive control, and fresh YMA broth (YMB) was used as a negative control. The plates were subsequently kept in the fridge for 30 min to allow the supernatants to be absorbed into the agar media,and incubated overnight at 37 °C. The inhibition zones were measured.

ANTIMICROBIAL ACTIVITIES AGAINST THE TEST BORNE PATHOGENS

The antimicrobial activity of strain Im33 was tested against a variety of foodborne test pathogens, namely, *Escherichia coli* O157:H7, *Escherichia coli* V517, *Escherichia coli* 0125, *Salmonella* Typhimurium, *Salmonella* Paratyphi, *Salmonella* Newport, *Salmonella* Braenderup, *Staphylococcus haemolyticus*, *Staphylococcus equorum*, *Enterococcus faecalis*, *Enterococcus cloacoe* 22x, *Bacillus cereus* K3, and *Klebsiella pneumonia* 14x. Strain Im33 was first grown in 5 mL of YMB with shaking at 28 °C for 7 days. Several colonies of each test pathogen were transferred to a tube of sterile saline until a 0.5 McFarland turbidity standard was achieved (OD_{625nm} = 0.08-0.13). Each suspension was swabbed onto a fresh MHA and several wells were made on the agar using a sterile cork borer (6 mm in diameter). The 7-day old broth culture was centrifuged at 10,000 rpm for 10 min. Fifty microliters of the supernatant were aliquoted in triplicates into each well. Twenty micrograms of ampicillin were used as a positive control, and fresh YMB was used as a negative control. The plates were subsequently kept in the fridge for 30 min to allow the supernatants to be absorbed into the agar media and incubated overnight at 37 °C. The inhibition zones were measured.

DETERMINATION OF MINIMUM INHIBITORY CONCENTRATION (MIC) AND MINIMUM BACTERICIDAL CONCENTRATION (MBC) OF THE CRUDE BIOACTIVE COMPOUNDS

MIC and MBC were determined using the modified broth microdilution method. The lyophilized crude extract was prepared in the concentration range between 0 and 1000 µg/mL. One hundred µL of each concentration was added in triplicates into each well in a 96-well plate. *E. coli* TOP10 was grown in MHA broth (MHB) with shaking at 37 °C for 6 hours. One hundred µL of the bacterial suspension was added to each well to an optical density of 0.001 at OD_{625nm}. One hundred mg/mL of ampicillin was used as a positive control. The plate was incubated with shaking at 37 °C overnight. The lowest concentration of the crude extract, which did not show any growth, was considered MIC. The cell suspensions from all the wells that did not show any growth were plated on MHA and incubated at 37 °C overnight. The lowest concentration, which produced no growth on the agar was considered as MBC of the crude extract against *E. coli* TOP10.

CARBON UTILIZATION TEST

The carbon utilization ability of strain Im33 was tested according to Shirling and Gottlieb (1966). Carbon sources such as arabinose, fructose, galactose, glucose, inositol, mannitol, mannose, raffinose, sorbitol, sucrose, and xylose were used. A basal medium without any carbon source was used as a negative control. Strain Im33 was spread on each plate in triplicate and incubated at 28 °C for 7 days, and the growth was observed.

RESULTS

MORPHOLOGICAL CHARACTERIZATION AND ANTIMICROBIAL PRODUCTION IN DIFFERENT MEDIA

The mycelial growth size of fungal strain Im33 waobserved in those media in descending order: MEA>YMA>SDA>LCA>CYA>PDA (Table 1). Spore formations were heavy on the MEA, YMA, and SDA and poor on the CYA, LCA, and PDA. It produced orange diffusible pigments on MEA, YMA, and SAB media, which turned the agar to orange. The colonies appeared white to yellow in CYA, LCA, and PDA media. The antimicrobial activity was strongest when it was grown in YMA, followed by MEA and SDA liquid media. No inhibition zone was observed when it was grown in LCA, CYA, and PDA (Table 1).

Under SEM, it was observed that the conidiophores of strain Im33 were biverticillate. The conidia were cylindrical to ellipsoidal with smooth-walled, which were about 1243-2219 nm long and 1034-1472 nm in diameter (Figure 1).

MOLECULAR CHARACTERIZATION AND PHYLOGENETIC ANALYSIS

BLAST sequence alignment analysis showed that strain lm33 exhibited 95% similarity to the fungus, *Talaromyces radicus*. A phylogenetic tree constructed based on the ITS1-5.8S-ITS2 rDNA sequences of strain Im33 and other closely related *Talaromyces* species clustered the strain into clade 2a (Figure 2).

SENSITIVITY TO CYCLOHEXIMIDE

No inhibition of growth was observed in all YMA supplemented with cycloheximide indicating that fungus strain Im33 was resistant to it.

ANTIMICROBIAL ACTIVITIES AGAINST TEST PATHOGENS

Strain lm33 inhibited the growth of all foodborne test pathogens, including Gram-negative *Escherichia* spp., *Salmonella* spp., *Enterococcus* spp., and *K. pneumonia* and Gram-positive *B. cereus*. It exhibited the strongest inhibition against *S. equorum* with the least activity against *E. coli* O157:H7. The diameters of the inhibition

zones are shown in Table 2.

TABLE 1. Colony morphology and antimicrobial activity of strain Im33 grown in different agar media

Agar medium	*Colony diameter (mm)	Colony morphology			Zonation	Sporulation	*Diameter of inhibition zone (mm)
		Texture	Surface color	Reverse color			
CYA	14.5 ± 0.8	Floccose	White to light yellow	White to pale yellow	Radially furrowed on the reverse	Poor	None
LCA	15.0 ± 0.4	Floccose	White to yellow	Bright yellow	Radially furrowed on the reverse	Poor	None
YMA	17.3 ± 0.5	Velvety	Yellow	Bright orange	Light zonation at the margin	Heavy	6.4 ± 0.4
MEA	17.6 ± 0.2	Velvety	Bright yellow	Bright orange	Light zonation at the margin	Heavy	6.2 ± 0.4
PDA	12.9 ± 0.3	Woolly	Light yellow	Yellow	None	Poor	None
SDA	15.7 ± 0.6	Floccose	White	Bright orange	Light zonation at the margin	Heavy	3.4 ± 0.4

*Data represents the mean of three replicates ± standard deviation

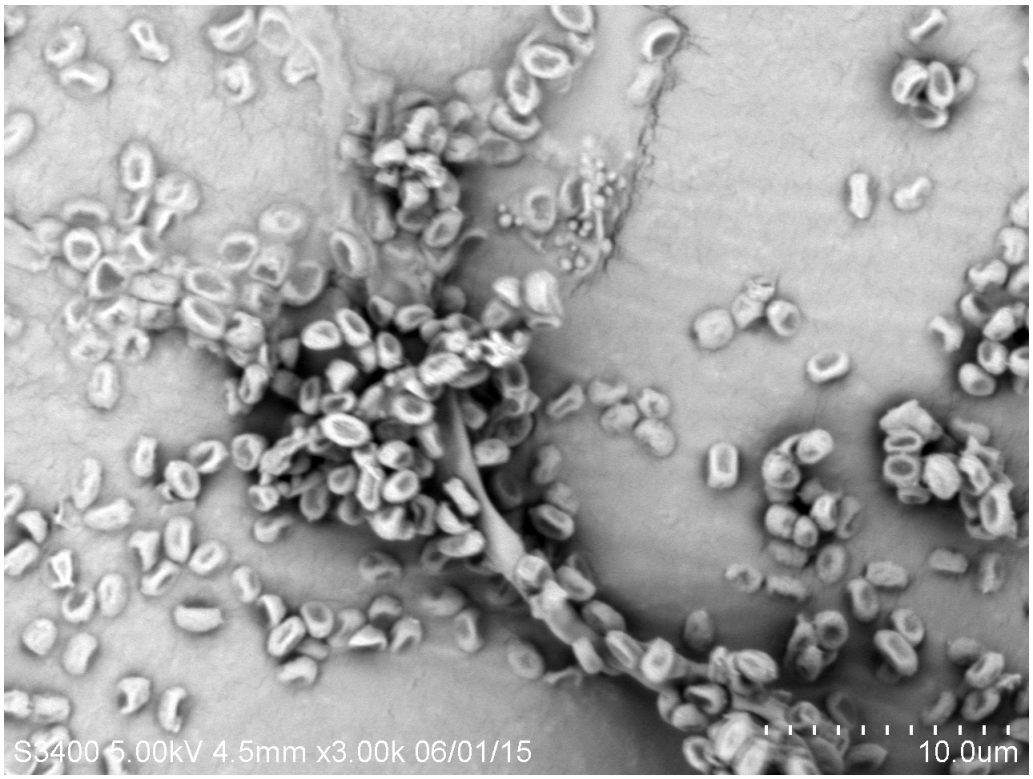

FIGURE 1. Spore morphology of strain Im33 observed under SEM

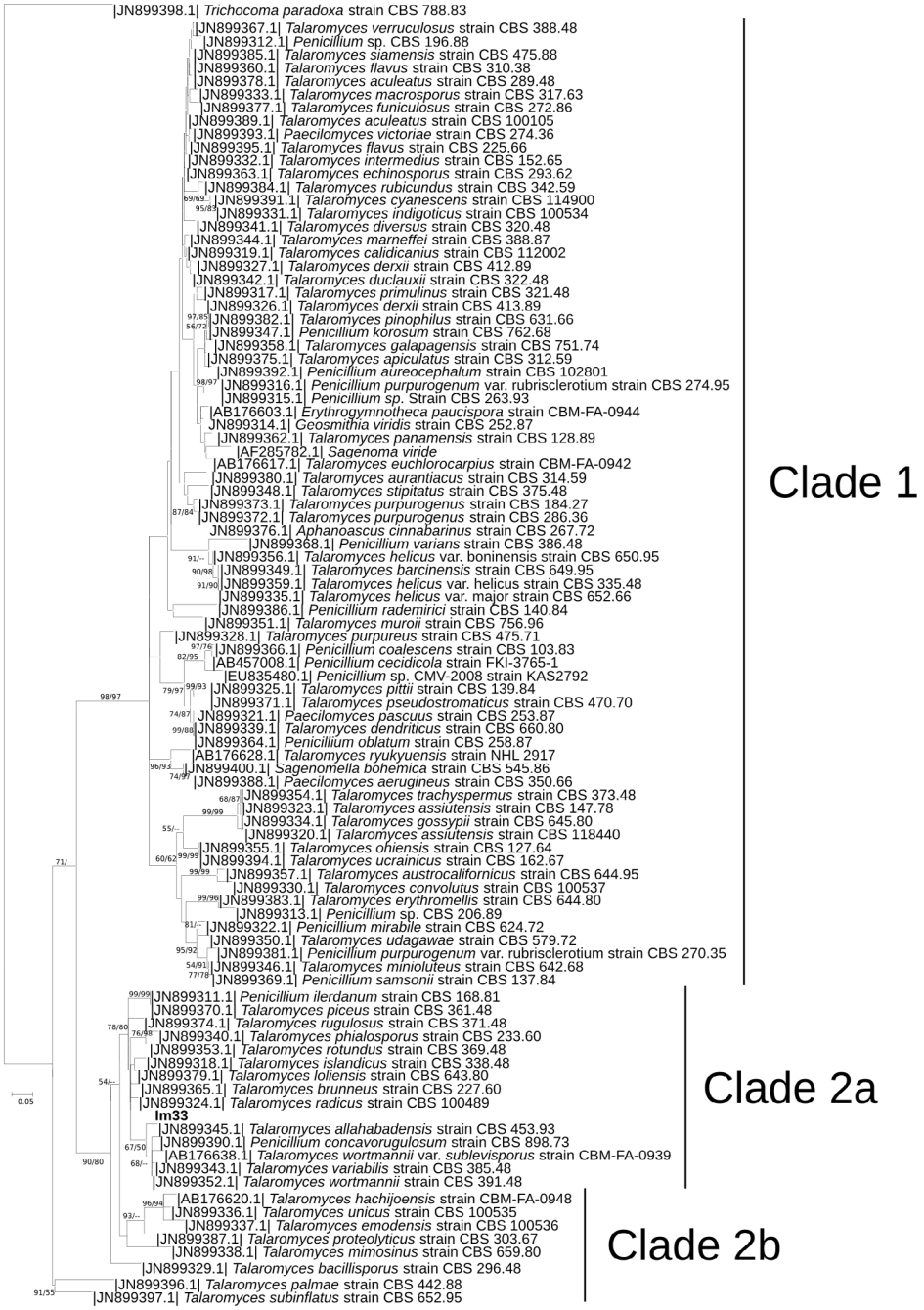

FIGURE 2. Phylogenetic tree of ITS1-5.8S-ITS2 rDNA sequences inferred by maximum likelihood method (using an alignment of 454 bp). *Trichocoma paradoxa* was used as an outgroup. The numbers shown next to the branches indicate bootstrap values of maximum likelihood (ML) and Maximum Parsimony (MP), respectively. Sequences used are presented with GenBank accession numbers followed by the name of the strain. The strain lm33 sequence reported in this paper is in bold (Clade 2a)

MIC AND MBC OF THE CRUDE BIOACTIVE COMPOUNDS AGAINST *E. coli* TOP10

The MIC and MBC of the crude extract against *E. coli* TOP10 were found to be 50 µg/mL and 75 µg/mL, respectively (Table 3).

CARBON UTILIZATION TEST

Bright yellow to orange colonies were observed in the media supplemented with fructose, galactose, glucose, inositol, mannitol, mannose, raffinose, sucrose, and xylose, while light yellow colonies were seen in the media supplemented with sorbitol and arabinose.

TABLE 2. Antimicrobial activities of strain Im33 against the test pathogens

Test pathogens	*Diameter of inhibition zone (mm)
E. coli O157:H7	10.6 ± 0.2
E. coli V517	11.5 ± 0.8
E. coli 0125	11.4 ± 0.5
S. Typhimurium	13.6 ± 0.6
S. Paratyphi	17.2 ± 0.6
S. Newport	14.4 ± 0.3
S. Braenderup	14.4 ± 0.9
S. haemolyticus	23.5 ± 0.5
S. equorum	27.9 ± 0.7
E. faecalis	24.2 ± 0.7
E. cloacoe 22x	12.1 ± 0.7
B. cereus K3	11.3 ± 0.2
K. pneumonia 14x	12.1 ± 0.7

*Data represents the mean of three replicates ± standard deviation

TABLE 3. Inhibitory effects of various concentrations of strain Im33 crude extract (µg/mL) against *E. coli*. (+) indicates inhibition; (-) indicates no inhibition

Conc. of crude extract (µg/mL)	The inhibition against *E. coli*		Conc. of crude extract (µg/mL)	The inhibition against *E. coli*	
	24-hr	48-hr		24-hr	48-hr
500	+	+	225	+	+
475	+	+	200	+	+
450	+	+	175	+	+
425	+	+	150	+	+
400	+	+	125	+	+
375	+	+	100	+	+
350	+	+	75	+	+
325	+	+	50	+	-
300	+	+	25	-	-
275	+	+	0	-	-
250	+	+			

DISCUSSION

The composition of a culture medium is an important factor in fungal identification. The vegetative growth, colony morphology, pigmentation, and sporulation of a fungus may vary in different media due to the differences in the type and concentration of carbon and nitrogen sources (C/N ratio) (Ajdari et al. 2011; Sharma & Pandey 2010). The C/N ratio was found to be one of the major parameters that affect the composition of fungal communities in soils sampled from the Arctic and Antarctic environments (Dennis et al. 2012; Fujimura & Egger 2012). In this study, six culture media were tested to determine a suitable basal medium for optimal growth, sporulation, and antimicrobial compound production of strain Im33. It was observed that strain Im33 grew better and produced more antimicrobial compounds in culture media with low C/N ratios such as MEA and YMA. These media contained high nitrogen sources like malt extract, yeast extract, and polypeptone, which seemed to provide better nutrients for the growth of strain Im33 compared to those with high C/N ratios such as CYA and PDA. The absence of inhibitory effect against *E. coli* TOP10 when it was grown in LCA, CYA, and PDA broths indicated that it did not produce antimicrobial compounds in these media, or that the yield of the antimicrobial compounds was too low to inhibit *E. coli* TOP10. Gupta, Manisha and Grover (2012) suggested that the presence of chloride ions in a culture medium could inhibit fungal sporulation, which explains why strain Im33 had poor sporulation in CYA and LCA. In addition, strain Im33 had heavy mycelial growth and poor sporulation in PDA. Although PDA is well known as one of the most common media for fungal growth and maintenance, it can be too rich for many fungi, which encourages excessive mycelial growth without sporulation (Nurbaya et al. 2014).

A phylogenetic tree constructed based on the ITS1-5.8S-ITS2 rDNA sequences of strain Im33 and other closely related *Talaromyces* species clustered the strain into a distinct, monophyletic branch within clade 2a, described by Samson et al. (2011), which diverged from other known species. It showed the highest similarity to *Talaromyces radicus* (96%), which was isolated from the rhizosphere of Australian wheat, and *Talaromyces brunneus* (96%), which was isolated from imported rice in Japan (Hocking, Whitelaw & Harden 1998; Udagawa 1959). The present study reported the first *Talaromyces* species isolated from Deception Island.

Cycloheximide is a eukaryotic protein synthesis inhibitor that is commonly used to suppress yeast and fungal growth (Dehoux, Davies & Cannon 1993) and is produced by an actinobacterium, *Streptomyces griseus* (Kominek 1975). Several cycloheximide-resistant *Talaromyces* species such as *T. islandicus* and *T. flavus* have been reported, but none of them have been isolated from their natural environments (Bagy et al. 1997; Ismail, Taligoola & Nakamya 2010). Hence, it remains unknown whether the resistance is natural or acquired. Strain Im33 was able to grow well on YMA supplemented with concentrations of cycloheximide up to 1,000 mg/L, suggesting that it might have a high level of natural resistance to cycloheximide. This finding is interesting, and the ability to resist cycloheximide probably provides an advantage to strain Im33 in competing with other microbes and fungi in the same habitat in the nutrient-limiting terrestrial soil on Deception Island. It will have no problem co-inhabiting a niche area with the cycloheximide-producing *Streptomyces* spp.

Members of the genus *Talaromyces* produce secondary metabolites with antimicrobial properties (Miao et al. 2012; Pretsch et al. 2014; Zang et al. 2016). Yamazaki et al. (2010) and Yamazaki, Ōmura and Tomoda (2010) discovered that *T. radicus* produces rugulosins which have antibacterial activity against methicillin-resistant *Staphylococcus aureus* (MRSA), and mitorubins which potentiate miconazole activity against *Candida albicans*. Crude extract from *T. wortmannii* exerts a strong inhibitory effect against an acne-inducing bacterium, *Propionibacterium acnes,* and possesses anti-inflammatory properties (Pretsch et al. 2014). Meanwhile, Zang et al. (2016) reported that *T. stipitatus* produces antimicrobial oligophenalenone dimers that inhibit the growth of human pathogenic bacteria. In this study, strain Im33 demonstrated a broad spectrum of antimicrobial activity against Gram-positive and Gram-negative bacteria. The result showed that soil fungi living on Deception Island have acquired peculiar adaptation strategies in order to survive in the extreme environment. The production of antimicrobial compounds to inhibit the growth or kill other microorganisms is likely one of the survival strategies to reduce the competition for space and nutrients in a niche area. This is consistent with their bacterial counterparts, which produce antimicrobial compounds as an added advantage to survive in nutrient-limited environments, as reported by Lo Guidice, Bruni

and Michaud (2007) and Lo Giudice et al. (2007).

Talaromyces species have been associated with soils and decaying organic matter. Some species were reported to produce various enzymes which were involved in the decomposition of organic materials and nutrient cycling in soils (Elíades et al. 2010; Tranchida et al. 2016). *T. udagawae* was isolated from soil under decaying corpses in Argentina, which demonstrated its role in the decomposition of human remains (Tranchida et al. 2016). Enzymes such as β–glucanases, cellulases, proteases, lipases, and xylanases have been isolated from *Talaromyces* species for biotechnological purposes (Inoue et al. 2014; Waters et al. 2011). It was observed that strain Im33 could fully utilize fructose, galactose, glucose, inositol, mannitol, mannose, raffinose, sucrose, and xylose, and partially degrade sorbitol and arabinose for growth and proliferation. The ability to utilize all carbon sources tested in this study suggested that strain Im33 might play a role in the decomposition of plant matter in soils in order to obtain nutrients for survival in adverse environmental conditions. This fungus's decomposition role corresponds to the location where it was discovered, which was under rotten grass on Deception Island, Antarctica.

Conclusions

Strain Im33 was discovered to be a *Talaromyces* species from Deception Island that produced broad-spectrum antibacterial compounds against Gram-positive and Gram-negative pathogens, as well as enzymes capable of digesting a variety of carbon sources. This suggests that Antarctic fungi, like their bacterial counterparts, need to evolve and acquire unique strategies to survive in harsh environments, such as the ability to not only degrade organic material but also to produce antimicrobial compounds to fend off competitors living in the same niche area. Future research should be done to further analyze the antibacterial chemicals produced by this strain, since they may be unique and have more widespread medical applications.

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