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Genome of *Diaporthe* sp. provides insights into the potential inter-phylum transfer of a fungal sesquiterpenoid biosynthetic pathway

Jose Guedes DE SENA FILHO[a,b,1], Maureen B. QUIN[c,1],
Daniel J. SPAKOWICZ[a], Jeffrey J. SHAW[a], Kaury KUCERA[a],
Brian DUNICAN[a], Scott A. STROBEL[a], Claudia SCHMIDT-DANNERT[c,*]

[a]Yale University, Dept. of Molecular Biophysics and Biochemistry, 800 West Campus Drive, West Haven, CT 06516, USA
[b]EMBRAPA — Empresa Brasileira de Pesquisa Agropecuária-Coastal Tablelands, Av. Beira Mar, 3250, Jardins, 49025-040 Aracaju, SE, Brazil
[c]University of Minnesota, Dept. of Biochemistry, Molecular Biology and Biophysics, 1479 Gortner Avenue, St Paul, MN 55108, USA

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ABSTRACT

Fungi have highly active secondary metabolic pathways which enable them to produce a wealth of sesquiterpenoids that are bioactive. One example is Δ6-protoilludene, the precursor to the cytotoxic illudins, which are pharmaceutically relevant as anticancer therapeutics. To date, this valuable sesquiterpene has only been identified in members of the fungal division Basidiomycota. To explore the untapped potential of fungi belonging to the division Ascomycota in producing Δ6-protoilludene, we isolated a fungal endophyte *Diaporthe* sp. BR109 and show that it produces a diversity of terpenoids including Δ6-protoilludene. Using a genome sequencing and mining approach 17 putative novel sesquiterpene synthases were identified in *Diaporthe* sp. BR109. A phylogenetic approach was used to predict which gene encodes Δ6-protoilludene synthase, which was then confirmed experimentally. These analyses reveal that the sesquiterpene synthase and its putative sesquiterpene scaffold modifying cytochrome P450(s) may have been acquired by inter-phylum horizontal gene transfer from Basidiomycota to Ascomycota. Bioinformatic analyses indicate that inter-phylum transfer of these minimal sequiterpenoid secondary metabolic pathways may have occurred in other fungi. This work provides insights into the evolution of fungal sesquiterpenoid secondary metabolic pathways in the production of pharmaceutically relevant bioactive natural products.

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Introduction

Higher fungi (divisions Ascomycota and Basidiomycota) are a valuable source of natural products. Fungi produce bioactive compounds to protect their mycelia and/or fruiting bodies against threats posed by competing microorganisms, invertebrates, insects, and larger animals (Gershenzon & Dudareva 2007; Aly *et al.* 2011; Alves *et al.* 2013; Schmidt-Dannert 2015). Some of these bioactive compounds are of value as pharmaceutical agents; as anticancer, antiviral, antimicrobial, and antifungal drugs (Abraham 2001; Misiek & Hoffmeister 2007; Elisashvili 2012; Evidente *et al.* 2014). However, chemical synthesis of these structurally complex molecules is frequently infeasible or economically impractical and as such, biosynthetic methods are required for their production. This can be achieved either by the native fungal producer or more commonly, in the case of low-yield or genetically intractable strains, by engineered, recombinant systems. Therefore, there is a need to identify and characterize the natural products biosynthetic enzymes and pathways for the development of such heterologous production systems, facilitating access to these chemically diverse scaffolds (Ajikumar *et al.* 2010; Wawrzyn *et al.* 2012a; Boettger & Hertweck 2013; Paddon *et al.* 2013; Lin *et al.* 2013; Tsunematsu *et al.* 2013; Wiemann *et al.* 2013; Lin *et al.* 2014; Wiemann & Keller 2014; Yaegashi *et al.* 2014; Spakowicz & Strobel 2015).

One of the largest classes of natural products is the terpenoids, with more than 40 000 compounds isolated. Several hundred different terpene scaffolds have been described, making this a highly diverse class of chemical structures (Christianson 2008). Among the fungi, mushroom-forming Basidiomycota are prolific producers of structurally diverse terpene natural products (Quin *et al.* 2014; Schmidt-Dannert 2015). Fungal terpenes are produced from the mevalonate pathway-derived five carbon precursors dimethylallyl diphosphate (DMAPP) or isopentenyl diphosphate (IPP) (Miziorko 2011). Condensation of monomers of DMAPP and IPP results in linear hydrocarbons of varying length, such as the C15 molecule farnesyl pyrophosphate ((2E,6E)-FPP), which is the precursor to the volatile sesquiterpenes. The ionization-dependent removal of inorganic pyrophosphate (PPi) from (2E,6E)-FPP, and the initial cyclization of the reactive carbocation is catalysed by enzymes known as sesquiterpene synthases (Christianson 2006; Miller & Allemann 2012). Different sesquiterpene synthases can catalyse distinct carbocation cyclization mechanisms: the enzyme can catalyse a 1,10 or 1,11 cyclization following removal of PPi from (2E,6E)-FPP (Lesburg *et al.* 1997), yielding a *E,E*-germacradienyl cation or *trans*-humulyl cation, respectively. Alternatively, the enzyme can cause (2E,6E)-FPP to undergo an initial isomerization yielding (3R)-nerolidol pyrophosphate (NPP) (Cane *et al.* 1981), followed by a 1,6 or 1,10 cyclization yielding a bisabolyl cation or *Z,E*-germacradienyl cation, respectively (Vedula *et al.* 2007). Subsequently, the carbocation undergoes a series of further cyclizations, ring rearrangements, methyl, and hydride shifts, until a final deprotonation mediated either by attack by a water molecule (Pinedo *et al.* 2008) or by the PPi (Chen *et al.* 2013) results in the release of the sesquiterpene from the enzyme active site. The sesquiterpene can then be further modified by accessory enzymes such as cytochrome P450 monoxygenases and other types of oxidoreductases that are typically located in biosynthetic gene clusters together with the terpene synthases in fungi, yielding the final bioactive sesquiterpenoid product (Agger *et al.* 2009).

Of particular interest are fungal sesquiterpene/oids derived from a 1,11 cyclization of (2E,6E)-FPP, *via* a *trans*-humulyl cation. Many of these chemicals are highly bioactive, and have potential as pharmaceutical agents (Abraham 2001). A large number of *trans*-humulyl cation derived sesquiterpenoids have been isolated from *Basidiomycota*, a significant portion of which appear to be derived from modified variants of the sesquiterpene scaffold Δ6-protoilludene (Abraham 2001; Quin *et al.* 2014; Schmidt-Dannert 2015). Δ6-protoilludene derived sesquiterpenoids have potent anticancer properties, and are currently being developed as therapeutics (McMorris *et al.* 2003; Schobert *et al.* 2011a, b). As part of a larger effort to identify and characterize the fungal biosynthetic pathways involved in Δ6-protoilludene derived sesquiterpenoid production, we previously biochemically characterized a number of *Basidiomycota* sesquiterpene synthases, including five Δ6-protoilludene synthases (Agger *et al.* 2009; Wawrzyn *et al.* 2012b; Quin *et al.* 2013a). Using our knowledge of the experimentally validated cyclization mechanisms of these enzymes we mined the rapidly expanding Joint Genome Initiative (JGI) database of fungal genomes (Cuomo & Birren 2010) to create a predictive framework (Wawrzyn *et al.* 2012b). Our framework enables the sequence-guided initial prediction of cyclization mechanism of putative fungal sesquiterpene synthases prior to cloning and characterization efforts, and has proven to be reliable in the directed discovery and characterization of additional sesquiterpene synthases from *Basidiomycota*, based upon cyclization mechanism of choice (Quin *et al.* 2013a).

In contrast to the *Basidiomycota*, relatively few studies have described sesquiterpene/oids isolated from *Ascomycota*. Of the *Ascomycota* sesquiterpenes, only a small number of those described are derived from the *trans*-humulyl cation. For example, α-humulene and koraiol (Brock *et al.* 2013) are produced by *Fusarium fujikuroi*; and presilphiperfolan-8β-ol (Pinedo *et al.* 2008; Wang *et al.* 2009) is produced by *Botrytis cinerea*; the corresponding sesquiterpene synthases have been identified and characterized from these major plant pathogens. Our previous phylogenetic analyses showed that these two Ascomycota enzymes form a clade that is distinct from the one that contains the Basidiomycota Δ6-protoilludene synthases identified and characterized by our group, indicating a difference in sequence (Schmidt-Dannert 2015). To the best of our knowledge, only one study has shown production of Δ6-protoilludene by the plant pathogenic Ascomycete *Ceratocystis piceae* (Hanssen *et al.* 1986), and the sesquiterpene synthase has not yet been identified. Bioinformatics analyses indicate that overall, Ascomycota have comparatively fewer putative sesquiterpene synthases encoded within their genomes compared to the sesquiterpene synthase rich Basidiomycota, which may explain why fewer sesquiterpene synthases have been characterized from Ascomycota (Schmidt-Dannert 2015). Nonetheless, the fact that *trans*-humulyl cation producing sesquiterpene synthases have already been identified and characterized; and that at least one Ascomycete is known to produce Δ6-protoilludene; indicates an underlying untapped potential of Ascomycota to produce bioactive sesquiterpenoids derived from a Δ6-protoilludane scaffold.

In this work we sought to identify 1,11-cyclizing sesquiterpene synthases, specifically Δ6-protoilludene synthases, in Ascomycota with the goal of accessing novel bioactive terpenoids. We focused our efforts on endophytic fungi which are known to be a source of pharmaceutically relevant terpenoids (de Souza et al. 2011; Chandra 2012; Barra et al. 2014), including monoterpenes that are synthesized by a recently discovered monoterpene synthase in the endophyte *Hypoxylon* sp. (Shaw et al. 2015a). *De novo* genome sequencing of a new environmentally isolated fungal endophyte, coded here as *Diaporthe* sp. BR109, and subsequent bioinformatics analyses, led to the discovery and characterization of the first Δ6-protoilludene synthase from an Ascomycete. Unexpectedly, our results also suggest a potential horizontal gene transfer of at least partial biosynthetic pathways leading to Δ6-protoilludene derived sesquiterpenoids, apparently across fungal divisions. These findings deepen our appreciation of the complex nature of evolution of secondary metabolic pathways in fungi.

Materials and methods

Endophytic fungal isolation, culturing, and sesquiterpene extractions

Caesalpinia pyramidalis Tul (Fabaceae) plant stem and leaf material were collected in northeast Brazil. The plant material was surface sterilized and plated on isolation media comprised of 1 X potato dextrose agar (PDA) (24 g L^{-1} potato dextrose), 0.1 X PDA (2.4 g L^{-1} potato dextrose) (EMD Millipore) or water agar (15 g L^{-1} agar) for isolation of *fungi*, as described elsewhere (Shaw et al. 2015a). A fungal isolate growing from the plated plant stem material was subcultured on a fresh 1 X PDA plate and was coded BR109. For detection of sesquiterpene production, BR109 was grown for 14 and 28 d in 100 mL potato dextrose broth (PDB) liquid media at 25 °C with shaking at 125 rpm. Fungal sesquiterpenes were extracted from the culture biomass using 2 × 30 mL chloroform and ethyl acetate. Extractions were filtered and were dried under vacuum prior to shipping to the University of Minnesota for GC/MS analyses.

GC/MS analysis of terpene/oids

GC/MS analysis was conducted on a HP GC 7890A chromatograph coupled to an anion-trap mass spectrometer HP MSD triple axis detector (Agilent Technologies, Santa Clara, CA, USA). Compounds were separated on a HP-5MS capillary column (30 m × 0.25 mm × 1.0 mm) with an injection port temperature of 250 °C and helium as carrier gas. The oven temperature started at 60 °C and was increased at 10 °C min^{-1} to a final oven temperature of 250 °C. Mass spectra were scanned over the range 5–300 amu at 1 s intervals. The retention indices and mass spectra of compound peaks were compared to reference spectra available in reference libraries in Mass Finder 4 (Joulain & Konig 1998) and the National Institute of Standards and Technology (NIST) standard reference database.

Phylogenetic analysis of fungal isolate BR109

The internal transcribed spacer (ITS) rDNA of fungal isolate BR109 was amplified by colony PCR using a modified method (van Zeijl et al. 1997), using trichoderma lysing enzyme (Sigma–Aldrich). The primers used for amplification were ITS1 (TCCGTAGGTGAACCTGCGG) and ITS4 (TCCTCCGCTTATTGATATGC). The resulting PCR product was sequenced by the W.M. Keck Foundation. The ITS sequence was aligned with homologues identified by BLAST using MUSCLE v3.8.31 and a maximum likelihood phylogenetic tree was constructed using RAxML v7.2.8 and MrBayes v3.2.0.

Genome sequencing of fungal isolate BR109

Genomic DNA was isolated from a 7 d old culture grown in potato dextrose media using a DNeasy Plant Mini kit (Qiagen), as described elsewhere (Gianoulis et al. 2012). Two libraries were prepared (450 bp and 3 kb mate-pair) according to Illumina protocols. Libraries were sequenced on the Illumina Hiseq 2000 using paired-end 2 × 250 bp reads and assembled Allpaths-LG v44034 (Gnerre et al. 2011). The genome data was submitted to GenBank (Bioproject ID PRJN288728).

Sesquiterpene synthase identification

Gene predictions were conducted using AUGUSTUS (Stanke et al. 2004), using reference species *Botrytis cinerea*, *Fusarium graminearum*, *Chaetomium globosum*, and *Magnaporthe grisea*. Amino acid predictions were manually checked for accuracy by creating a sequence alignment using ClustalW (Thompson et al. 1994) with previously characterized sesquiterpene synthases to check for the presence and correct alignment of conserved metal binding motifs present in all sesquiterpene synthases (Lesburg et al. 1998). For predictions of cyclization mechanism of putative sesquiterpene synthases, the curated list of amino acid sequences were aligned, and phylogenetic analyses were carried out using MEGA 6 (Tamura et al. 2013) with the default parameters for the Neighbor-Joining (Saitou & Nei 1987) method and a bootstrap test of phylogeny (500 replicates). Biosynthetic gene clusters surrounding the putative sesquiterpene synthases were manually annotated using AUGUSTUS and BLAST. Further details of bioinformatics methods, all gene sequences, and protein sequences, are provided in the Supporting Information.

Cloning and expression of sesquiterpene synthase in Escherichia coli

Putative sesquiterpene synthase Dia1 was synthesized with codon optimization for expression in *E. coli* and cloned into plasmid backbones pUC57-Kan using restriction sites NcoI and XmaI (GENEWIZ). We subcloned Dia1 into our in-house plasmid pUCBB (Vick et al. 2011) that allows for constitutive expression using restriction sites BamHI and SpeI. Plasmid pUCBB-Dia1 was transformed into *E. coli* BL21 and single colonies were isolated on Lysogeny Broth (LB) agar supplemented with ampicillin (100 μg mL^{-1}). Single colonies were used to inoculate 2L flasks of LB broth (500 mL) supplemented with ampicillin (100 μg mL^{-1}), and the cultures were incubated overnight at 30 °C with shaking at 225 rpm. The headspace of flasks was sampled the next day for volatile sesquiterpenes for 10 min using a solid-phase microextraction (SPME) fibre, followed by GC–MS analysis.

Results

Endophytic fungal isolate BR109 produces mono- and sesquiterpenes

In our search for terpenoid producing endophytic fungi that produce pharmaceutically relevant *trans*-humulyl derived sesquiterpenes, we serendipitously isolated an uncharacterized fungal endophyte (coded BR109) from a flowering tree that is endemic to northeastern Brazil. The endophyte isolate produced a range of mono- and sesquiterpenoids, including Δ6-protoilludene (*vide infra*) and was identified as *Diaporthe* (*Phomopsis*) sp. by ITS sequencing. Phylogenetic analyses showed that fungal isolate BR109 was most closely related to *Diaporthe anacardii* and *Diaporthe foeniculaceae* (Fig 1) (Gomes *et al.* 2013). Like the Δ6-protoilludene producing *Ceratocystis piceae* (Ascomycota, Sordariomycetes, Hypocreomycetidae) (Hanssen *et al.* 1986) and the recently genome sequenced *Hypoxylon* sp. (Ascomycota, Sordariomycetes, Xylariomycetidae) which encodes a monoterpene synthase (Shaw *et al.* 2015a), this fungus also belongs to the Sordariomycetes but is a representative of the third subclass, Sordariomycetidae, within this fungal class.

To identify the terpenoids produced by the fungal isolate BR109, metabolites produced by the fungus were solvent extracted from culture biomass. GC/MS analysis of the extracts confirmed that the isolate produced a variety of terpene/oids (Fig 2), indicating that the fungus likely expressed a diversity of terpene synthases, including the sought after Δ6-protoilludene synthase. Several peaks in the GC/MS chromatogram had corresponding mass spectra that could be assigned using reference libraries as C10 monoterpenes and monoterpenoids: terpinen-4-ol **1**, *trans*-piperitol **2**, γ-terpineol **3**, and piperitone epoxide **4**. Several other peaks could be assigned as C15 sesquiterpenes and sesquiterpenoids: neotrifaradiene **5**, Δ6-protoilludene **6**, 3,7-di-epi-trifara-9,14-diene **7**, β-elemene (the heat-induced Cope rearrangement product of germacrene A) **8**, thujopsene **9**, nardosina-7,9,11-triene **10**, aristolene **11**, α-muurolene **12**, α-bulnesene **13**, guaia-9,11-diene **14**, norpatchulenol **15**, and maaliol **16** (Figs 2 and 3). Other peaks which could not be confidently assigned using reference libraries, had mass spectra with parent ions corresponding to a *m/z* 206, 216, 222, 234, 235, and 236, which are indicative of modified sesquiterpenoids.

The presence of a wide range of sesquiterpene products suggested that fungal isolate BR109 expressed a complement
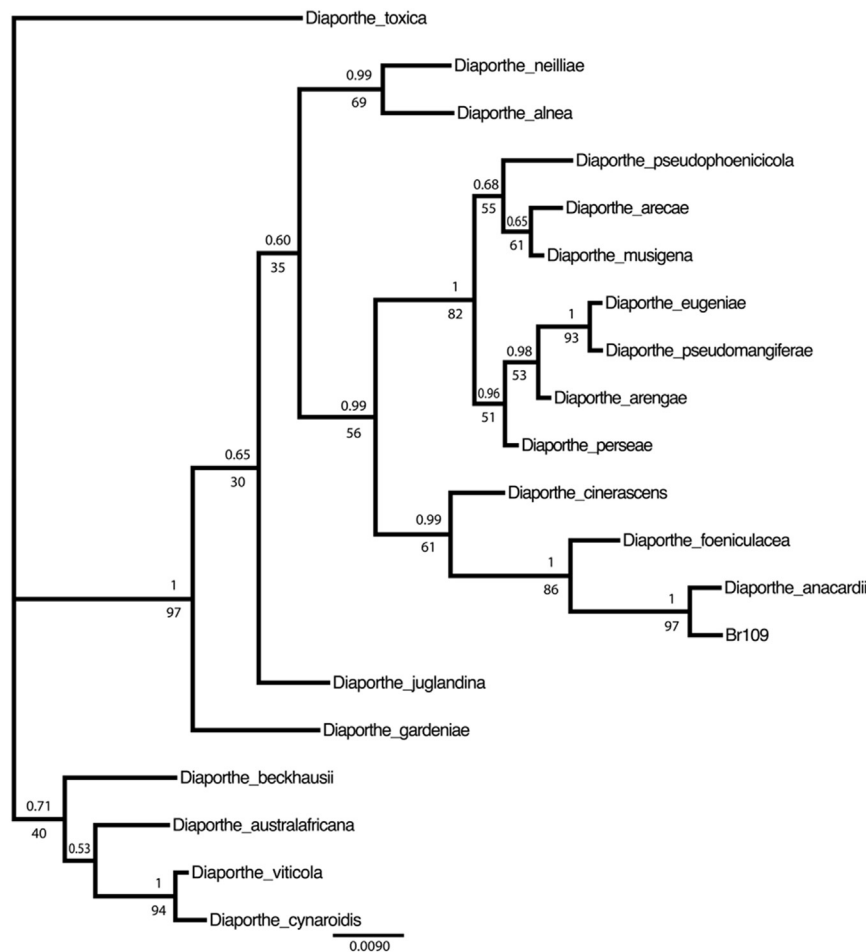

Fig 1 — Phylogenetic analyses of fungal isolate BR109. ITS sequencing shows that BR109 is most closely related to *Diaporthe anacardii* and *Diaporthe foeniculacea*.
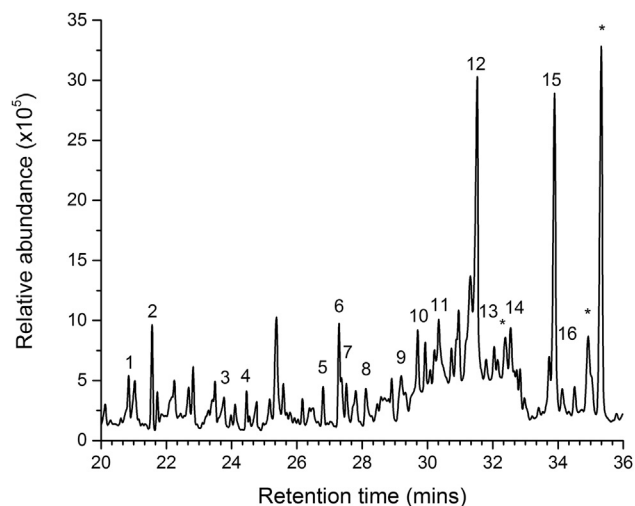
Fig 2 — **GC/MS analysis of the terpenes/terpenoids produced by fungal isolate BR109. Peaks that could be assigned based on comparison of mass spectra to known libraries of terpenes are labelled with numbers. Numbering of peaks on the chromatogram correspond to the structures shown in Fig 3. Peaks that could not be assigned, but had *m/z* parent ions likely related to modified sesquiterpenoids, are labelled with an asterisk *.**

of terpene synthases that catalyse different types of cyclization reactions. For example, neotrifaradiene **5** and 3,7-di-epi-trifara-9,4-diene **7** share a trifarane backbone which has been proposed to be derived from nerolidol (Sonwa *et al.* 2001). BR109 therefore may express an acyclic sesquiterpene synthase, nerolidol synthase, which has so far only been described from plants (Nagegowda *et al.* 2008; Green *et al.* 2012), bacteria (Nakano *et al.* 2011), and from the endophyte *Hypoxylon* sp. (Shaw *et al.* 2015a). Furthermore, the spectrum of sesquiterpenes made by the fungus suggested that it expressed cyclic sesquiterpene synthases responsible for almost all possible initial cyclization reactions of FPP; for example, thujopsene **9** has been proposed to be derived from a 1,6 cyclization of NPP *via* a bisabolyl cation (Wu *et al.* 2005); one of the most abundant products α-muurolene **12**, and the guaiane skeleton-derived products **13** and **14** have been proposed to be synthesized from a direct 1,10 cyclization of (2E,6E)-FPP *via* a E,E-germacradienyl cation (de Kraker *et al.* 1998; Wawrzyn *et al.* 2012b); and Δ6-protoilludene **6** is the result of a 1,11 cyclization of (2E,6E)-FPP *via* a *trans*-humulyl cation (Seemann *et al.* 2002; Wawrzyn *et al.* 2012b; Quin *et al.* 2013a, 2015). None of the products identified, however, appeared to be derived from a 1,10 cyclization of NPP *via* a Z,E-germacradienyl cation.
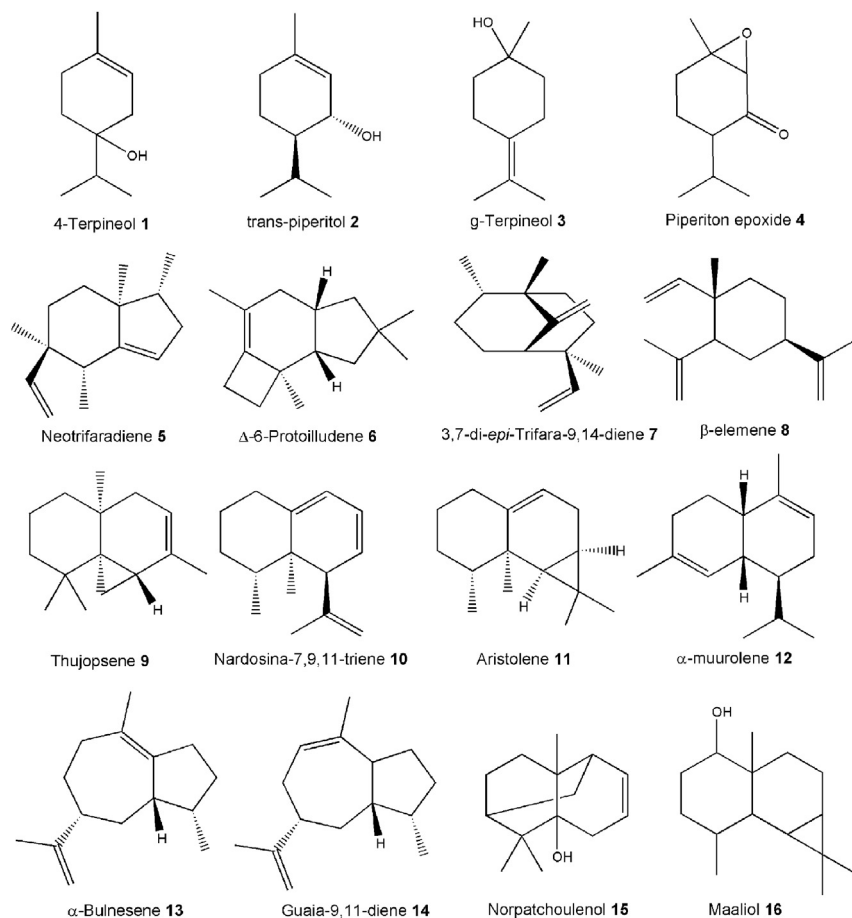

Fig 3 — **Chemical structures of terpenoids produced by fungal isolate BR109. Identified terpenes/oids are numbered according to the peak labelling in Fig 2. Relative stereochemistries of structures are shown.**

Genome and complement of putative sesquiterpene synthases in BR109

Owing to the fact that fungal isolate BR109 likely expressed a diversity of sesquiterpene synthases, and produced Δ6-protoilludene **6**, we set out to sequence the genome of this uncharacterized endophyte in order to map its terpene synthase complement and identify the Δ6-protoilludene synthase. Following *de novo* genome sequencing of fungal isolate BR109, the final genome assembly length was estimated to be 56 Mbp in size across 145 scaffolds, with an N50 of 1.8 Mbp, which is similar to other reported endophyte genomes (Gianoulis *et al.* 2012; Shaw *et al.* 2015a, b). A total of 16 469 predicted genes were identified (Table S1).

To identify genes encoding putative sesquiterpene synthases in BR109 we carried out BLAST searches using the sequences of diverse fungal sesquiterpene synthases previously cloned and characterized by our group: Cop1–6 from the *Basidiomycete Coprinus cinereus* (Agger *et al.* 2009; Lopez-Gallego *et al.* 2010a, b); Omp1–11 from the Basidiomycete *Omphalotus olearius* (Wawrzyn *et al.* 2012b; Quin *et al.* 2013b); and Stehi159379, Stehi128017, Stehi25180, Stehi64702, and Stehi73029 from the Basidiomycete *Stereum hirsutum* (Quin *et al.* 2013a, 2015). We also included sequences of sesquiterpene synthases characterized from Ascomycetes by other groups: presilphiperfolan-8β-ol synthase BcBOT2 from *Botrytis*

cinerea (Wang *et al.* 2009), koraiol synthase Ffsc4, and acorenol synthase Ffsc6 from *Fusarium fujikuroi* (Brock *et al.* 2013), trichodiene synthase FsTS from *Fusarium sporotrichioides* (Hohn & Vanmiddlesworth 1986), longiborneol synthase FgCLM1 from *Fusarium graminearum* (McCormick *et al.* 2010), aristolochene synthase PrAS from *Penicillium roqueforti* (Caruthers *et al.* 2000), as well as 11 terpene synthases Hyp1–11 recently identified in *Hypoxylon* sp. (Shaw *et al.* 2015a). Using our searches we identified a total of 17 genes encoding putative sesquiterpene synthases in the genome of BR109, named Dia1–17 (Fig 4, Supporting Information).

We have previously shown in Basidiomycota that phylogenetic analyses comparing putative sesquiterpene synthases to characterized enzymes are predictive of the cyclization mechanisms (Wawrzyn *et al.* 2012b; Quin *et al.* 2013a). Using this same approach, we noted that the potential sesquiterpene synthases from BR109 clustered in distinct clades with other characterized enzymes, potentially according to cyclization mechanism (Fig 4). Most of the predicted Dia sesquiterpene synthases clustered most closely with homologues from other Ascomycota. Dia6–8 clustered in a clade with Ascomycota terpene synthases Hyp1, 2, 5, 6, 7, and 8 from *Hypoxylon* sp. Dia6 was located on a branch with Hyp7, an inactive enzyme; Dia7 was located on a branch with Hyp6, an inactive enzyme; and Dia8 was located on a branch with Hyp2, which produces δ-cadinene (Shaw *et al.* 2015a). It is not reliable to draw
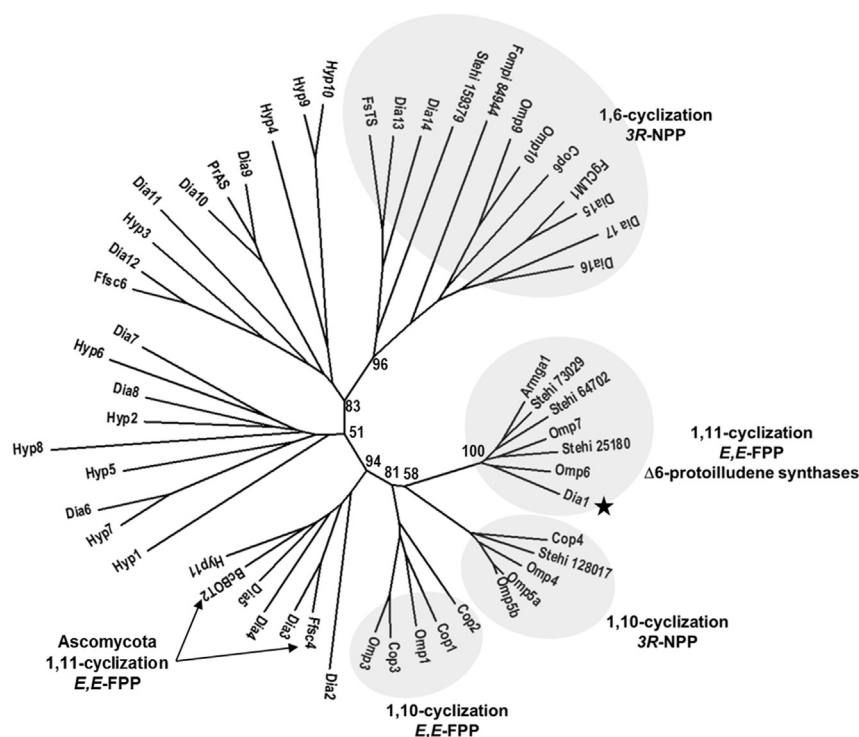

Fig 4 — Phylogenetic analyses of the 17 putative sesquiterpene synthases Dia1-17 identified in the genome of fungal isolate BR109. Putative sesquiterpene synthases Dia1-17 cluster in distinct clades alongside other characterized sesquiterpene synthases from *Basidiomycota* and *Ascomycota*, apparently according to cyclization mechanism. Clusters that contain sesquiterpene synthases previously characterized by our group with known cyclization mechanisms are highlighted with a shaded oval. The sesquiterpene synthase that we characterize in this study, Dia1, is highlighted with a star. Dia1 clusters closely with other previously characterized Δ6-protoilludene synthases from *Basidiomycota*. Bootstrap values (1000 replicates) are shown for the first internal nodes (see Supporting Information).

conclusions regarding putative cyclization mechanisms for this particular cluster of Dia enzymes because so few of the characterized Hyp enzymes with which they share sequence identity were active. The next distinct clade contained putative terpene synthases Dia9–12; Dia9 and Dia10 are closely related to aristolochene synthase PrAS which catalyses a 1,10 cyclization (Caruthers *et al.* 2000) and Dia12 was closely related to acorenol synthase Ffsc6 which may catalyse a 1,6 cyclization (Brock *et al.* 2011). Dia11 is not located on the same branch as any other sesquiterpene synthase in this cluster. Notably, this particular cluster contains previously characterized Ascomycota enzymes catalysing apparently diverse cyclizations, raising the possibility that our predictive framework may not be as reliable for predicting the activity of Ascomycota sesquiterpene synthases as it is for Basidiomycota (Quin *et al.* 2013a). The largest complement of putative Dia sesquiterpene synthases clustered with Ascomycota NPP 1,6 cyclizing, bisabolyl cation producing enzymes: Dia13 and Dia14 were most closely related to trichodiene synthase FsTS (Hohn & Vanmiddlesworth 1986), Dia15 was most closely related to longiborneol synthase FgCLM1 (McCormick *et al.* 2010), and Dia16 and Dia17 were located on a separate branch from Dia15.

Finally, four of the putative sesquiterpene synthases Dia2–5 clustered separately with the Ascomycota sesquiterpene synthases BcBOT2 (Wang *et al.* 2009) and Ffsc4 (Brock *et al.* 2011) that catalyse a 1,11 cyclization of 2E,6E-FPP, and which we have previously shown cluster separately from the 1,11-cyclizing Basidiomycota enzymes (Quin *et al.* 2014; Schmidt-Dannert 2015). Surprisingly, one single putative sesquiterpene synthase, Dia1, clustered very closely with previously characterized 1,11 cyclizing Basidiomycota Δ6-protoilludene synthases (Engels *et al.* 2011; Wawrzyn *et al.* 2012b; Quin *et al.* 2013a), providing strong support that this particular enzyme may be responsible for the observed Δ6-protoilludene production by the endophyte BR109.

Evidence of horizontal gene transfer in Δ6-protoilludene synthases

Our phylogenetic analyses indicated that, for the most part, the cyclization mechanism of Ascomycota sesquiterpene synthases cannot be inferred by their relationship to Basidiomycota enzymes, as the Dia putative sesquiterpene synthases generally were most similar to Ascomycota enzymes, regardless of their cyclization mechanism. For example, Dia9 and Dia10 clustered with the *Ascomycete* (2E,6E)-FPP 1,10 cyclizing, (E,E)-germacradienyl cation producing enzyme aristolochene synthase PrAS (Caruthers *et al.* 2000); not with the *Basidiomycete* versions of this subset of sesquiterpene synthases, Cop1–3 and Omp1–3 (Agger *et al.* 2009; Wawrzyn *et al.* 2012b), which are located distantly on the phylogenetic tree (Fig 4). It was therefore intriguing that Dia1 was so closely related to previously characterized Basidiomycota 1,11 cyclizing Δ6-protoilludene synthases Omp6&7, Stehi25180, Stehi64702, and Stehi73029, and Armga1 (Engels *et al.* 2011; Wawrzyn *et al.* 2012b; Quin *et al.* 2013a), as opposed to other 1,11 cyclizing *Ascomycota* sesquiterpene synthases Ffsc4 (Brock *et al.* 2011) and BcBOT2 (Wang *et al.* 2009), with which Dia2–5 associate on a separate clade (Fig 4). This obvious difference in primary sequence led us to question whether Dia1 had been acquired *via* a cross-phyla horizontal gene transfer event between *Basidiomycota* and *Ascomycota*; a phenomenon that has been described for a small number of fungal secondary metabolic genes and pathways (Slot & Hibbett 2007; Slot & Rokas 2011; Wisecaver *et al.* 2014). The gene encoding Dia1 also shares a more similar intron splicing pattern with genes encoding *Basidiomycota* 1,11 cyclizing sesquiterpene synthases than with genes encoding Ascomycota 1,11 cyclizing enzymes (Fig 5A, Supporting Information), further supporting the theory that horizontal gene transfer may have resulted in the presence of a Basidiomycete-like gene encoding a Δ6-protoilludene synthase in an Ascomycete genome.

In order to determine whether Dia1 encoded a predicted Δ6-protoilludene synthase, we synthesized a codon optimized variant of the Dia1 gene, and cloned and expressed the enzyme in *Escherichia coli* and analysed its activity using previously used methods (Engels *et al.* 2011; Wawrzyn *et al.* 2012b; Quin *et al.* 2013a). The major volatile sesquiterpene produced by *E. coli* cells overexpressing Dia1 was the *trans*-humulyl cation derived Δ6-protoilludene **6** (Fig 6), confirming that our prediction of cyclization mechanism and activity was correct. Further, minor peaks were also observed including pentalenene **17**, 2-sterpurene **18**, african-1-ene **19**, brasila-5(10),6-diene **20** (Fig 6), all of which are 1,11 cyclization products; as well as the 1,10 cyclization product β-elemene **8** (a heat induced rearrangement product of germacrene A), which has been observed in the headspace of other heterologously overexpressed Δ6-protoilludene synthases (Quin *et al.* 2013a).

Horizontal gene transfer of fungal sesquiterpenoid secondary metabolic pathways

With the confirmation of Dia1 as a Δ6-protoilludene synthase that is most closely related to *Basidiomycota* enzymes with the same activity (Figs 4 and 5A), we hypothesized that Dia1 was likely acquired by BR109 or its ancestors by horizontal gene transfer from a *Basidiomycota* source. We next questioned whether such a cross-phyla transfer of a *Basidiomycota* Δ6-protoilludene synthase could be detected in other *Ascomycota*, or whether this was a rare case limited to BR109 and closely related endophytic *Fungi*. Homology searches of 317 *Ascomycota* genomes available at the Joint Genome Institutes MycoCosm genome database with the Dia1 protein sequence as a search template identified 20 putative sesquiterpene synthases homologues that had high sequence identity (E-values $< 1E^{-60}$) to Dia1. Interestingly, these homologues were identified in the genomes of fungi belonging to two related fungal classes; the Sordariomycetes and Leotiomycetes (Table S2), suggesting that the *Basidiomycota* gene may be acquired by a shared ancestor of these two fungal classes, and was maintained by some, but lost by other members of these two classes. Several of the identified Dia1 homologues share similar intron splicing patterns of their predicted gene architectures (most notably, introns 2 and 3 are separated by a small exon) suggesting a common evolutionary origin (Fig 5B).

All of the previously characterized *Basidiomycota* Δ6-protoilludene synthases characterized by our group are located in predicted biosynthetic gene clusters (Wawrzyn *et al.* 2012b; Quin *et al.* 2013a). The initial Δ6-protoilludene scaffold
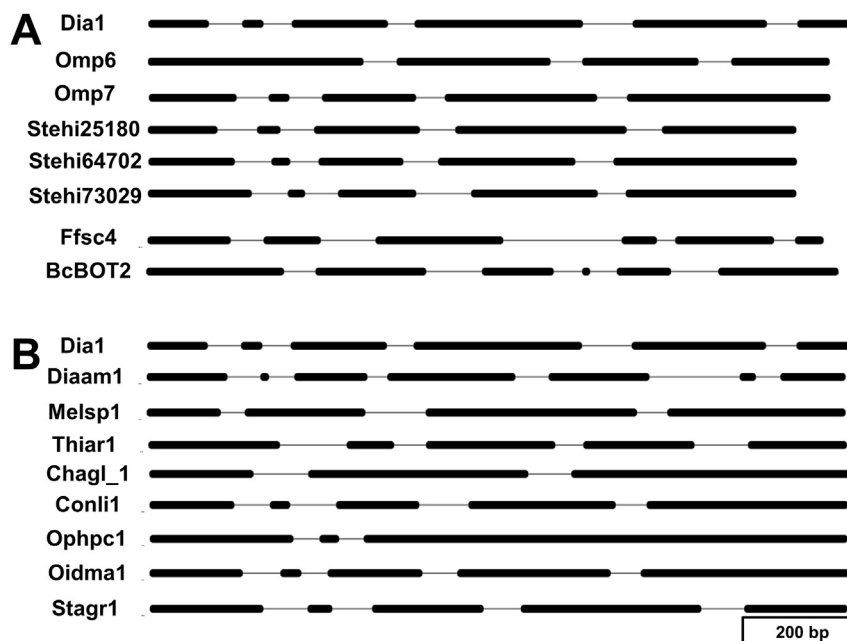
Fig 5 – Intron splicing patterns of *Basidiomycota* and *Ascomycota* genes encoding 1,11 cyclizing sesquiterpene synthases differ. (A) The gene architecture of Dia1 is compared to characterized *Basidiomycota* genes encoding 1,11 cyclizing sesquiterpene synthases Omp6, Omp7, Stehi25180, Stehi64702, and Stehi73029; as well as characterized *Ascomycota* genes encoding 1,11 cyclizing sesquiterpene synthases Ffsc4 and BcBOT2. The splicing patterns between characterized *Basidiomycota* and *Ascomycota* genes are different; Dia1 most closely matches the splicing pattern of *Basidiomycota* genes. (B) The gene architecture of Dia1 is compared to putative *Ascomycota* genes that may encode sesquiterpene synthases as determined by sequence comparisons. Terpene synthase gene names refer to those indicated in Fig 7. Exons are indicated by black rounded rectangles, introns are indicated by grey lines. The scale bar represents 200 bp.
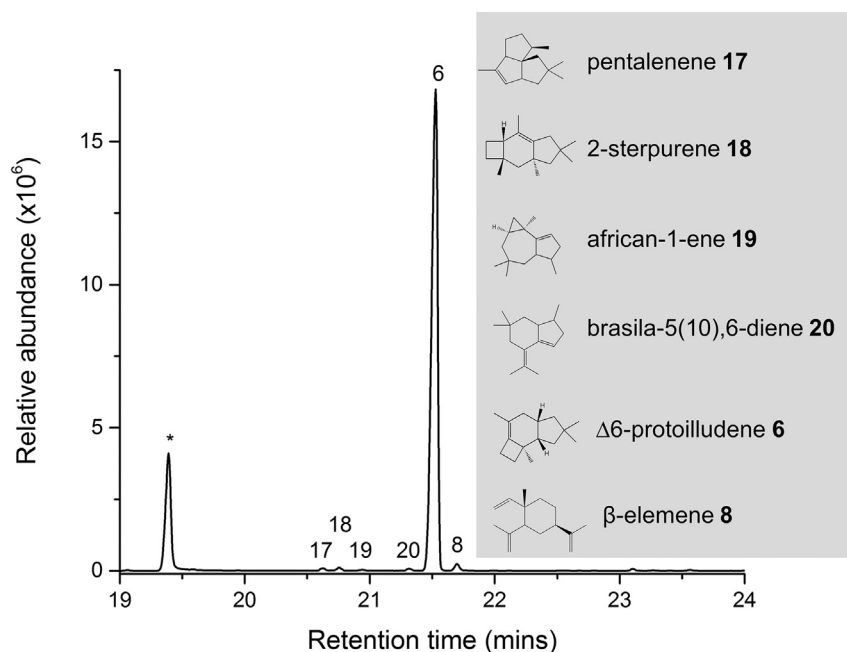

Fig 6 – GC/MS analysis of the volatile sesquiterpenes produced by *E. coli* overexpressing Dia1. Headspace analysis of *E. coli* cells overexpressing Dia1 reveals Δ6-protoilludene 6 as a major peak on the chromatogram, as well as minor peaks corresponding to pentalenene 17, 2-sterpurene 18, African-1-ene 19, and brasila-5(10),6-diene 20, which are all derived from a 1,11 cyclization of (2E,6E)-FPP. β-elemene 8 is a heat induced rearrangement product of a 1,10 cyclization of (2E,6E)-FPP. Peaks that could be assigned based on comparison of mass spectra to known libraries of terpenes are labelled with numbers, and chemical structures are shown in the grey box. Indole, highlighted with an asterisk (*), is a breakdown product of tryptophan naturally produced by *E. coli*, and serves as an internal standard.

is modified into to a wide diversity of bioactive sesquiterpenoids (Abraham 2001; Quin *et al.* 2014). These modifications are likely catalysed by enzymes such as cytochrome P450 monooxygenases, oxidoreductases, and methyltransferases. We therefore searched within the genomic regions surrounding these 20 putative sesquiterpene synthase homologues, as well as Dia1, for putative associated biosynthetic genes. Eight of the homologues, as well as Dia1, appear to be part of putative biosynthetic gene clusters that we manually annotated (Fig 7, Table S2). These clusters vary in size, containing anywhere between two and 16 genes encoding putative transporters, transcription factors, scaffold modifying enzymes (e.g. methyltransferases), P450s and oxidoreductases. The presence of genes encoding P450s and oxidoreductases surrounding Δ6-protoilludene synthase Dia1, as well as the other eight homologues, suggests that these biosynthetic genes likely modify the Δ6-protoilludene scaffold into bioactive

secondary metabolites. For example, the gene cluster associated with Diaam1|5282 identified in the recently sequenced genome of the grapevine trunk pathogen *Diaporthe ampelina* may play an important role in its pathogenicity (Morales-Cruz *et al.* 2015).

It is notable that every biosynthetic gene cluster that we have identified as being associated with a (putative) Δ6-protoilludene synthase contains at least one cytochrome P450 monooxygenase (Fig 7) (Wawrzyn *et al.* 2012b; Quin *et al.* 2013a), which may indicate that P450 monooxygenases have an essential function in the biosynthesis of modified sesquiterpenoids, although this remains to be verified. All of the putative biosynthetic gene clusters identified for Dia1 and its eight homologues have a P450 enzyme located adjacent to the predicted terpene synthase (Fig 7). If a modification catalysed by a P450 is essential for the biosynthesis of modified bioactive sesquiterpenoids derived from Δ6-protoilludene;
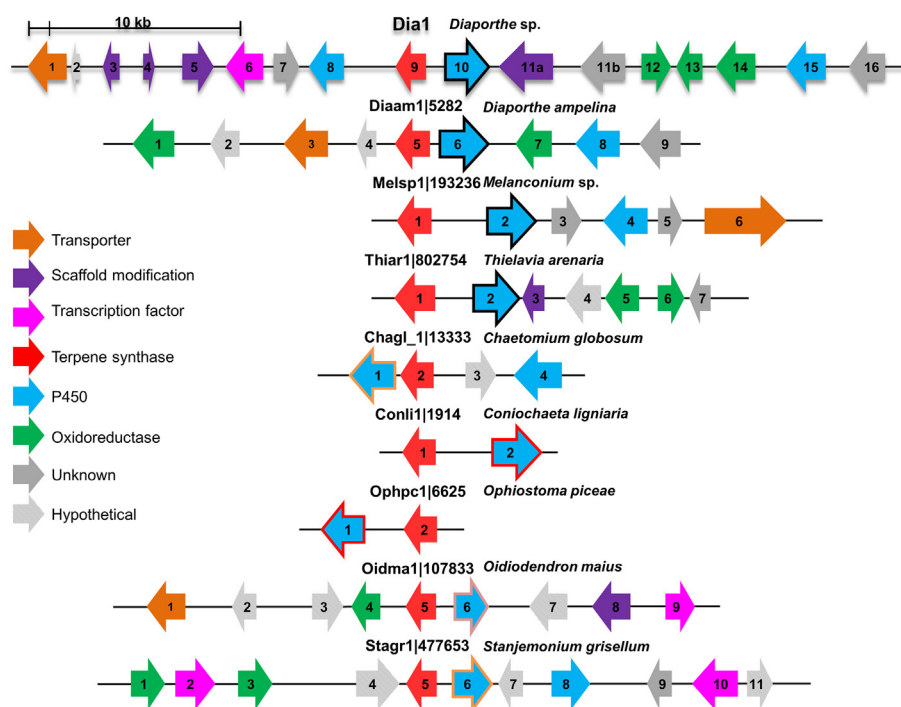

Fig 7 – **Putative sesquiterpene synthases and biosynthetic gene clusters associated with Δ6-protoilludene synthase Dia1 and its closely related *Ascomycota* homologues, and classification of the P450 most closely associated with these putative terpene synthases. Homologues of Δ6-protoilludene synthase Dia1 were identified by BLAST searches of *Ascomycota* genomes in JGI using a cutoff value of 1E−60. Putative terpene synthases are indicated by a red arrow, with the JGI identifier and species name provided above the arrow. Potential biosynthetic genes clustered around the terpene synthase were manually annotated using AUGUSTUS and BLAST. Identified were genes putatively encoding transporters, enzymes involved in scaffold modification, transcription factors, cytochrome P450 monooxygenases, and oxidoreductases (coloured arrows show their putative functions). Genes with unknown function or annotated as hypothetical are indicated by grey arrows. The numbers within arrows refer to gene model prediction from AUGUSTUS outputs. The P450 most closely associated with the putative terpene synthases (bold arrow outline) was categorized according to CYP family using Dr. Nelson's P450 database and BLAST server (http://drnelson.uthsc.edu/CytochromeP450.html). Dia_g10 (3e-167), Diaam_g6 (1e-128), Melsp_g2 (2e-109), Thiar_g2 (5e-165) belong to CYP family 5032 (black arrow outline) associated with *Basidiomycota*, while the other P450s are most closely related to *Ascomycota* CYP families: Chagl_g1 (2e-143), Stagr_g6 (9e-172) belong to CYP family 65 (orange arrow outline); Conli_g2 (0), Ophpc_g1 (0) belong to CYP 582 (rose arrow outline); and Oidma_g6 (2e-52) to CYP 682 (pink arrow outline). E-values for top P450 hits are shown in parentheses as an indicator of significance of CYP family assignments (see Supporting Information for sequences). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)**

the cytochrome P450 and terpene synthase may potentially be horizontally transferred together to yield a partial or complete secondary metabolic pathway that provides a fitness advantage to the host (Slot & Rokas 2011). Our analyses of the predicted P450s located adjacent to Dia1 and the other predicted Δ6-protoilludene synthase homologues (Fig 7) showed that some were highly related in sequence and potentially in function (CYP family) to *Basidiomycota* P450s (Supporting Information). Putative P450s associated with (putative) sesquiterpene synthases Dia1, Diaam1, Melsp1, and Thiar1 were classified according to sequence as belonging to CYP5037, a cytochrome P450 family that is enriched in *Basidiomycota* (Syed *et al.* 2014). Furthermore, the closest match identified by BLAST search for these four putative P450s belongs to a *Basidiomycete*, suggesting that at least in these clusters, a terpene synthase and a P450 may have been acquired together from a *Basidiomycota* source by horizontal gene transfer. This is in contrast to the other five P450s associated with the *Ascomycota* sesquiterpene synthase homologues, which were more similar in sequence to *Ascomycota* P450s and these clusters likely recruited a cytochrome P450 from an existing complement of enzymes.

Discussion

Sesquiterpenoids belong to a large and diverse class of natural products, many of which have potential as pharmaceutical agents due to their bioactivities (Fraga 2013). Fungi represent one of the greatest sources of bioactive sesquiterpenoids (Abraham 2001), therefore the discovery and characterization of fungal sesquiterpenoid biosynthetic pathways is of key interest. The goal of this work was to explore the biosynthetic potential of the relatively understudied fungal division *Ascomycota* in respect to their production of bioactive sesquiterpenoids derived from the Δ6-protoilludene scaffold that is typically associated with *Basidiomycota*. Here, we have conducted *de novo* genome sequencing of an environmentally isolated fungal endophyte which produces both monoterpenoids and sesquiterpenoids (Figs 2 and 3), and we used a genome mining and phylogenetic approach to identify and characterize the first Δ6-protoilludene synthase (Fig 6) from an *Ascomycete*.

Previously, we have shown that our predictive framework was reliable for the targeted discovery of novel sesquiterpene synthases from *Basidiomycota* based on cyclization mechanism (Quin *et al.* 2013a). This has the potential to streamline the discovery and characterization of new enzymes, in particular, those that catalyse a 1,11 cyclization of (2*E*,6*E*)-FPP to produce *trans*-humulyl cation derived sesquiterpene scaffolds, such as Δ6-protoilludene. This study shows that predicting cyclization mechanism of putative sesquiterpene synthases from *Ascomycota* based upon phylogenetic clustering may not be as well defined as it is for *Basidiomycota* (Fig 4). This may be related to the fact that relatively fewer sesquiterpene synthases have been identified and characterized from *Ascomycota* than *Basidiomycota* (Schmidt-Dannert 2015); or it could be due to the fact that in this study we purposefully compared *Ascomycota* and *Basidiomycota* sequences. Our results indicate that there is an underlying difference in gene architecture and amino sequence between *Ascomycota* and

Basidiomycota sesquiterpene synthases (Figs 4 and 5), which may make phylogenetic analyses more difficult. Future studies depend upon the availability of a more diverse set of experimentally characterized *Ascomycota* sesquiterpene synthases. Coincidently, using this comparative approach led us to identify an unexpected case of horizontal gene transfer across fungal phyla.

Horizontal gene transfer from species to species across divisions and classes is a commonly recognized mechanism in fungal genomic evolution that drives metabolic diversification (Fitzpatrick 2012; Wisecaver *et al.* 2014). Gene duplication and horizontal gene transfer likely accounts for the wide-spread presence of Δ6-protoilludene synthases and associated gene clusters (Wawrzyn *et al.* 2012b; Quin *et al.* 2013a) in different members of the division *Basidiomycota*. Similarly, a Δ6-protoilludene synthase and associated genes may have been transferred from a *Basidiomycete* to one or several members within the *Ascomycota* division, followed by species to species transfer within the division, for example, between the closely related *Diaporthe* sp. BR109 and *Diaporthe ampelina*. So far, our analysis has identified 20 Δ6-protoilludene synthase homologues in the sequenced genomes of fungi from only two closely related *Ascomycota* classes: *Sordariomycetes* and *Leotiomycetes*, which are known to be more proficient in horizontal gene transfer of metabolic genes, and especially clustered genes, in comparison to other fungal divisions and classes (Wisecaver *et al.* 2014). Eight of the putative Δ6-protoilludene synthase homologues are located in a biosynthetic gene cluster and in four of those fungi, the terpene synthase and an associated P450 are most closely related to *Basidiomycota* homologues, suggesting that they likely have originally been transferred as a cluster. This strongly suggests that uptake of these genes, despite the expense of alternative splicing arrangements of genes, must provide an evolutionary fitness to the host (Lawrence & Roth 1996).

It is not known which, if any, of the fungal strains that we have identified by sequence analysis produce Δ6-protoilludene and/or modified sesquiterpenoids derived from this scaffold, nor is it known what bioactivities such modified sesquiterpenoids could have and how those activities could benefit the host. Nonetheless, the conserved presence of a cytochrome P450 in all putative Δ6-protoilludene synthase containing biosynthetic gene clusters, which is some cases contain only a sesquiterpene synthase and (a) cytochrome P450(s) (Fig 7), could indicate a putative minimal operon architecture required for function. Likewise, the apparent horizontal transfer of both a sesquiterpene synthase and one cytochrome P450 in at least some of the *Ascomycota* species could suggest a minimal operon architecture required for evolutionary fitness. Future work will require the characterization of cytochrome P450s within these clusters, and studies of the modified sesquiterpene scaffolds that they may be involved in creating, to determine whether any of these hypotheses are correct.

In general, more natural product related studies have been carried out with *Ascomycota* than *Basidiomycota*, despite the fact that *Basidiomycota* are a rich resource for bioactive sesquiterpenoids. This may be due to several factors, including the fact that reliable laboratory cultivation techniques for natural products isolation are comparably well established for filamentous fungi and endophytes (Posch *et al.*

2013; Venugopalan & Srivastava 2015); more genome sequences of *Ascomycetes* are publically available (Schmidt-Dannert 2015); and the genetics of *Ascomycetes* are better understood, enabling the development of genetic manipulation techniques (Brakhage & Schroeckh 2011; Brakhage 2013; Scharf & Brakhage 2013). *Ascomycota* could therefore serve as a useful platform for the discovery and/or production of further modified bioactive sesquiterpenoids such as those derived from the Δ6-protoilludene scaffold. Furthermore, fungal endophytes such as the *Ascomycete Diaporthe* (*Phomopsis*) sp. produce a diversity of interesting and bioactive sesquiterpene scaffolds, such as cadinanes (Silva *et al.* 2006), drimanes (Zang le *et al.*, 2012) and meroterpenoids (Tajima *et al.* 2004; Hemtasin *et al.* 2011; Ma *et al.* 2015) and as we have shown here, *trans*-humulene scaffolds. *Diaporthe* (*Phomopsis*) sp. is also known to produce monoterpenoids (Sassa *et al.* 2003; Singh *et al.* 2011) as we have also shown here; as well as diterpenoids (Toyomasu *et al.* 2008) and triterpenoids (Zhang *et al.* 2013). This fungal species therefore represents a rich source of terpene synthases that could potentially be characterized. Increased availability of *Diaporthe* (*Phomopsis*) sp. genome sequences, such as the one we present here, or other novel species (Koloniuk *et al.* 2014) will facilitate further studies in this area.

Conclusion

This work describes the first characterization of a Δ6-protoilludene synthase from an *Ascomycete*, and provides insights into the evolutionary pathway of individual genes and potentially minimal sesquiterpenoid secondary metabolic pathways across fungal phyla. These results offer a basis towards the discovery and characterization of further novel biotechnologically relevant enzymes involved in the biosynthesis of bioactive natural products in fungi.

Author contributions

Conceived and designed experiments: JGSF, MBQ, CS-D; conducted experiments: JGSF, MBQ, DJS, JJS, KK, BFD; analysed data: JGSF, MBQ, CS-D; provided reagents: JGSF, SAS, CS-D; wrote the manuscript: MBQ, CS-D.

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Appendix A. Supplementary data

Supplementary data related to this article can be found at http://dx.doi.org/10.1016/j.funbio.2016.04.001.

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