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Peacock tail with a fungal cocktail: first assessment of the mycobiota associated with the brown alga

Padina pavonica

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Abstract

The microbial diversity of the Mediterranean Sea is still poorly investigated, and a greater effort is needed to reveal marine fungal biodiversity associated with algal substrates. This study is the first description of the cultivable mycobiota associated with the calcareous brown alga *Padina pavonica*. Twenty algal thalli were analysed with a polyphasic approach, combining morphological and molecular data for fungal identification. Our data reveal a surprising richness of fungal species associated with a single brown alga: 268 isolates belonging to 134 taxa ascribable to Ascomycota (95.3 %), Basidiomycota (5.2 %), and Mucoromycota (0.7 %) were retrieved. Twenty-nine species were reported for the first time in marine environment. The analyses of the fungal community revealed possible substrate specificity. In addition, a number of sterile strains form separate clusters within the Diaporthales, Hypocreales, and Pleosporales, indicating that putative new lineages may arise from the marine environment.

Keywords: marine fungi; Mediterranean Sea; cultivable mycobiota; microbial diversity; algicolous fungi

Introduction

Biodiversity of fungi represent one of the most challenging and interesting fields in marine biology. Marine fungi can be defined as an ecologically diverse and cosmopolitan group of organisms distributed in all oceans and seas (Hyde et al., 1998), although the patterns and processes of their local and global diversity are yet to be disclosed. Functioning as saprobes, parasites and mutualistic symbionts (Jones, 2011; Raghukumar, 2017), marine fungi are heavily involved in biogeochemical cycling (Rédou et al., 2015). They produce numerous interesting compounds and enzymes, which, beside their ecological significance, have been acknowledged for their astonishing bioactivity (Mouad et al., 2011, 2012; Burgaud et al., 2014; Bonugli-Santos et al., 2015; Imhoff, 2016; Sridhar, 2017).

Jones et al. (2015) listed more than 1,100 species of marine fungi, belonging to Ascomycota, Basidiomycota, Blastocladiomycota, and Chytridiomycota. Nevertheless, more than 10,000 species are estimated as yet to be discovered (Jones and Pang, 2012). This major gap is mainly due to the scarcity of habitats/substrates thoroughly explored for the presence of these organisms and to the low number of researchers currently working in this field.

In this context, the Mediterranean Sea, notwithstanding it is known as a hotspot of biodiversity for flora and fauna, is still a poorly investigated area (Coll et al., 2010). Only few data are available, in particular regarding algicolous fungi. Garzoli et al. (2014) presented the first characterisation of the fungal community associated with a red alga, *Asparagopsis taxiformis*, observing only 5 fungal taxa on 24 thalli; more recently, Gnavi et al. (2017), analysing the green alga *Flabellia petiolata*, detected 64 fungal taxa.

The present work is part of an extensive survey aimed to unravel the microbial diversity of the Mediterranean Sea by means of a polyphasic approach combining morphological, physiological, and molecular studies (Panno et al., 2013; Gnavi et al., 2014; Garzoli et al., 2014; 2015; Gnavi et al., 2017;). The focus of the current report is on the culturable mycobiota associated with the brown alga *Padina pavonica* (Phaeophyceae, Dictyotales, Dictyotaceae), a widely distributed warm-temperate species (Guiry et al., 2014). Due to its fan-shaped thallus, *P. pavonica* is known also as Peacock's tail and it is commonly found in the Mediterranean Sea (Cormaci et al., 2012). This alga is rich in carbohydrates (mainly alginates and

laminarans), lipids (fucosterol), vitamins, and mineral salts, and it is known for its slight bioactivity against microbial pathogens (Kamenarska et al., 2002; Awad et al., 2008; Omezzine et al., 2009). Although previous attempts have been made to study its mycobiota (Cuomo et al., 1983; Abdel-Gawad et al., 2014), the published data were exclusively based on morphological observations and did not provide a complete list of fungal species associated with this alga. To the best of our knowledge, this study represents the first description of the culturable mycobiota associated with *P. pavonica*.

Materials and methods

Sampling

Samples of *P. pavonica* were collected in March 2010 in the coastal waters of Elba Island (Livorno, Italy) in the Tyrrhenian Sea (NW Mediterranean Sea). The same two sampling sites considered by Gnani et al. (2017) for the presence of fungi associated with the green alga *F. petiolata* were chosen in the seagrass meadows of *Posidonia oceanica*: (1) Ghiaie (WGS84 42°49'04''N, 10°19'20''E) and (2) Margidore (WGS84 42°45'29''N, 10°18'24''E). Twenty thalli (10 thalli for each sampling site) were harvested at two different depths (5 thalli/each depth): USL, Upper Sea Level (average depth: 3-5 m bsl); ISL, Intermediate Sea Level (average depth: 14-15 m bsl). Algae were maintained in sterile dark containers at 4 °C.

Fungal isolation

Algal thalli were sonicated (30 s each time) and serially washed in artificial sterilized SeaWater (SW, 3.4 % w/v Sea Salt mix - Sigma-Aldrich, Saint Louis, USA - in ultrapure distilled water ddH₂O) three times to remove unrefined sediments. According to the procedure described by Gnani et al. (2017), each thallus was homogenized in 20 mL of filtered seawater by means of Ultra-Turrax (IKA) sterile device. The homogenates were further diluted 1:10 in sterilized seawater and 1 mL of the resulting solution was plated in sterile Petri dishes (120 mm) containing 30 mL of one of two media: 1) Corn Meal Agar SeaWater medium (CMASW, 17 g CMA - Sigma-Aldrich Saint Louis, USA - dissolved in 1 L of filtered SW) and 2) *Padina* Agar

SeaWater medium (PASW, 1 g fw of *P. pavonica* in 100 mL of SW boiled for 30 min at 60 °C and filtered; 18 g agar; SW up 1 L) (Panno, 2014). Both media were supplemented with antibiotics (Gentamicin 80 mg/L, Tazocin 100 mg/L). Plates were prepared in triplicate, incubated at 15 °C for 15 d and subsequently placed at 24 °C for 45 d to allow the isolation of both psychrotolerant and mesophilic colonies. Colony forming units per gram of dry weight for each thallus (CFU/g dw) were recorded and strains from each fungal morphotype and from each sampling site were isolated in pure culture and preserved at the *Mycoteca Universitatis Taurinensis* (MUT). Accession records and descriptions are available at MUT website (www.mut.unito.it/en); Supp. Mat. 1).

Fungal identification

Strains were firstly identified on the basis of their macro/microscopic morphological and physiological features according to specific taxonomical keys as described in Ainsworth (2008). Subsequently, specific markers were amplified in a Biometra TGradient Thermocycler (Biometra, Göttingen, Germany): the nuclear ribosomal nrDNA partial regions (ITS or LSU and SSU when necessary) were amplified using the universal primers ITS1/ITS4 (Schoch et al., 2012; White et al., 1990), LR0R/LR7 (Lapeyre et al., 1993), and NS1/NS4 (White et al., 1990). For yeasts, NL1/NL4 primers were used to amplify the D1/D2 region of LSU (Kurtzman and Robnett, 1997). For strains belonging to *Aspergillus* spp. and *Penicillium* spp., the β -tubulin gene was amplified using the primer pair Bt2a/Bt2b (Glass and Donaldson, 1995); ACT512F/ACT783R (Carbone and Kohn, 1999) were used to amplify the Actin gene for *Cladosporium* spp.. Finally, for *Stachybotrys* and *Alternaria* spp., it was necessary to amplify respectively Calmodulin and glyceraldehyde-3-phosphate dehydrogenase genes, using primers CL-1/CL-2 (O'Donnell et al., 2000) and GPD1/GPD2 (Berbee et al., 1999). PCR products were then sequenced using Sanger sequencing techniques at MacroGen (Seoul Korea). The resulting electropherograms (ABI-files) were analysed with Sequencer software, version 5.2 (Gene Codes Corp., Ann Arbor, MI, USA). Newly generated sequences were compared to those available in public databases (GenBank - nblast; mismatch 1/-2; gap costs linear; Mycobank) and deposited at NCBI (Suppl. Mat. 1). Sterile mycelia and strains with morphological features that did not match any

available species description and showed low sequence similarity with those available in public databases were further characterised through phylogenetic inference.

Phylogenetic Analysis

A full phylogenetic analysis was performed on ITS sequences. Three datasets were composed for Diaporthales, Hypocreales and Pleosporales, following the Outline of Ascomycota (Lumbsch and Huhndorf, 2011). Sequences from the Fungal Biodiversity Center CBS type strains were preferred, when available; other sequences were chosen on the basis of specific taxonomic studies and retrieved from NCBI GenBank database. Alignments were performed with MUSCLE, implemented in MEGA 7.0, using default conditions for gap openings and gap extension penalties and trimmed by TrimAl (v 1.2) (<http://trimal.cgenomics.org>) with the AUTOMATED1 setting. Phylogenetic analyses were performed using a Bayesian Inference approach (BI; MrBayse 3.2.2), as described in Gnani et al. (2017). Bayesian posterior probability (BPP) values over 0.6 are reported in the resulting trees.

Statistical analysis

The biodiversity within sampling sites and depth was evaluated calculating Shannon-Weaver's index (H'), Gini-Simpson's index ($1-\lambda$), and Pielou's evenness (J').

Statistical analyses were mainly performed using PRIMER v 7.0 for multivariate ecological research (Clarke and Gorley, 2015). Differences among thalli were evaluated through ANalysis Of SIMilarity (ANOSIM). Differences within sampling site and depth were evaluated by applying a Permutational Multivariate Analysis of Variance (PERMANOVA; pseudo-F index; $P < 0.05$) and visualised by Non-Metric Multi-Dimensional Scaling (NMDS) in R environment (R Core Team, 2015). The contribution of single species (expressed in percentage) to the diversity observed within and between groups was assessed by SIMilarity PERcentage (SIMPER) analysis. Possible ecological roles of retrieved taxa were inferred by querying the FUNGuild public database (Nguyen et al., 2016, <http://www.stbates.org/guilds/>)

Results

All algal samples were colonized by fungi. The colonisation rates ranged between 898 CFU/g dw in samples from Margidore ISL and 1,760 CFU/g dw in samples collected from Ghiaie ISL (Tab. 1, Suppl. Mat. 2). A total of 268 isolates belonging to 134 fungal taxa were retrieved (Tab.2) and 292 sequences were newly generated and deposited in NCBI database (Suppl. Mat. 2). Sixty-four percent of the strains were identified at species level, 13 % at genus level, 11 % at family level, 5 % at order level, 4 % at class level, and 2 % at phylum level.

Most species required specific media: 67 taxa were exclusively isolated from CMASW, 34 exclusively from PASW, and 33 were present on both media.

Most of the isolated taxa belonged to Ascomycota (93.3 %). A few Basidiomycota (5.2 %) and Mucoromycota (0.7 %) were also detected. No Chytridiomycota or Cryptomycota were observed.

The isolated taxa belonged to 7 classes, 19 orders and 34 families. Among Ascomycota, the most represented classes were Dothideomycetes (45.5 %, mainly Pleosporales and Capnodiales - 26.1 % and 14.4 %, respectively) and Sordariomycetes (27.6 %, mainly Hypocreales and Diaporthales - 14.9 % and 3.0 %, respectively), followed by Eurotiomycetes (11.9 %), while Leotiomycetes represented only a small percentage of the detected taxa (3.7 %). Within Basidiomycota, the organisms retrieved belonged to Agaricomycetes (3.0 %), Microbotriomycetes (1.5 %) and Wallemiomycetes (0.7 %).

The phylogenetic analysis showed that 68 sterile or morphologically cryptic isolates were affiliated to Pleosporales order (Fig. 3), 10 isolates were comprised in the Hypocreales (Fig. 4), 5 isolates fell within Diaporthales (Fig. 5). The majority of these strains, showing low homology with ITS sequences available in public databases (Blastn similarity < 96 %), form separate clusters within the three orders.

The genus found with the highest frequency and the highest diversity of species was *Cladosporium* (20.7 % of total fungal load, 13 different species), followed by *Penicillium* (20.2 % of total fungal load, 8 species). *Penicillium antarcticum* was the most abundant species in terms of fungal load (13,883 CFU/g dw, 8.8 % of total isolates), followed by *Cladosporium halotolerans* (12,106 CFU/g dw, 7.6 % of total isolates), *P. roseopurpureum* (7,189 CFU/g dw, 4.5 % of total isolates), *C. sphaerosphaermum* (6,106 CFU/g dw, 3.8 %

of total isolates) and *Acrostalagmus luteoalbus* (5,070 CFU/g dw, 3.2 % of total isolates). The remaining taxa were recorded at < 3 %. *Penicillium antarcticum* was also the most widespread species (4 sites, 9 thalli), followed by *A. luteoalbus* (4 sites, 5 thalli), *Pyrenochaetopsis* sp.3 (3 sites and 5 thalli), *Pyrenochaetopsis* sp.2 (3 sites and 4 thalli), *C. sphaerospermum* and *P. steckii* (3 sites and 3 thalli).

ANOSIM analysis revealed a significant variability among thalli (among 95 and 100 %) and the majority of taxa retrieved was restricted to a single thallus (Fig. 1). Significant differences in species composition were found between sampling sites ($p=0.002$), between depths ($p=0.001$) (Fig.2), and with a significant effect of the interaction between sampling sites and depths ($p = 0.002$). *Cladosporium halotolerans* (14.1 %), *P. antarcticum* (7.9 %), *P. roseopurpureum* (7.4 %), *C. sphaerospermum* (5.2 %), *C. cladosporioides* (3.3 %) and *A. luteoalbus* (3.3 %) were the most frequent taxa recorded on Ghiaie samples, while *P. antarcticum* (9.6 %), *P. brevicompactum* (5.4 %), *Pyrenochaetopsis* sp.1 (4.3 %), *Pyrenochaetopsis* sp. 3 (4.0 %), and *C. pseudocladosporioides* (3.8 %) on Margidore samples. As for different depths, *P. antarcticum* (9.7 %), *P. roseopurpureum* (9.4 %), *A. luteoalbus* (4.4 %), *C. sphaerospermum* (4.1 %) and *Pyrenochaetopsis* sp.1. (4.1 %) were the dominant taxa in terms of abundance in USL samples, while *C. halotolerans* (14.8 %), *P. antarcticum* (7.7 %), *P. brevicompactum* (5.6 %), *C. sphaerospermum* (3.6 %) and *C. xylophilum* (3.1 %) in ISL samples. Other species were recorded with frequencies lower than 3 %.

SIMPER analysis highlighted dissimilarities between sites (99.53 %) and depths (99.50 %). The analysis identified *P. antarcticum*, *C. halotolerans* and *P. roseopurpureum* as the species mostly contributing to the diversities of both factors.

Discussion

Padina pavonica is a brown alga widespread in the Mediterranean and Black Sea, as well as in the Atlantic Ocean. However, previous attempts to describe its associated mycobiota have been incomplete: the number of analysed samples was not specified, no molecular identification was performed, and only a few

taxa were detected (Cuomo et al., 1983; Abdel-Gawad et al., 2014). Thus, this study represents the first survey of the fungal community associated with *P. pavonica*.

The analyses of the mycobiota indicate a high biodiversity (134 isolated taxa). Almost all the identified taxa belong to Ascomycota, confirming the dominance of this phylum in the marine environment, as underlined by Pang and Jones (2017). Dothideomycetes, Sordariomycetes and Eurotiomycetes, the most widespread fungal classes at a global level (Jones and Pang, 2012), were also dominant in our samples. By contrast, no Chytridiomycota or Cryptomycota were isolated. These two phyla have been retrieved in marine environments mainly in water columns and sediments (Richards et al., 2015) or through culture independent studies (Nagahama and Nagano, 2012). Indeed, these microorganisms are difficult to isolate. In addition, the algal substrate itself may not represent their preferred substratum. Our results demonstrate that site and depth can influence the community structure observed on *P. pavonica* thalli. Nonetheless, a huge variability (in terms of species recorded on each thallus) was recorded. Most of the species were restricted to a single algal thallus. Indeed, the shape of the rarefaction curve relative to Ghiaie and Margidore sites (data not shown) suggests that a much higher number of thalli would be necessary to estimate the entire richness of the culturable mycobiota.

Our data are remarkable in terms of detected biodiversity if compared with other algal substrates of the Mediterranean Sea. Thalli of *P. pavonica* analysed in the present study were sampled in the same locations and period as those of the green alga *Flabellia petiolata* investigated by Gnavi et al. (2017). Fungal biodiversity, in terms of species richness, was twice as high as the one recorded on the brown alga in the same number of thalli. This is in line with previous findings that indicates brown algae as major fungal hosts in the marine habitats (Zuccaro and Mitchell, 2005).

Only 13 species were shared by the two algae: *Acremonium sclerotigenum*, *Acrostalagmus luteoalbus*, *Arthrinium arundinis*, *A. phaeospermum*, *Aureobasidium pullulans*, *Cladosporium allicinum*, *C. cladosporioides*, *C. sphaerospermum*, *Gibellulopsis nigrescens*, *Massarina rubi*, *Schizophyllum commune*, *Penicillium antarcticum* and *P. brevicompactum*. These species, common in marine habitats (Pang and Jones, 2017; Bovio et al., 2018), were retrieved on both algae, confirming their ubiquity and their ability to face

different environmental conditions. Interestingly, eight of these species (*A. luteoalbus*, *A. arundinis*, *A. phaeospermum*, *A. pullulans*, *C. cladosporioides*, *C. sphaerospermum*, *P. brevicompactum* and *S. commune*) are known as plant endophytes and/or pathogens in terrestrial habitats (FUNGuild.org).

Most of the taxa retrieved on *P. pavonica* were not observed on *F. petiolata* and *viceversa*: in identical abiotic conditions (site and depth, Fig. 6), these two algae seem to recruit different fungal communities, suggesting the importance of the substrate in shaping the associated mycobiota. Host-specificity recruitment is supported by data previously obtained in a broader context. A comparison of the mycobiotas retrieved from *P. pavonica* and other Mediterranean substrata confirms that only a few taxa are shared with other algae (*Asparagopsis taxiformis*, 5 taxa retrieved, 1 species in common) (Garzoli et al., 2014), seagrasses (*Posidonia oceanica*, 88 taxa retrieved, 8 species in common) (Panno et al., 2013), wood samples (40 taxa retrieved, 7 species in common) (Garzoli et al., 2015), and sponges (*Psammocinia* sp., 89 taxa retrieved, 8 species in common) (Paz et al., 2010).

Twenty-nine species were retrieved for the first time from a marine environment (*Aaosphaeria arxii*, *A. brunnescens*, *Acremonium vitellinum*, *Alternaria metachromatica*, *Arthrinium marii*, *Bjerkandera adusta*, *Cladosporium delicatulum*, *C. iranicum*, *C. subtilissimum*, *C. xylophylum*, *Devriesia lagerstroemiae*, *Libertella blepharis*, *Paecilomyces inflatus*, *Paraconiothyrium variabile*, *Paraphaeosphaeria neglecta*, *Pestalotia olivacea*, *Plectosporium tabacinum*, *Pochonia clamydosporia*, *Pyrenochaetopsis microspora*, *Ramichloridium strelitziae*, *Sarocladium glaucum*, *Sporothrix inflata* and *Toxicocladosporium strelitziae*). The majority of these have been previously recorded in terrestrial environments as animal or plant pathogens or saprobic fungi (FUNGuild.org; Walker, 1980; Domsch et al., 1980; Guarro et al., 2012; Crous et al., 2013). *Aspergillus conicus*, *A. jeyangensis*, *Chamaeleomyces granulomatis*, *Ochrocladosporium frigidarii*, *Penicillium caseifulvum*, *Scopulariopsis humicola*, previously found in marine substrates, are typical terrestrial inhabitants. Members of *Penicillium*, *Cladosporium*, and *Aspergillus* are the dominant taxa at all sites and depths, although their high sporulation rate may result in an overestimation of the substrate colonization. These genera are ubiquitous in the marine environment, and represent a prominent source of secondary metabolites even though their ecological role is still debated (Imhoff et al., 2011).

The most frequently retrieved species in our samples was *P. antarcticum*, being isolated from all sites and depths. Even though this species was originally described from soil in Antarctica (McRae et al., 1999), it is widespread in all marine environments, including different Mediterranean substrata such as *F. petiolata* (Gnavi et al., 2017), water, and sediments (Bovio et al., 2017). *Penicillium roseopurpureum* and *P. brevicompactum* were also found with high frequency. In the Mediterranean Sea, *P. brevicompactum* is reported from water and sediments (Bovio et al., 2017), holothurians (*Holothuria polii*) (Marchese et al., 2016), ascidians (*Cystodytes dellechiajei*, *Didemnum fulgen*) (Lopez-Legentil et al., 2015), marine sponges (*Psammocinia* sp.) (Paz et al., 2010), green algae (*F. petiolata*) (Gnavi et al., 2017) and seagrasses (*P. oceanica*), (Panno et al., 2013). *Penicillium roseopurpureum*, reported also on *H. polii* (Marchese et al., 2016), is an ubiquitous species (Houbraken et al., 2011). *Cladosporium halotolerans*, a highly halotolerant species (Zajc et al., 2012), is dominant at the Ghiaie site and at maximum depths. This species has also been reported from sea water and driftwood (Garzoli et al., 2015; Bovio et al., 2017). *Cladosporium sphaerospermum*, reported from *P. oceanica* (Panno et al., 2013), *F. petiolata* (Gnavi et al., 2017) and *H. polii* (Marchese et al., 2016), is a species that also dominates all sites and depth.

A number of isolates remained sterile in axenic culture, which is common for many marine strains (Gnavi et al., 2017). They presented low homology (< 96 %) with sequences available in public databases. Phylogenetic inference demonstrated that several strains group in clades that are separated from species currently belonging to Diaporthales, Hypocreales, and Pleosporales (Fig. 3,4,5). In light of the peculiarity of their isolation sources, it is reasonable to hypothesise that these strains may represent new species. Nonetheless, since many type strains of the species belonging to these orders lack reference sequences and are described only on the bases of their anamorphic and/or telomorphic stage, attempts to induce sporulation are ongoing, to better characterize these putative new species of marine origin.

Conclusion

Comparing our data with those available for the Mediterranean Sea clearly demonstrates the magnitude of fungal biodiversity in marine environment, which seems to be even higher than what was hypothesised by

several authors. More than 800 marine algae and plant species inhabit the Mediterranean Sea and less than a dozen of these substrates have been systematically surveyed for the presence of fungi. Our data, together with previous ones, indicate that about 30 % of taxa isolated from Mediterranean substrates cannot be identified at species level. If we apply the ratio employed by Hawksworth (1991) of 5.9 fungi associated with a plant in a given location, we can estimate the number of marine fungi still to be discovered to be approximately 1,400 species. This estimate is very conservative, since the average number of taxa isolated from Mediterranean plant and algae is approximately 70 for each substratum, raising the number of discoverable fungi to 16,800. Intriguingly, considering that recent molecular advances indicate that less than 2 % of the total fungal biodiversity is detected with cultivable studies, nearly a million of species may be waiting to be discovered.

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CAPTIONS TO ILLUSTRATIONS

Figure 1. Non-Metric Multi Dimensional Scaling (NMDS) plot of fungal taxa associated with different algal thalli over sampling sites. Thalli are indicated as dots, ellipses represent the dispersion of data along the principal axes. Color-code: dark blue = Ghiaie Upper Sea Level USL, light blue = Ghiaie Intermediate Sea Level ISL, dark orange = Margidore USL, light orange Marginore ISL.

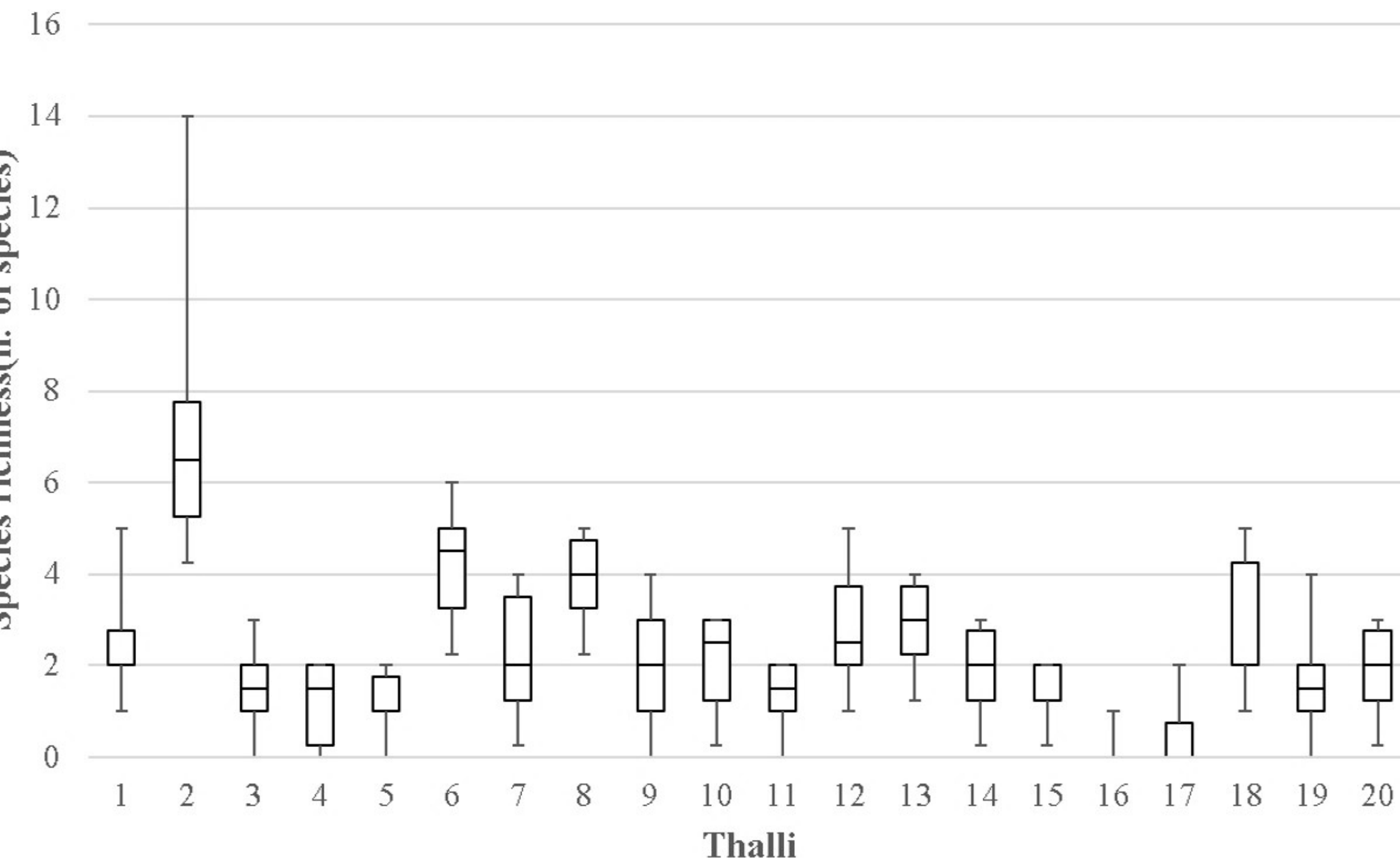
Figure 2. Boxplot of species richness recorded on twenty algal thalli. The horizontal lines represent the median, the boxes the interquartile range and the vertical lines span maximum and minimum values.

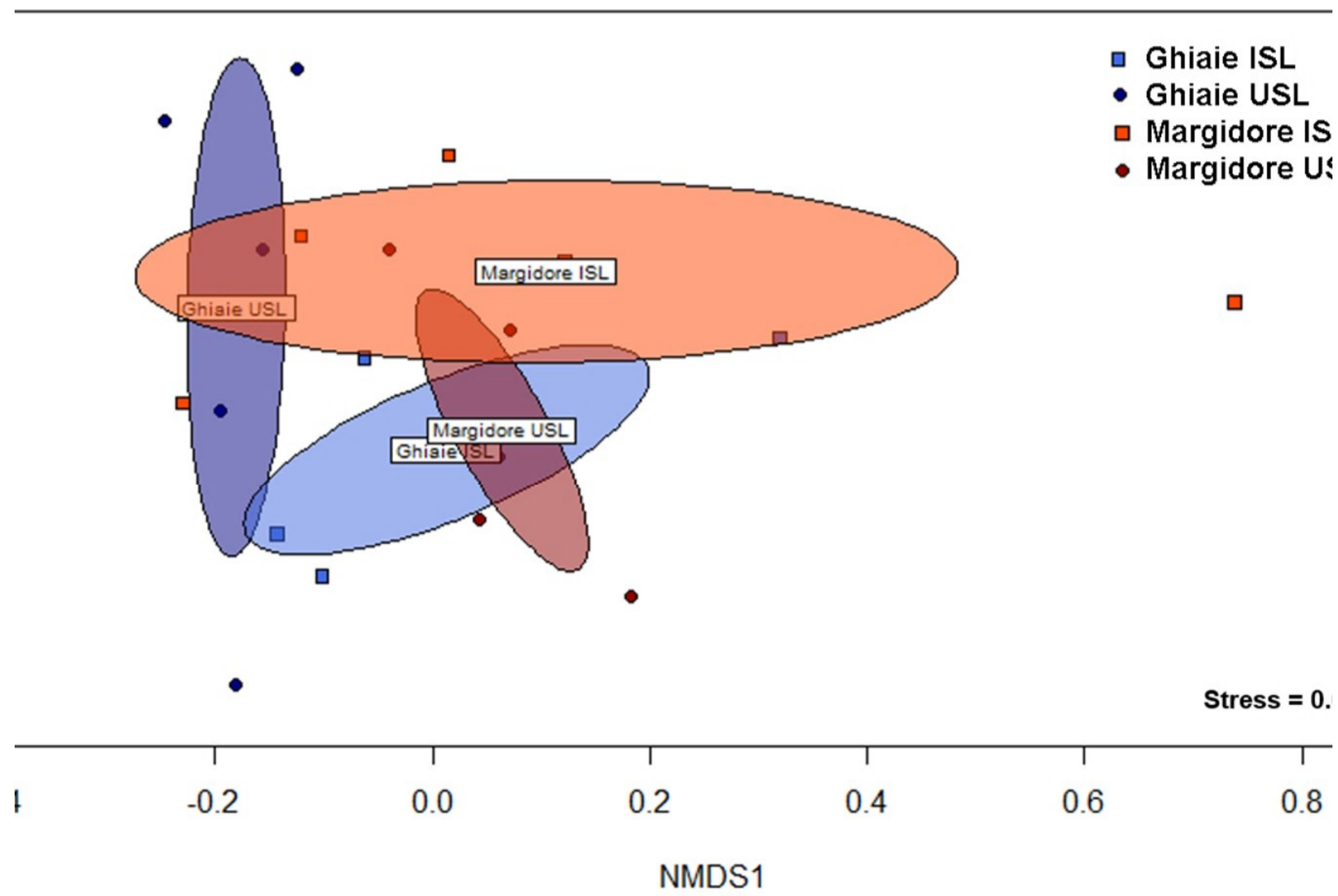
Figure 3. Bayesian phylogeny of Pleosporales (Dothideomycetes) based on Internal Transcribed Spacer nrDNA (ITS). Branch numbers indicate BPP above 0.70. Sixty-eight fungal isolates (indicated as MUT) are included. Bar = expected changes per site (0.2).

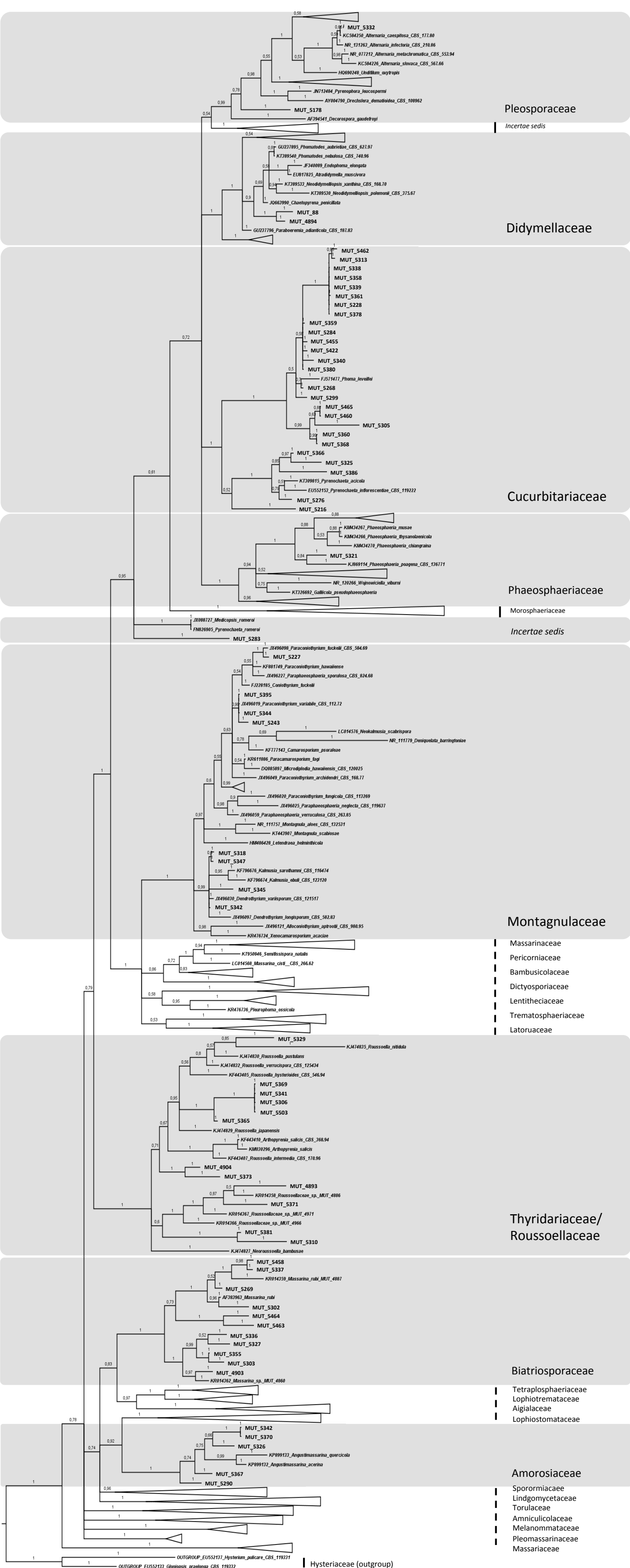
Figure 4. Bayesian phylogeny of Hypocreales (Soradiomycetes) based on Internal Transcribed Spacer nrDNA (ITS). Branch numbers indicate BPP above 0.70. Eight fungal isolates (indicated as MUT) are included. Bar = expected changes per site (0.07).

Figure 5. Bayesian phylogeny of Diaporthales (Soradiomycetes) based on Internal Transcribed Spacer nrDNA (ITS). Branch numbers indicate BPP above 0.70. Five fungal isolates (indicated as MUT) are included. Bar = expected changes per site (0.2).

Figure 6. Venn diagrams showing the total number of taxa and shared taxa between the green alga *F. petiolata* (Gnavi et al., 2017) and *P. pavonica* in the two different sampling sites (Ghiaie and Margidore, Elba Island).







Pleosporaceae

Incertae sedis

Didymellaceae

Cucurbitariaceae

Phaeosphaeriaceae

Morosphaeriaceae

Incertae sedis

Montagnulaceae

Massariaceae

Periconiaceae

Bambusicolaceae

Dictyosporiaceae

Lentitheciaceae

Trematosphaeriaceae

Latoruaceae

Thyrideriaceae/
Rousoellaceae

Biatrisporaceae

Tetraplophaeriaceae

Lophiotremataceae

Aigialaceae

Lophiostomataceae

Amorosiaceae

Sporormiaceae

Lindgomycetaceae

Torulaceae

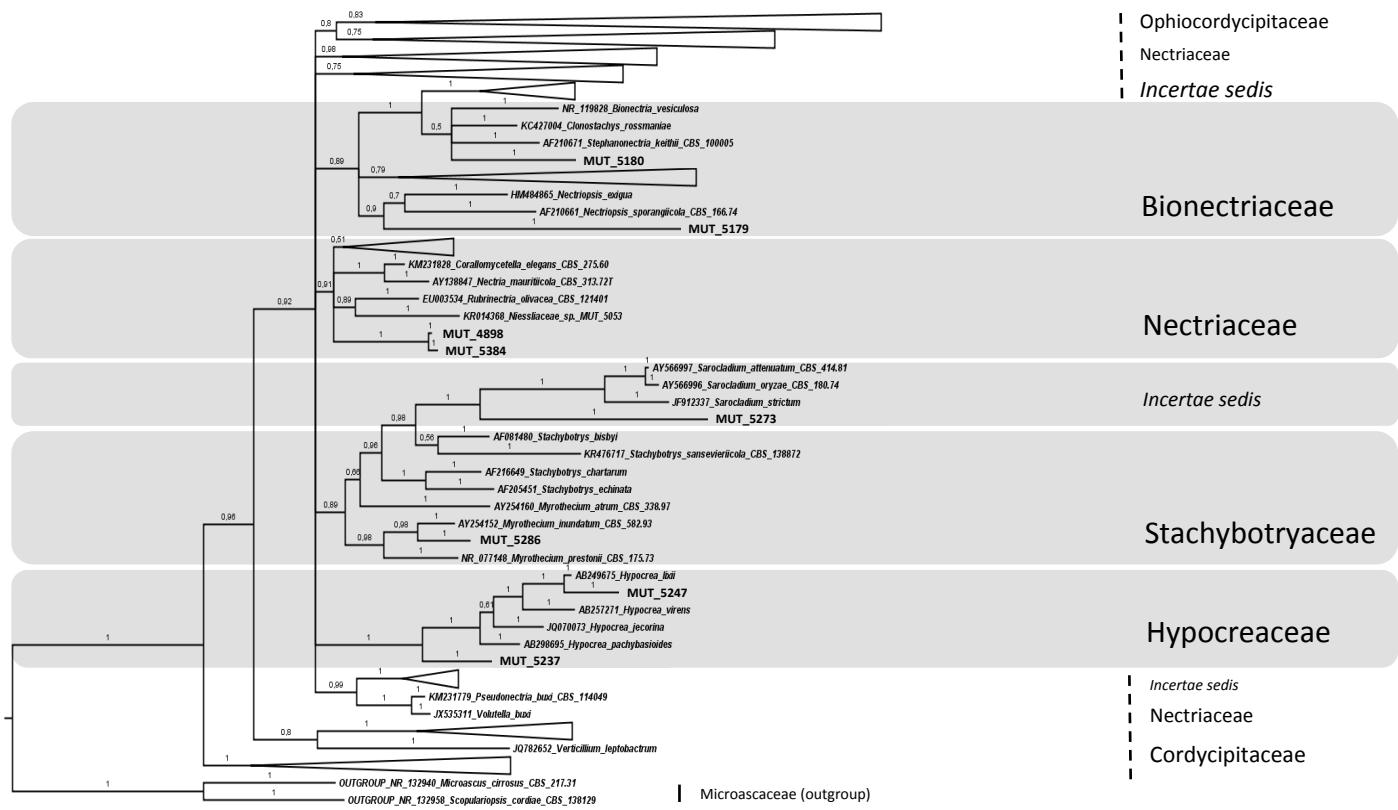
Amniculicolaceae

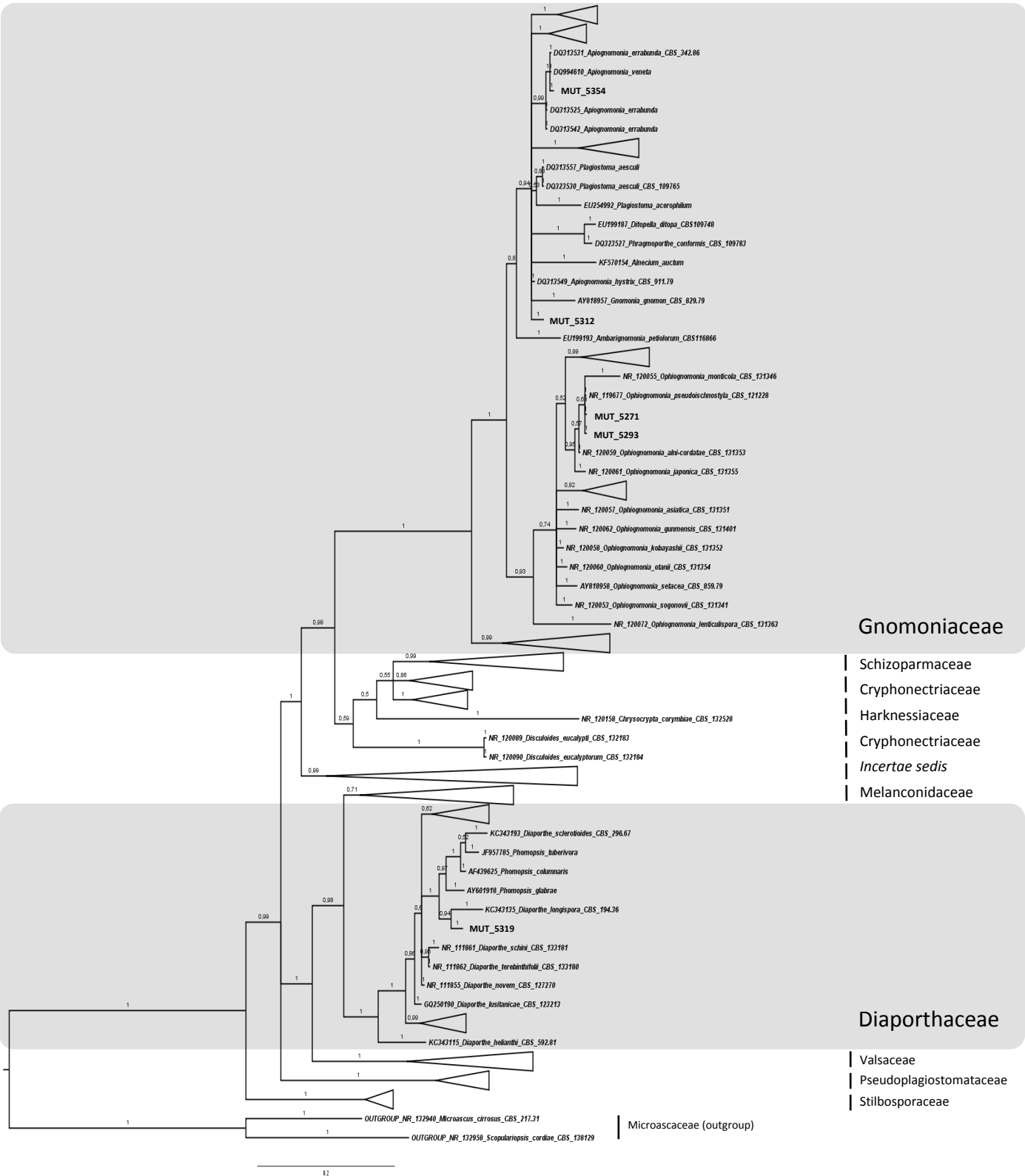
Melanommataceae

Pleomassariniaceae

Massariaceae

Hysteriaceae (outgroup)





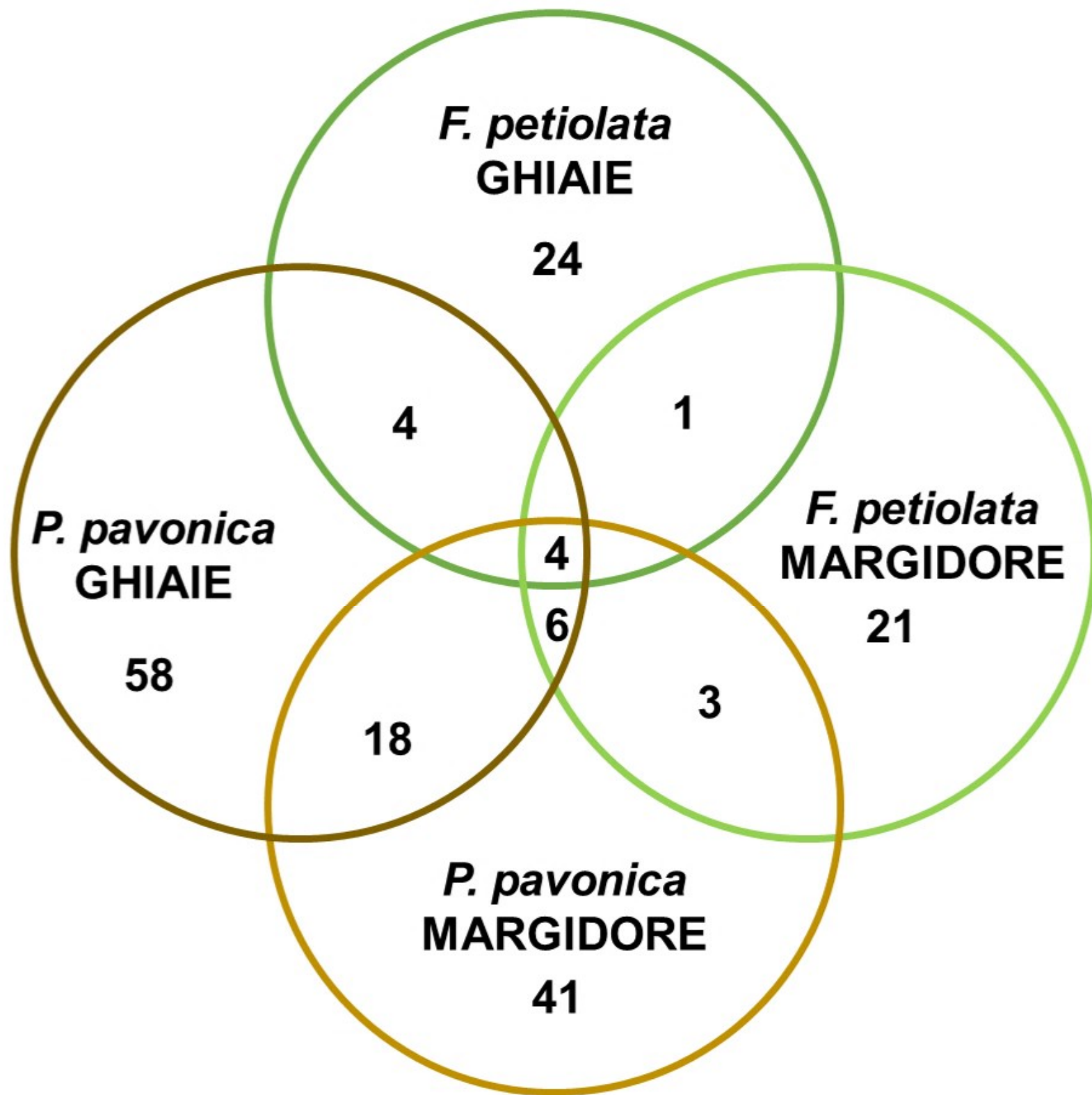


Table 1. Average fungal load (CFU/gdw±SE) and number of fungal entities isolated from *P. pavonica* specimens in different sites and depth. Biodiversity within sampling sites: Shannon-Weaver's index (H'), Gini-Simpson's index (1-Lambda) and Pielou's evenness (J').

Sites	Ghiaie				Margidore			
	USL 3-5m depth		ISL 14-15m depth		USL 3-5m depth		ISL 14-15m depth	
Depth media	PASW	CMASW	PASW	CMASW	PASW	CMASW	PASW	CMASW
CFU/g dw±SE	1,485±52	1,007±94	1,760±56	1,500±79	1,523±45	1,083±71	1,343±90	898±71
Average CFU/gdw	1,246±41		1,630±51		1,303±37		1,121±41	
	1,438±69				1,212±72			
Num. of exclusive fungal taxa	15(21)	8(17)	21(42)	13(30)	13(31)	7(22)	13(24)	4(15)
(total number of taxa retrieved)	23(35)		37(64)		23(44)		17(33)	
	65(90)				44(69)			
	Diversity indices							
H'	3.203		3.413		3.512		3.226	
1-lambda	0.938		0.920		0.962		0.947	
J'	0.901		0.821		0.928		0.923	

Table 2. Marine fungal entities isolated from *Padina pavonica* and recovered in other marine substrates and environments.

Taxa	From Mediterranean Sea	From brown algae	From Marine environment worldwide
<i>Aaosphaeria arxii</i> (Aa) Aptroot	FR	FR	FR
<i>Acremonium brunnescens</i> W. Gams	FR	FR	FR
<i>Acremonium furcatum</i> (Moreau & V. Moreau) ex W. Gams	[11]	FR	[7]
<i>Acremonium sclerotigenum</i> (Moreau & R. Moreau ex Valenta) W. Gams	[2], [5]	FR	[2], [5]
<i>Acremonium vitellinum</i> W. Gams	FR	FR	FR
<i>Acrostalagmus luteoalbus</i> (Link) Zare, W. Gams & Schroers	[2], [6]	FR	[7]
* Agaricales sp.	/	/	/
<i>Alternaria metachromatica</i> E.G. Simmons	FR	FR	FR
* <i>Alternaria</i> sp.	/	/	/
* <i>Apiognomonina</i> sp.	/	/	/
<i>Arthrimum arundinis</i> (Corda) Dyko & B. Sutton	[1], [2], [5]	[13]	[1], [2], [5], [13]
<i>Arthrimum marii</i> Larrondo & Calvo	FR	FR	FR
<i>Arthrimum phaeospermum</i> (Corda) M.B. Ellis	[1], [2], [5], [6]	FR	[1], [2], [5], [6]
* Ascomycota sp.1	/	/	/
* Ascomycota sp.2	/	/	/
* Ascomycota sp.3	/	/	/
<i>Aspergillus conicus</i> Blochwitz	FR	FR	FR
<i>Aspergillus fumigatus</i> Fresen.	[1], [4], [5]	[16]	[7]
<i>Aspergillus heyangensis</i> Z.T. Qi, Z.M. Sun & Yu X. Wang	FR	FR	FR
<i>Aspergillus insuetus</i> (Bainier) Thom & Church	[5], [6], [14]	FR	[7]
<i>Aspergillus insulicola</i> Montem. & A.R. Santiago	FR	FR	[7]
<i>Aspergillus terreus</i> Thom	[3], [5], [10]	[10], [16]	[7]
<i>Aureobasidium pullulans</i> (de Bary) G. Arnaud	[2], [6]	FR	[7]
<i>Aureobasidium pullulans</i> var. <i>melanogenum</i> Herm.-Nijh.	[2], [6]	FR	[7]
<i>Bionectria ochroleuca</i> (Schwein.) Schroers & Samuels	FR	FR	[7]
* Bionectriaceae sp.	/	/	/
* <i>Bjerkandera adusta</i> (Willd.) P. Karst.	FR	FR	FR

* Botryosphaeriaceae sp. 1	/	/	/
* Capnodiales sp.1	/	/	/
* Capnodiales sp.2	/	/	/
* Capnodiales sp.3	/	/	/
<i>Chaetomium bostrychodes</i> Zopf	FR	FR	[17]
<i>Chamaeleomyces granulomatis</i> Sigler	FR	FR	FR
<i>Cladosporium allicinum</i> (Fr. : Fr.) Bensch, U. Braun & Crous	[2]	[2]	[2]
<i>Cladosporium bruhnei</i> Linder	[5]	FR	[5]
<i>Cladosporium cladosporioides</i> (Fresen.) G.A. de Vries	[1], [2], [5], [9], [10]	FR	[7]
<i>Cladosporium delicatulum</i> Cooke, Grevillea	FR	FR	FR
<i>Cladosporium halotolerans</i> Zalar, de Hoog & Gunde-Cim.	[5], [11]	FR	[5], [11]
<i>Cladosporium iranicum</i> Bensch, Crous & U. Braun	FR	FR	FR
<i>Cladosporium pseudocladosporioides</i> Bensch, Crous & U. Braun	[5], [9]	FR	[5], [9]
<i>Cladosporium ramotenellum</i> K. Schub., Zalar, Crous & U. Braun	FR	FR	[18]
<i>Cladosporium sphaerospermum</i> Penz.	[1], [2], [6]	FR	
<i>Cladosporium subtilissimum</i> K. Schub., Dugan, Crous & U. Braun	FR	FR	FR
<i>Cladosporium uredinicola</i> Speg.	FR	FR	[7]
<i>Cladosporium xylophilum</i> Bensch, Shabunin, Crous & U. Braun	FR	FR	FR
<i>Cladosporium</i> sp.	/	[16]	/
* <i>Clonostachys</i> sp.	/	/	/
* <i>Coprinellus</i> sp.	/	/	/
* Cucurbitariaceae sp.1	/	/	/
* Cucurbitariaceae sp.2	/	/	/
<i>Devriesia lagerstroemiae</i> Crous & M.J. Wingfield	FR	FR	FR
* <i>Diaporthe</i> sp.	/	/	/
* Didymellaceae sp.	/	/	/
* Didymosphaeriaceae sp.	/	/	/
* Dohideomycetes sp.1	/	/	/
* Dohideomycetes sp.2	/	/	/
* Dohideomycetes sp.3	/	/	/
* Dothideomycetes sp.4	/	/	/
* Dothideomycetes sp.5	/	/	/

<i>Exophiala aquamarina</i> de Hoog, Vicente, Najafzadeh, Harrak, Badali, Seyedmousavi & Nyaoke	[19]		
<i>Fusarium oxysporum</i> Schltdl.	[5], [11]	[13]	[5], [11], [13]
<i>Gibellulopsis nigrescens</i> (Pethybr.) Zare, W. Gams & Summerb.	[1], [2], [5], [6]	[13]	[1], [2], [5], [6], [13]
* <i>Gnomoniaceae</i> sp.	/	/	/
* <i>Helotiales</i> sp.1	/	/	/
* <i>Helotiales</i> sp.2	/	/	/
* <i>Hydropiosphaera</i> sp.	/	/	/
* <i>Lachnum</i> sp.	/	/	/
* <i>Lemonniera</i> sp.	/	/	/
<i>Libertella blepharis</i> A.L. Sm.	FR	FR	FR
* <i>Lophiotrema rubi</i> (Fuckel) Yin. Zhang, C.L. Schoch & K.D. Hyde	[1], [2]	-	[1], [2]
* <i>Lophiotremataceae</i> sp.1	/	/	/
* <i>Lophiotremataceae</i> sp.2 =Flb MUT4887	/	/	/
* <i>Lophiotremataceae</i> sp.3	/	/	/
<i>Microsphaeropsis olivacea</i> (Bonorden) Höhnel	FR	FR	[20]
<i>Mortierella alpina</i> Peyronel		FR	[21]
* <i>Myrothecium inundatum</i> Tode			[7]
* <i>Nectriaceae</i> sp. 1	/	/	/
<i>Ochrocladosporium frigidarii</i> Crous & U. Braun	FR	FR	FR
* <i>Ophiognomonia</i> sp.	/	/	/
<i>Paecilomyces inflatus</i> (Burnside) J.W. Carmich.	FR	FR	FR
* <i>Paraconiothyrium variabile</i> Riccioni, Damm, Verkley & Crous	FR	FR	FR
* <i>Paraconiothyrium</i> sp.	/	/	/
<i>Paraphaeosphaeria neglecta</i> Verkley, Riccioni & Stielow	FR	FR	FR
<i>Penicillium antarcticum</i> A.D. Hocking & C.F. McRae	[2], [5], [6]	-	[2], [5], [6]
<i>Penicillium brevicompactum</i> Dierckx	[1], [2], [3], [4], [5], [6], [10]	[10]	[7]
<i>Penicillium caseifulvum</i> Lund, Filt. & Frisvad	FR	FR	FR
<i>Penicillium citrinum</i> Thom	[3], [5], [6], [10]	[10], [12]	[7]
<i>Penicillium roseopurpureum</i> Dierckx	[6]	[6]	[6]
<i>Penicillium spinulosum</i> Thom	[1]	-	[7]

<i>Penicillium steckii</i> K.M. Zalessky	[3], [6]	-	[3], [6]
<i>Penicillium</i> sp.	/	[16]	/
<i>Pestalotia olivacea</i> Guba	FR	FR	FR
* <i>Pezizomycotina</i> sp.	/	/	/
* <i>Phaeosphaeria</i> sp.	/	/	/
* <i>Phaeosphaeriaceae</i> sp. 1	/	/	/
<i>Plectosporium tabacinum</i> (J.F.H. Beyma) M.E. Palm, W. Gams & Nirenberg	FR	FR	FR
* <i>Pleosporaceae</i> sp.	/	/	/
* <i>Pleosporales</i> sp.1	/	/	/
* <i>Pleosporales</i> sp.2	/	/	/
* <i>Pleosporales</i> sp.3	/	/	/
<i>Pochonia chlamydosporia</i> (Goddard) Zare & W. Gams	FR	FR	FR
* <i>Pyrenochaeta</i> sp.1	/	/	/
* <i>Pyrenochaeta</i> sp.2	/	/	/
* <i>Pyrenochaeta</i> sp.3	/	/	/
* <i>Pyrenochaeta</i> sp.4	/	/	/
<i>Pyrenochaetopsis microspora</i> (Gruyter & Boerema) Gruyter, Aveskamp & Verkley	FR	FR	FR
* <i>Pyrenochaetopsis</i> sp.1	/	/	/
* <i>Pyrenochaetopsis</i> sp.2	/	/	/
* <i>Pyrenochaetopsis</i> sp.3	/	/	/
<i>Ramichloridium strelitziae</i> Arzanlou, W. Gams & Crous	FR	FR	FR
<i>Rhodotorula aurantiaca</i> (Saito) Lodder	FR	FR	[7]
* <i>Roussoellaceae</i> sp.1	/	/	/
* <i>Roussoellaceae</i> sp.2	/	/	/
* <i>Roussoellaceae</i> sp.3	/	/	/
* <i>Roussoellaceae</i> sp.4 =FLAB4886 e 4971	/	/	/
* <i>Roussoellaceae</i> sp.5	/	/	/
<i>Sarocladium glaucum</i> (W. Gams) Summerbell	FR	FR	FR
* <i>Sarocladium</i> sp.	/	/	/
* <i>Schizophyllum commune</i> Fr.	[1], [2]	-	[7]

<i>Scopulariopsis humicola</i> G.L. Barron	FR	FR	FR
* <i>Sordariomycetes</i> sp.1	/	/	/
* <i>Sordariomycetes</i> sp.2	/	/	/
* <i>Sporidiobolales</i> sp.	/	/	/
<i>Sporothrix inflata</i> de Hoog	FR	FR	FR
* <i>Stachybotryna</i> sp.	/	/	/
<i>Stachybotrys chartarum</i> (Ehrenberg) S. Hughes	[5], [6], [11]	-	[7]
* <i>Thelebolus</i> sp.	/	/	/
<i>Toxicocladosporium strelitziae</i> P.W. Crous	FR	FR	FR
<i>Trichoderma aureoviride</i> Rifai	FR	FR	[7]
<i>Trichoderma harzianum</i> Rifai	[1], [3], [4], [5], [6]	[8]	[7]
<i>Trichoderma koningi</i> Oudemans	[1], [5]	-	[7]
* <i>Trichoderma</i> sp.	/	[16]	/
<i>Wallemia sebi</i> (Fr.) Arx	[1]	[15]	[7]
* Fungal sp.1	/	/	/

*Identification confirmed with phylogenetic analyses.

References: FR First Record, [1] Panno et al., 2013, [2] Gnavi et al., 2017, [3] Paz et al., 2010, [4] Lopez et al., 2015, [5] Bovio et al., 2017, [6] Marchese et al., 2016, [7] Jones et al., 2015, [8] Thirunavukkarasu et al., 2015, [9] Garzoli et al., 2014, [10] Atalla et al., 2010, [11] Garzoli et al., 2015, [12] Smetanina et al., 2016, [13] Hong et al., 2015, [14] Lopez-Gresa et al., 2009, [15] Kuncic et al., 2010, [16] Flewelling et al., 2015, [17] Clipson et al., 2001, [18] Li and Li, 2014, [19] de Hoog et al. 2011, [20] Keusgen et al., 1996, [21] Landy and Jones, 2006.

Supplementary material 1. List of marine fungal strains isolated from *Padina pavonica*. Mycotheca Universitatis Taurinensis (MUT) accession number (available on: <http://www.mut.unito.it/en/Database>) and GenBank Accession Numbers are indicated.

MUT Accession number	Taxa	Genbank accession number							
		ITS	LSU	SSU	ACT	CL	BT	NL	GPD
5333	<i>Aaosphaeria arxii</i> (Aa) Aptroot	KU158145							
5198	<i>Acremonium brunnescens</i> W. Gams	KT699144	KT699149						
5297	<i>Acremonium brunnescens</i> W. Gams	KU255047							
5296	<i>Acremonium furcatum</i> (Moreau & V. Moreau) ex W. Gams	KU255046							
4854	<i>Acremonium sclerotigenum</i> (Moreau & R. Moreau ex Valenta) W. Gams	KT699120	KT699145	KT699150					
4896	<i>Acremonium vitellinum</i> W. Gams	KT699123		KT699152					
5173	<i>Acrostalagmus luteoalbus</i> (Link) Zare, W. Gams & Schroers	KT699135							
5230	<i>Acrostalagmus luteoalbus</i> (Link) Zare, W. Gams & Schroers								
5252	<i>Acrostalagmus luteoalbus</i> (Link) Zare, W. Gams & Schroers								
5264	<i>Acrostalagmus luteoalbus</i> (Link) Zare, W. Gams & Schroers	KT715714							
5265	<i>Acrostalagmus luteoalbus</i> (Link) Zare, W. Gams & Schroers								
5274	<i>Acrostalagmus luteoalbus</i> (Link) Zare, W. Gams & Schroers								
5275	<i>Acrostalagmus luteoalbus</i> (Link) Zare, W. Gams & Schroers	KT715723							
5280	<i>Acrostalagmus luteoalbus</i> (Link) Zare, W. Gams & Schroers	KT715728							
5203	Agaricales sp.	KM355987							
5334	<i>Alternaria metachromatica</i> E.G. Simmons	KU158146							KU198155
5335	<i>Alternaria metachromatica</i> E.G. Simmons	KU158147		KU158174					KU198156
5332	<i>Alternaria</i> sp.	KU158144		KU158173					KU198154
5354	<i>Apiognomonina</i> sp.	KU158163							
5254	<i>Arthrinium arundinis</i> (Corda) Dyko & B. Sutton	KT715713							
5343	<i>Arthrinium arundinis</i> (Corda) Dyko & B. Sutton	KU158155							
5452	<i>Arthrinium arundinis</i> (Corda) Dyko & B. Sutton								
5267	<i>Arthrinium marii</i> Larrondo & Calvo	KT715716							
5288	<i>Arthrinium marii</i> Larrondo & Calvo								
5317	<i>Arthrinium marii</i> Larrondo & Calvo	KU255061							
4906	<i>Arthrinium phaeospermum</i> (Corda) M.B. Ellis	KT699131							
5443	Ascomycota sp.1	KU314971							
5449	Ascomycota sp.2	KU314977		KU314978					
5309	Ascomycota sp.3	KU255056							
78	<i>Aspergillus conicus</i> Blochwitz	KT699116					KT779529		
5253	<i>Aspergillus fumigatus</i> Fresen.						KU198177		
5387	<i>Aspergillus heyangensis</i> Z.T. Qi, Z.M. Sun & Yu X. Wang						KU198178		
4895	<i>Aspergillus insuetus</i> (Bainier) Thom & Church	KT699122		KT699151			KT779532		
102	<i>Aspergillus insulicola</i> Montem. & A.R. Santiago						KT779530		
5168	<i>Aspergillus terreus</i> Thom	KT699133							

72	<i>Aureobasidium pullulans</i> (de Bary) G. Arnaud	KT699115	
5266	<i>Aureobasidium pullulans</i> var. <i>melanogenum</i> Herm.-Nijh.	KT715715	
4900	<i>Bionectria ochroleuca</i> (Schwein.) Schroers & Samuels	KT699125	KT699147
5292	Bionectriaceae sp.	KU255042	KU255043
5195	<i>Bjerkandera adusta</i> (Willd.) P. Karst.	KM355986	
4901	Botryosphaeriaceae sp. 1	KT699126	KT699154
5176	Botryosphaeriaceae sp. 1	KT699137	
5445	Capnodiales sp.1	KU314973	KU314974
4905	Capnodiales sp.2	KT699130	
5441	Capnodiales sp.3	KU314969	
5244	<i>Chaetomium bostrychodes</i> Zopf	KT715709	
5385	<i>Chamaeleomyces granulomatis</i> Sigler		KU314964
5277	<i>Cladosporium allacinum</i> (Fr. : Fr.) Bensch, U. Braun & Crous	KT715725	
5454	<i>Cladosporium bruhnei</i> Linder		KU198173
5295	<i>Cladosporium cladosporioides</i> (Fresen.) G.A. de Vries	KU314943	
5316	<i>Cladosporium cladosporioides</i> (Fresen.) G.A. de Vries	KU255060	KU158139
5379	<i>Cladosporium cladosporioides</i> (Fresen.) G.A. de Vries		KU198168
109	<i>Cladosporium delicatulum</i> Cooke, Grevillea		KU158126
5287	<i>Cladosporium halotolerans</i> Zalar, de Hoog & Gunde-Cim.		KU158129
5289	<i>Cladosporium halotolerans</i> Zalar, de Hoog & Gunde-Cim.		KU158130
5353	<i>Cladosporium halotolerans</i> Zalar, de Hoog & Gunde-Cim.		KU198159
5362	<i>Cladosporium halotolerans</i> Zalar, de Hoog & Gunde-Cim.		KU198160
5372	<i>Cladosporium halotolerans</i> Zalar, de Hoog & Gunde-Cim.		KU198161
5374	<i>Cladosporium halotolerans</i> Zalar, de Hoog & Gunde-Cim.		KU198162
5375	<i>Cladosporium halotolerans</i> Zalar, de Hoog & Gunde-Cim.		KU198163
5376	<i>Cladosporium halotolerans</i> Zalar, de Hoog & Gunde-Cim.		KU198164
5298	<i>Cladosporium iranicum</i> Bensch, Crous & U. Braun	KU255048	KU158133
5330	<i>Cladosporium pseudocladosporioides</i> Bensch, Crous & U. Braun	KU158142	KU158172
5356	<i>Cladosporium pseudocladosporioides</i> Bensch, Crous & U. Braun	KU158165	
5364	<i>Cladosporium pseudocladosporioides</i> Bensch, Crous & U. Braun		KU198167
5388	<i>Cladosporium pseudocladosporioides</i> Bensch, Crous & U. Braun	KU314967	KU198170
5323	<i>Cladosporium ramotenellum</i> K. Schub., Zalar, Crous & U. Braun		KU158140
5324	<i>Cladosporium ramotenellum</i> K. Schub., Zalar, Crous & U. Braun		KU158141
5451	<i>Cladosporium</i> sp.	KU314979	KU198172
89	<i>Cladosporium sphaerospermum</i> Penz.		KU158125
5307	<i>Cladosporium sphaerospermum</i> Penz.		KU158138
5450	<i>Cladosporium sphaerospermum</i> Penz.		KU198171
5301	<i>Cladosporium subtilissimum</i> K. Schub., Dugan, Crous & U. Braun		KU158134
5363	<i>Cladosporium subtilissimum</i> K. Schub., Dugan, Crous & U. Braun		KU198166
5250	<i>Cladosporium uredinicola</i> Speg.		KU158127
5357	<i>Cladosporium uredinicola</i> Speg.		KU198165

5457	<i>Cladosporium xylophilum</i> Bensch, Shabunin, Crous & U. Braun		
5180	<i>Clonostachys</i> sp.	KT699140	
4897	<i>Coprinellus</i> sp.	KM355983	KM355995
5167	<i>Coprinellus</i> sp.	KT699132	
5171	<i>Coprinellus</i> sp.	KT699134	
5313	Cucurbitariaceae sp.1	KU255059	
5462	Cucurbitariaceae sp.1	KU314985	
5299	Cucurbitariaceae sp.2	KU255049	
5473	<i>Devriesia lagerstroemiae</i> Crous & M.J. Wingfield	KU314992	
5319	<i>Diaporthe</i> sp.	KU255063	
88	Didymellaceae sp.	KT699118	
4894	Didymellaceae sp.	KM355999	KM355994
5242	Didymosphaeriaceae sp.1	KT715707	
5318	Didymosphaeriaceae sp.1	KU255062	
5345	Didymosphaeriaceae sp.1	KU158157	
5347	Didymosphaeriaceae sp.1	KU158159	
5383	Dohideomycetes sp.1	KU314962	
4902	Dohideomycetes sp.2	KT699127	KT699155
5270	Dohideomycetes sp.2	KT715719	KU158128
5448	Dohideomycetes sp.2	KU314976	
4899	Dohideomycetes sp.3	KM356000	KM355996
5279	Dohideomycetes sp.3	KT715727	
5308	Dohideomycetes sp.3	KU255055	
5346	Dohideomycetes sp.3	KU158158	
5278	Dothideomycetes sp.4		KT715726
5459	Dothideomycetes sp.5		
5352	<i>Exophiala aquamarina</i> de Hoog, Vicente, Najafzadeh, Harrak, Badali, Seyedmousavi & Nyaoke	KU158162	
5226	Fungal sp. 1	KM355988	
5215	<i>Fusarium oxysporum</i> Schltdl.		
5351	<i>Gibellulopsis nigrescens</i> (Pethybr.) Zare, W. Gams & Summerb.	KU158161	
5382	<i>Gibellulopsis nigrescens</i> (Pethybr.) Zare, W. Gams & Summerb.	KU314961	KU198169
5312	Gnomoniaceae sp.	KU255058	
5470	Helotiales sp.1	KU314990	
5177	Helotiales sp.2	KT699138	
5179	<i>Hydropiosphaera</i> sp.	KT699139	
84	<i>Lachnum</i> sp.	KT699117	
5444	<i>Lemonniera</i> sp.	KU314972	
5165	<i>Libertella blepharis</i> A.L. Sm.	KM355984	
5302	<i>Lophiotrema rubi</i> (Fuckel) Yin. Zhang, C.L. Schoch & K.D. Hyde	KU255051	KU158135
4903	Lophiotremataceae sp.1	KT699128	
5303	Lophiotremataceae sp.1	KU255052	KU158136

5327	Lophiotremataceae sp.1	KU255071		KU198174
5336	Lophiotremataceae sp.1	KU158148		KU198157
5355	Lophiotremataceae sp.1	KU158164		
5269	Lophiotremataceae sp.2 =Flb MUT4887	KT715718		
5337	Lophiotremataceae sp.2 =Flb MUT4887	KU158149		
5458	Lophiotremataceae sp.2 =Flb MUT4887	KU314982		
5463	Lophiotremataceae sp.3	KU314986		
5464	Lophiotremataceae sp.3			
5331	<i>Microsphaeropsis olivacea</i> (Bonorden) Höhnelt	KU158143		
5172	<i>Mortierella alpina</i> Peyronel		KT699148	
5194	<i>Mortierella alpina</i> Peyronel	KT699142		
5286	<i>Myrothecium inundatum</i> Tode	KU255039		
4898	Nectriaceae sp. 1	KT699124	KT699146	KT699153
5384	Nectriaceae sp. 1	GENBPP11		
5502	<i>Ochrocladosporium frigidarii</i> Crous & U. Braun	KU314963		
5271	<i>Ophiognomonia</i> sp.	KT715720		
5293	<i>Ophiognomonia</i> sp.	KU255044		
5272	<i>Paecilomyces inflatus</i> (Burnside) J.W. Carmich.	KT715721		
5227	<i>Paraconiothyrium</i> sp.	KT715702		
5243	<i>Paraconiothyrium variabile</i> Riccioni, Damm, Verkley & Crous	KT715708		
5344	<i>Paraconiothyrium variabile</i> Riccioni, Damm, Verkley & Crous	KU158156		
5395	<i>Paraconiothyrium variabile</i> Riccioni, Damm, Verkley & Crous	KU314968		
5229	<i>Paraphaeosphaeria neglecta</i> Verkley, Riccioni & Stielow	KT715703		
5170	<i>Penicillium antarcticum</i> A.D. Hocking & C.F. McRae			
5184	<i>Penicillium antarcticum</i> A.D. Hocking & C.F. McRae			
5186	<i>Penicillium antarcticum</i> A.D. Hocking & C.F. McRae			
5187	<i>Penicillium antarcticum</i> A.D. Hocking & C.F. McRae			KT779536
5199	<i>Penicillium antarcticum</i> A.D. Hocking & C.F. McRae			KT779541
5201	<i>Penicillium antarcticum</i> A.D. Hocking & C.F. McRae			KT779542
5206	<i>Penicillium antarcticum</i> A.D. Hocking & C.F. McRae			
5207	<i>Penicillium antarcticum</i> A.D. Hocking & C.F. McRae			KT779544
5211	<i>Penicillium antarcticum</i> A.D. Hocking & C.F. McRae			
5212	<i>Penicillium antarcticum</i> A.D. Hocking & C.F. McRae			
5218	<i>Penicillium antarcticum</i> A.D. Hocking & C.F. McRae			
5219	<i>Penicillium antarcticum</i> A.D. Hocking & C.F. McRae			KT779547
5220	<i>Penicillium antarcticum</i> A.D. Hocking & C.F. McRae			
5221	<i>Penicillium antarcticum</i> A.D. Hocking & C.F. McRae			
5222	<i>Penicillium antarcticum</i> A.D. Hocking & C.F. McRae			
5223	<i>Penicillium antarcticum</i> A.D. Hocking & C.F. McRae			
5225	<i>Penicillium antarcticum</i> A.D. Hocking & C.F. McRae			KU198175
5232	<i>Penicillium antarcticum</i> A.D. Hocking & C.F. McRae			

5233	<i>Penicillium antarcticum</i> A.D. Hocking & C.F. McRae		
5234	<i>Penicillium antarcticum</i> A.D. Hocking & C.F. McRae		
5235	<i>Penicillium antarcticum</i> A.D. Hocking & C.F. McRae		
5314	<i>Penicillium antarcticum</i> A.D. Hocking & C.F. McRae		
5315	<i>Penicillium antarcticum</i> A.D. Hocking & C.F. McRae		
5169	<i>Penicillium brevicompactum</i> Dierckx		KT779535
5183	<i>Penicillium brevicompactum</i> Dierckx		
5191	<i>Penicillium brevicompactum</i> Dierckx		
5193	<i>Penicillium brevicompactum</i> Dierckx		KT779540
5208	<i>Penicillium brevicompactum</i> Dierckx		
5166	<i>Penicillium caseifulvum</i> Lund, Filt. & Frisvad		KT779534
5213	<i>Penicillium caseifulvum</i> Lund, Filt. & Frisvad		
5202	<i>Penicillium citrinum</i> Thom		KT779543
5217	<i>Penicillium citrinum</i> Thom		KT779546
5236	<i>Penicillium citrinum</i> Thom		KU198176
4892	<i>Penicillium roseopurpureum</i> Dierckx	KT699121	KT779531
5164	<i>Penicillium roseopurpureum</i> Dierckx		KT779533
5174	<i>Penicillium roseopurpureum</i> Dierckx		
5181	<i>Penicillium roseopurpureum</i> Dierckx		
5185	<i>Penicillium roseopurpureum</i> Dierckx		
5196	<i>Penicillium roseopurpureum</i> Dierckx		
5205	<i>Penicillium roseopurpureum</i> Dierckx		
5209	<i>Penicillium roseopurpureum</i> Dierckx	KT715699	KT779545
5188	<i>Penicillium</i> sp.	KT699141	KT779537
5245	<i>Penicillium</i> sp.		
5189	<i>Penicillium spinulosum</i> Thom		KT779538
5182	<i>Penicillium steckii</i> K.M. Zalesky		
5192	<i>Penicillium steckii</i> Zaleski		KT779539
5224	<i>Penicillium steckii</i> Zaleski		KT779548
5214	<i>Pestalotia olivacea</i> Guba	KT715700	
5241	<i>Pestalotia olivacea</i> Guba		
5285	Pezizomycotina sp.	KU255038	
5321	<i>Phaeosphaeria</i> sp.	KU255065	
5328	Phaeosphaeriaceae sp. 1	KU255072	KU255073
5175	<i>Plectosporium tabacinum</i> (J.F.H. Beyma) M.E. Palm, W. Gams & Nirenberg	KT699136	
5178	Pleosporaceae sp.	KM355985	
5283	Pleosporales sp.1	KU255035	KU255036
5326	Pleosporales sp.2	KU255069	KU255070
5342	Pleosporales sp.2	KU158154	KU158177
5370	Pleosporales sp.2	KU314949	KU314950
5290	Pleosporales sp.3	KU255040	KU158131

5367	Pleosporales sp.3	KU314945	KU198158
5320	<i>Pochonia chlamydosporia</i> (Goddard) Zare & W. Gams	KU255064	
5216	Pyrenochaeta sp.1	KT715701	
5386	Pyrenochaeta sp.2	KU314965	KU314966
5276	Pyrenochaeta sp.3	KM356002	KT715724
5325	Pyrenochaeta sp.4	KU255067	KU255068
5366	Pyrenochaeta sp.4	KU158171	KU158180
5268	<i>Pyrenochaetopsis microspora</i> (Gruyter & Boerema) Gruyter, Aveskamp & Verkley	KM355992	KT715717
5228	Pyrenochaetopsis sp.1	KM355989	
5338	Pyrenochaetopsis sp.1	KU158150	
5339	Pyrenochaetopsis sp.1	KU158151	KU158175
5358	Pyrenochaetopsis sp.1	KU158166	
5361	Pyrenochaetopsis sp.1	KU158169	
5378	Pyrenochaetopsis sp.1	KU314955	KU314956
5284	Pyrenochaetopsis sp.2	KU255037	
5340	Pyrenochaetopsis sp.2	KU158152	
5359	Pyrenochaetopsis sp.2	KU158167	
5380	Pyrenochaetopsis sp.2	KU314957	KU314958
5442	Pyrenochaetopsis sp.2	KU314970	
5455	Pyrenochaetopsis sp.2	KU314980	
5304	Pyrenochaetopsis sp.3		KU158137
5305	Pyrenochaetopsis sp.3	KU255053	
5360	Pyrenochaetopsis sp.3	KU158168	KU158178
5368	Pyrenochaetopsis sp.3	KU314946	
5460	Pyrenochaetopsis sp.3	KU314983	KU314984
5465	Pyrenochaetopsis sp.3	KU314987	KU314988
5504	<i>Ramichloridium strelitziae</i> Arzanlou, W. Gams & Crous	KU314994	
5471	<i>Rhodotorula aurantiaca</i>		KU314991
5329	Roussoellaceae sp.1	KU314944	
5306	Roussoellaceae sp.2	KU255054	
5341	Roussoellaceae sp.2	KU158153	KU158176
5365	Roussoellaceae sp.2	KU158170	KU158179
5369	Roussoellaceae sp.2	KU314947	KU314948
5503	Roussoellaceae sp.2	KU314993	
4904	Roussoellaceae sp.3	KT699129	
5373	Roussoellaceae sp.3	KU314953	KU314954
4893	Roussoellaceae sp.4	KM355998	KM355993
5371	Roussoellaceae sp.4 =FLAB4886 e 4971	KU314951	KU314952
5310	Roussoellaceae sp.5	KU255057	
5381	Roussoellaceae sp.5	KU314959	KU314960
5294	<i>Sarocladium glaucum</i> (W. Gams) Summerbell	KU255045	

5273	<i>Sarocladium</i> sp.	KT715722		
5200	<i>Schizophyllum commune</i> Fr.	KT715697		
5204	<i>Schizophyllum commune</i> Fr.	KT715698		
5240	<i>Schizophyllum commune</i> Fr.	KM355991	KT715706	
5456	<i>Scopulariopsis humicola</i> G.L. Barron	KU314981		
4926	Sordariomycetes sp.1	KM356001	KM355997	
5282	Sordariomycetes sp.2	KT715730		
73	Sporidiobolales sp.			KU158181
5197	<i>Sporothrix inflata</i> de Hoog	KT699143		
5466	<i>Stachybotryna</i> sp.	KU314989		
5322	<i>Stachybotrys chartarum</i> (Ehrenberg) S. Hughes	KU255066		
5350	<i>Stachybotrys chartarum</i> (Ehrenberg) S. Hughes	KU158160		KU198179
5447	<i>Stachybotrys chartarum</i> (Ehrenberg) S. Hughes	KU314975		
5281	<i>Thelebolus</i> sp.	KT715729		
5300	<i>Thelebolus</i> sp.	KU255050		
5291	<i>Toxicocladosporium strelitziae</i> P.W. Crous	KU255041		KU158132
5231	<i>Trichoderma aureoviride</i> Rifai	KU314942		
5238	<i>Trichoderma harzianum</i> Rifai	KT715704		
5239	<i>Trichoderma harzianum</i> Rifai	KT715705		
5247	<i>Trichoderma harzianum</i> Rifai	KT715711		
5248	<i>Trichoderma harzianum</i> Rifai			
5505	<i>Trichoderma koningi</i> Oudemans	KU314996		
5190	<i>Trichoderma koningii</i> Oudemans			
5246	<i>Trichoderma koningii</i> Oudemans	KT715710		
5249	<i>Trichoderma koningii</i> Oudemans	KT715712		
5237	<i>Trichoderma</i> sp.	KM355990		
103	<i>Wallemia sebi</i> (Fr.) Arx	KT699119		

Supplementary material 2. The colonisation rates (Colony Forming Unit per gram of dry weight CFU/g dw \pm Standard Error SE) of the taxa retrieved on thalli of *Padina pavonica* per each site analyzed (Ghiaie and Margidore) and for each depth (Upper Sea Level USL and Intermediate Sea Level ISL).

Sites Depth Media	Ghiaie (CFU/gdw \pm SE)				Margidore (CFU/gdw \pm SE)			
	USL 3-5m depth		ISL 14-15m depth		USL 3-5m depth		ISL 14-15m depth	
	PASW	CMASW	PASW	CMASW	PASW	CMASW	PASW	CMASW
	CFU \pm ES	CFU \pm ES	CFU \pm ES	CFU \pm ES	CFU \pm ES	CFU \pm ES	CFU \pm ES	CFU \pm ES
<i>Aaosphaeria arxii</i> (Aa) Aptroot	0	0	0	0	0	0	0	0
<i>Acremonium brunnescens</i> W. Gams	0	0	0	0	112 \pm 249	45.5 \pm 102	0	0
<i>Acremonium furcatum</i> (Moreau & V. Moreau) ex W. Gams	0	0	0	0	0 \pm 0	0	0	40.8 \pm 91.3
<i>Acremonium sclerotigenum</i> (Moreau & R. Moreau ex Valenta) W. Gams	0	0	0	0	0 \pm 0	0	0	0
<i>Acremonium vitellinum</i> W. Gams	0	0	0	26.8 \pm 59.9	0 \pm 0	0	0	0
<i>Acrostalagmus luteoalbus</i> (Link) Zare, W. Gams & Schroers	118 \pm 264	39.4 \pm 88.1	0	29.6 \pm 66.2	23.7 \pm 52.9	45.5 \pm 102	40.8 \pm 91.3	40.8 \pm 91.3
* Agaricales sp.	0	73.2 \pm 109	0	0	0	0	0	0
<i>Alternaria metachromatica</i> E.G. Simmons	0	0	29.6 \pm 66.2	0	0	44.7 \pm 100	0	0
* <i>Alternaria</i> sp.	0	48.9 \pm 109	0	0	0	0	0	0
* <i>Apiognomonina</i> sp.	0	0	0	0	0	0	32.5 \pm 72.7	0
<i>Arthrinium arundinis</i> (Corda) Dyko & B. Sutton	0	0	21.3 \pm 47.7	0	0	44.7 \pm 100	85.8 \pm 192	0
<i>Arthrinium marii</i> Larrondo & Calvo	0	0	0	14.8 \pm 33.1	0	0	0	68.9 \pm 94.6
<i>Arthrinium phaeospermum</i> (Corda) M.B. Ellis	0	0	0	0	0	27.9 \pm 62.4	0	0
* Ascomycota sp.1	0	0	0	28.6 \pm 64	0	0	0	0
* Ascomycota sp.2	0	0	0	0	0	0	0	40.8 \pm 91.3
* Ascomycota sp.3	0	0	28.6 \pm 64	0	0	44.7 \pm 100	0	0
<i>Aspergillus conicus</i> Blochwitz	0	0	0	0	0	0	0	32.5 \pm 72.7
<i>Aspergillus fumigatus</i> Fresen.	0	0	0	0	0	0	42.9 \pm 96	0
<i>Aspergillus heyangensis</i> Z.T. Qj, Z.M. Sun & Yu X. Wang	0	0	0	0	0	0	0	0
<i>Aspergillus insuetus</i> (Bainier) Thom & Church	0	0	0	14.2 \pm 31.6	0	0	0	0
<i>Aspergillus insulicola</i> Montem. & A.R. Santiago	29.8 \pm 66.5	0	0	0	0	0	0	0
<i>Aspergillus terreus</i> Thom	0	0	0	0	23.7 \pm 52.9	0	0	0
<i>Aureobasidium pullulans</i> (de Bary) G. Arnaud	0	29.8 \pm 66.5	0	0	0	0	0	0
<i>Aureobasidium pullulans</i> var. <i>melanogenum</i> Herm.-Nijh.	0	39.4 \pm 88.1	0	0	0	0	0	0
<i>Bionectria ochroleuca</i> (Schwein.) Schroers & Samuels	0	0	0	0	0	27.9 \pm 62.4	0	0
* Bionectriaceae sp.	0	0	0	0	0	23.7 \pm 52.9	0	0
* <i>Bjerkandera adusta</i> (Willd.) P. Karst.	0	48.9 \pm 109	0	0	0	0	0	0
* Botryosphaeriaceae sp. 1	0	0	0	53.6 \pm 120	0	0	0	0
* Capnodiales sp.1	0	0	0	0	27.9 \pm 62.4	0	0	0
* Capnodiales sp.2	0	0	0	29.6 \pm 66.2	0	0	0	0
* Capnodiales sp.3	0	0	0	0	0	45.5 \pm 102	0	0
<i>Chaetomium bostrychodes</i> Zopf	0	0	24.7 \pm 55.2	0	0	44.7 \pm 100	0	0

<i>Chamaeleomyces granulomatis</i> Sigler	0	0	0	0	0	0	0	0
<i>Cladosporium allicinum</i> (Fr. : Fr.) Bensch, U. Braun & Crous	0	0	28.6 ± 64	0	0	44.7 ± 100	0	0
<i>Cladosporium bruhnei</i> Linder	45.5 ± 102	0	0	0	0	0	0	0
<i>Cladosporium cladosporioides</i> (Fresen.) G.A. de Vries	29.8 ± 66.5	0	104 ± 232	57.2 ± 128	0	44.7 ± 100	0	0
<i>Cladosporium delicatulum</i> Cooke, Grevillea	39.4 ± 88.1	0	0	0	0	0	0	0
<i>Cladosporium halotolerans</i> Zalar, de Hoog & Gunde-Cim.	0	0	0	354 ± 584	0	0	0	0
<i>Cladosporium iranicum</i> Bensch, Crous & U. Braun	29.8 ± 66.5	0	0	0	0	0	0	0
<i>Cladosporium pseudocladosporioides</i> Bensch, Crous & U. Braun	0	0	0	0	45.5 ± 102	0	32.5 ± 72.7	107 ± 162
<i>Cladosporium ramotenellum</i> K. Schub., Zalar, Crous & U. Braun	0	0	0	121 ± 232	0	0	0	0
<i>Cladosporium sphaerospermum</i> Penz.	0	97.4 ± 218	0	198 ± 443	112 ± 249	0	0	0
<i>Cladosporium subtilissimum</i> K. Schub., Dugan, Crous & U. Braun	0	0	21.3 ± 47.7	0	0	90.3 ± 124	0	0
<i>Cladosporium uredinicola</i> Speg.	48.7 ± 109	0	0	0	0	22.8 ± 50.9	0	0
<i>Cladosporium xylophilum</i> Bensch, Shabunin, Crous & U. Braun	0	0	0	0	0	0	0	172 ± 384
<i>Cladosporium</i> sp.	0	0	0	0	24.7 ± 55.2	0	0	0
* <i>Clonostachys</i> sp.	0	59.5 ± 133	0	0	0	0	0	0
* <i>Coprinellus</i> sp.	0	0	0	0	71 ± 159	0	0	0
* Cucurbitariaceae sp.1	0	0	0	28.6 ± 64	0	114 ± 255	0	0
* Cucurbitariaceae sp.2	0	0	0	0	0	0	0	32.5 ± 72.7
<i>Devriesia lagerstroemiae</i> Crous & M.J. Wingfield	0	0	53.6 ± 120	0	0	44.7 ± 100	0	0
* <i>Diaporthe</i> sp.	0	0	21.3 ± 47.7	0	0	44.7 ± 100	0	0
* Didymellaceae sp.	0	89.3 ± 200	0	0	0	0	0	0
* Didymosphaeriaceae sp.	29.8 ± 66.5	78.8 ± 176	14.8 ± 33.1	0	0	44.7 ± 100	0	0
* Dohideomycetes sp.1	0	0	0	0	0	0	34.3 ± 76.8	0
* Dohideomycetes sp.2	0	0	14.8 ± 33.1	0	0	44.7 ± 100	36.4 ± 81.4	36.4 ± 81.4
* Dohideomycetes sp.3	48.9 ± 109	0	59.2 ± 132	0	0	44.7 ± 100	0	0
* Dohideomycetes sp.4	0	0	14.8 ± 33.1	0	0	44.7 ± 100	0	0
* Dohideomycetes sp.5	0	0	0	0	0	0	0	40.8 ± 91.3
<i>Exophiala aquamarina</i> de Hoog, Vicente, Najafzadeh, HARRAK, Badali, Seyedmouza	0	0	0	21.3 ± 47.7	0	0	0	0
<i>Fusarium oxysporum</i> Schltdl.	0	0	0	28.6 ± 64	0	0	0	0
<i>Gibellulopsis nigrescens</i> (Pethybr.) Zare, W. Gams & Summerb.	0	48.7 ± 109	0	0	0	0	0	0
* Gnomoniaceae sp.	0	0	28.6 ± 64	0	0	44.7 ± 100	0	0
* Helotiales sp.1	45.5 ± 102	0	0	0	0	0	0	0
* Helotiales sp.2	0	0	0	0	0	23.7 ± 52.9	0	0
* <i>Hydropiosphaera</i> sp.	0	0	0	0	0	27.9 ± 62.4	0	0
* <i>Lachnum</i> sp.	0	0	0	0	0	45.5 ± 102	0	0
* <i>Lemonniera</i> sp.	0	0	26.8 ± 59.9	0	0	44.7 ± 100	0	0
<i>Libertella blepharis</i> A.L. Sm.	0	0	0	44.4 ± 99.4	0	0	0	0
* <i>Lophiotrema rubi</i> (Fuckel) Yin. Zhang, C.L. Schoch & K.D. Hyde	0	0	0	21.3 ± 47.7	0	0	0	0
* Lophiotremataceae sp.1	0	0	49.4 ± 110	0	22.8 ± 50.9	124 ± 127	0	0
* Lophiotremataceae sp.2 =Flb MUT4887	0	0	28.6 ± 64	28.3 ± 63.3	23.7 ± 52.9	44.7 ± 100	0	0

* Lophiotremataceae sp.3	0	0	24.7 ± 55.2	0	22.8 ± 50.9	44.7 ± 100	0	0
<i>Microsphaeropsis olivacea</i> (Bonorden) Höhnel	0	0	14.8 ± 33.1	0	0	44.7 ± 100	0	0
<i>Mortierella alpina</i> Peyronel	29.8 ± 66.5	0	14.8 ± 33.1	0	0	44.7 ± 100	0	0
* <i>Myrothecium inundatum</i> Tode	0	0	0	0	0	0	0	0
* Nectriaceae sp. 1	0	0	28.6 ± 64	0	27.9 ± 62.4	44.7 ± 100	0	0
<i>Ochrocladosporium frigidarii</i> Crous & U. Braun	0	0	0	0	0	27.9 ± 62.4	0	0
* <i>Ophiognomonia</i> sp.	0	0	0	0	0	27.9 ± 62.4	0	34.3 ± 76.8
<i>Paecilomyces inflatus</i> (Burnside) J.W. Carmich.	0	24.3 ± 54.4	0	0	0	0	0	0
* <i>Paraconiothyrium variabile</i> Riccioni, Damm, Verkley & Crous	0	0	82.2 ± 121	0	0	29.4 ± 65.8	0	0
* <i>Paraconiothyrium</i> sp.	0	0	0	0	0	0	0	32.5 ± 72.7
<i>Paraphaeosphaeria neglecta</i> Verkley, Riccioni & Stielow	0	0	0	0	24.7 ± 55.2	0	0	0
<i>Penicillium antarcticum</i> A.D. Hocking & C.F. McRae	289 ± 407	0	53.6 ± 120	96.3 ± 113	23.7 ± 52.9	227 ± 394	232 ± 359	34.3 ± 76.8
<i>Penicillium brevicompactum</i> Dierckx	0	0	14.8 ± 33.1	0	0	44.7 ± 100	81.6 ± 183	182 ± 407
<i>Penicillium caseifulvum</i> Lund, Filt. & Frisvad	0	0	0	0	137 ± 305	0	0	0
<i>Penicillium citrinum</i> Thom	0	0	0	28.3 ± 63.3	0	0	0	0
<i>Penicillium roseopurpureum</i> Dierckx	0	424 ± 511	0	0	55.8 ± 125	0	0	0
<i>Penicillium spinulosum</i> Thom	0	0	0	0	0	55.8 ± 125	0	0
<i>Penicillium steckii</i> K.M. Zalessky	0	73 ± 163	0	0	0	0	36.4 ± 81.4	0
<i>Penicillium</i> sp.	0	0	26.8 ± 59.9	0	0	68.4 ± 101	0	0
<i>Pestalotia olivacea</i> Guba	0	0	0	14.2 ± 31.6	0	23.7 ± 52.9	0	0
* Pezizomycotina sp.	0	29.8 ± 66.5	0	0	0	0	0	0
* <i>Phaeosphaeria</i> sp.	0	0	0	0	0	0	0	40.8 ± 91.3
* Phaeosphaeriaceae sp. 1	0	0	0	0	0	23.7 ± 52.9	0	0
<i>Plectosporium tabacinum</i> (J.F.H. Beyma) M.E. Palm, W. Gams & Nirenberg	0	0	0	14.2 ± 31.6	0	0	0	0
* Pleosporaceae sp.	0	0	0	0	0	0	0	0
* Pleosporales sp.1	0	0	0	0	0	0	0	32.5 ± 72.7
* Pleosporales sp.2	48.9 ± 109	48.9 ± 109	0	14.8 ± 33.1	0	0	0	0
* Pleosporales sp.3	0	0	0	57.2 ± 128	0	0	0	65 ± 145
<i>Pochonia chlamydosporia</i> (Goddard) Zare & W. Gams	0	0	0	0	0	0	0	32.5 ± 72.7
* Pyrenochaeta sp.1	59.5 ± 133	0	0	0	0	0	0	0
* Pyrenochaeta sp.2	0	0	14.8 ± 33.1	0	0	44.7 ± 100	0	0
* Pyrenochaeta sp.3	0	0	0	0	0	0	0	32.5 ± 72.7
* Pyrenochaeta sp.4	0	0	0	0	0	0	68.9 ± 94.6	0
* <i>Pyrenochaetopsis microspora</i> (Gruyter & Boerema) Gruyter, Aveskamp & Verkley	0	0	0	0	0	0	0	32.5 ± 72.7
* <i>Pyrenochaetopsis</i> sp.1	0	0	0	14.8 ± 33.1	69.2 ± 102	138 ± 205	0	0
* <i>Pyrenochaetopsis</i> sp.2	0	0	21.3 ± 47.7	0	48.4 ± 66.2	116 ± 165	32.5 ± 72.7	32.5 ± 72.7
* <i>Pyrenochaetopsis</i> sp.3	0	0	14.8 ± 33.1	26.8 ± 59.9	68.3 ± 153	72.6 ± 104	0	97.5 ± 218
<i>Ramichloridium strelitziae</i> Arzanlou, W. Gams & Crous	0	39.4 ± 88.1	0	0	0	0	0	0
<i>Rhodotorula aurantiaca</i> (Saito) Lodder	39.4 ± 88.1	0	0	0	0	0	0	0
* Roussoellaceae sp.1	0	0	0	0	0	27.9 ± 62.4	0	0

* Roussoellaceae sp.2	0	0	0	0	50.7 ± 70	22.8 ± 50.9	72.8 ± 163	0
* Roussoellaceae sp.3	0	0	0	0	45.5 ± 102	0	32.5 ± 72.7	0
* Roussoellaceae sp.4 =FLAB4886 e 4971	0	0	14.8 ± 33.1	21.3 ± 47.7	0	44.7 ± 100	0	0
* Roussoellaceae sp.5	0	0	53.6 ± 120	0	0	44.7 ± 100	0	0
<i>Sarocladium glaucum</i> (W. Gams) Summerbell	0	0	0	0	0	27.9 ± 62.4	0	0
* <i>Sarocladium</i> sp.	0	0	26.8 ± 59.9	0	0	44.7 ± 100	0	0
* <i>Schizophyllum commune</i> Fr.	0	0	21.3 ± 47.7	0	0	95.4 ± 96.1	0	0
<i>Scopulariopsis humicola</i> G.L. Barron	0	78.8 ± 176	0	0	0	0	0	0
* Sordariomycetes sp.1	0	45.5 ± 102	0	0	0	0	0	0
* Sordariomycetes sp.2	29.8 ± 66.5	0	0	0	0	0	0	0
* Sporidiobolales sp.	0	29.8 ± 66.5	0	0	0	0	0	0
<i>Sporothrix inflata</i> de Hoog	0	0	0	0	0	0	0	40.8 ± 91.3
* <i>Stachybotryna</i> sp.	0	0	0	26.8 ± 59.9	0	0	0	0
<i>Stachybotrys chartarum</i> (Ehrenberg) S. Hughes	0	0	26.8 ± 59.9	26.8 ± 59.9	0	44.7 ± 100	0	40.8 ± 91.3
* <i>Thelebolus</i> sp.	0	0	0	44.4 ± 99.4	0	0	36.4 ± 81.4	0
<i>Toxicocladosporium strelitziae</i> P.W. Crous	0	39.4 ± 88.1	0	0	0	0	0	0
<i>Trichoderma aureoviride</i> Rifai	0	0	0	14.2 ± 31.6	0	0	0	0
<i>Trichoderma harzianum</i> Rifai	0	0	49.4 ± 110	0	0	68.4 ± 101	0	0
<i>Trichoderma koningi</i> Oudemans	0	0	143 ± 280	0	0	39.2 ± 87.6	0	0
* <i>Trichoderma</i> sp.	0	0	28.6 ± 64	0	0	44.7 ± 100	0	0
<i>Wallemia sebi</i> (Fr.) Arx	45.5 ± 102	0	0	0	0	45.5 ± 102	0	0
* Fungal sp.1	0	0	0	0	23.7 ± 52.9	0	0	0