

Identification of a Fungal 1,8-cineole Synthase from *Hypoxylon* sp. with Common Specificity
Determinants to the Plant Synthases*

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*Running Title: *Identification of fungal 1,8-cineole synthase*

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Background: 1,8-cineole, a commercially important monoterpene, was identified as a fungal product.

Results: The 1,8-cineole synthase was identified from a *Hypoxylon* fungal genome and mutagenesis revealed a critical asparagine residue.

Conclusions: The fungal 1,8-cineole synthase uses a mechanism similar to the plant version.

Significance: This is the first identified fungal monoterpene synthase and may facilitate future terpene synthase identification and production.

ABSTRACT

Terpenes are an important and diverse class of secondary metabolites widely produced by fungi. Volatile compound screening of a fungal endophyte collection revealed a number of isolates in the family Xylariaceae, producing a series of terpene molecules including 1,8-cineole. This compound is a commercially important component of eucalyptus oil used in pharmaceutical applications and has been explored as a potential biofuel additive. The genes that produce terpene molecules such as 1,8-cineole have been little explored in fungi, providing an opportunity to explore the biosynthetic origin of these compounds. Through genome sequencing of cineole producing isolate E7406B we were able to

identify eleven new terpene synthase genes. Expressing a subset of these genes in *E. coli* allowed identification of the *hyp3* gene, responsible for 1,8-cineole biosynthesis, the first monoterpene synthase discovered in fungi. In a striking example of convergent evolution, mutational analysis of this terpene synthase revealed an active site asparagine critical for water capture and specificity during cineole synthesis, the same mechanism used in an unrelated plant homologue. These studies have provided insight into the evolutionary relationship of fungal terpene synthases to those in plants and bacteria, and further established fungi as a relatively untapped source of this important and diverse class of compounds.

Fungi have long been studied for the ability to produce secondary metabolites with useful properties (1). Many of the most well-studied molecules are bioactive natural products that may have antimicrobial or other properties useful in medicine or agriculture (2, 3). More recently there has been an increased focus on biological compounds that may serve as biofuels, commodity chemicals or their precursors (4, 5). These molecules are often volatile organic compounds

(VOCs) that mimic the properties of compounds found in petroleum mixtures.

Terpenoids represent the largest class of secondary metabolites with over 40,000 known structures, and are produced as VOCs from many fungal species (6). This large amount of chemical diversity is generated by the terpene synthase enzymes (TPS) that produce these molecules (7, 8). These enzymes take a prenyl diphosphate precursor and, through a variety of cyclizations and rearrangements of a carbocation intermediate, produce the final terpene scaffold. The prenyl diphosphate precursors can have variable chain-lengths in 5 carbon intervals, which adds to the diversity of this compound class. For example, monoterpenes (C_{10}) derive from geranyl pyrophosphate (GPP), sesquiterpenes (C_{15}) from farnesyl pyrophosphate (FPP) and diterpenes (C_{20}) from geranylgeranyl pyrophosphate (GGPP). The terpene backbone can be further modified, often through oxidation by P450 enzymes, to create a huge array of natural products.

The diversity of terpene products is due in large part to the plasticity of terpene synthase enzyme active sites. The TPS enzymes can be either specific or promiscuous, synthesizing anywhere from a single product to more than 50 different compounds. The identity and number of compounds produced by a TPS enzyme is determined in the active site, where the substrate is activated by a metal binding motif (DDxxD/E) to form a carbocation intermediate, and guided through a variety of cyclization mechanisms. Structurally, all TPS enzymes share a common terpene synthase fold which is conserved in bacteria, fungi and plants, however outside of the DDxxD/E motif there is only limited sequence similarity between plant and microbial enzymes (9, 10). Evidence from plants suggests that terpene synthases have evolved rapidly and that sequence similarity is dominated by species relationships rather than the terpene product (8, 11, 12). The “evolvability” and plasticity of these enzymes has recently allowed for directed evolution and rational engineering of TPS activity (13, 14). Site-directed mutagenesis was used by Yoshikuni et al. to identify plasticity residues in a promiscuous γ -humulene synthase and convert it into a variety of more specific synthases (15). Furthermore, Kampranis et al. were able to convert a 1,8-cineole synthase from the sage plant *Salvia fruticosa* to

produce non-oxygenated monoterpenes sabinene or limonene as well as sesquiterpenes by mutation of a single asparagine residue (16). Such plasticity has also been observed in a fungal trichodiene synthase, demonstrating that this is a conserved feature of TPS enzymes (17).

Many terpenoids are bioactive and may have medicinal properties such as anticancer (taxanes) antimicrobial, or antimalarial activity (artemisinin)(18–21). These compounds, particularly the mono- and sesquiterpenes, are often used as fragrance or flavoring compounds. More recently a number of terpene hydrocarbons have been studied as potential biofuels. Farnesane and bisabolane, fully reduced forms of the sesquiterpenes farnesene and bisabolene, have both been produced as alternative diesel fuels (22). These molecules have an energy density similar to that of diesel fuel and much greater than that of ethanol, currently the most widely used biofuel. In addition these terpene derived fuels are immiscible in water and compatible with current engines which are further advantages over ethanol. Monoterpenes have also been studied as biofuel targets. Pinene can be chemically dimerized for use as a potential jet-fuel while limonene has been studied for use as a biofuel and precursor for commodity chemicals (23–25). Both of these compounds are traditionally derived from plant biomass, but alternative biosynthetic production platforms have been explored.

Because of the interest in terpenes for a variety of uses, the pathways that produce these molecules have been engineered for increased production in *Sacharomyces cerevisiae* and *Escherichia coli*. In *E. coli*, this involved expression of components of the yeast mevalonate pathway in addition to the endogenous DXP pathway in the bacterium. This pathway was originally developed for the over-production of amorpha-4,11-diene, a sesquiterpene precursor of the antimalarial drug artemisinin (26–28). Additional optimization and expression of a bisabolene synthase allowed the pathway to be adapted for production of the biofuel precursor bisabolene at a yield of 900 mg/L (22). Recently, this pathway was adapted for expression of the monoterpene limonene by replacing the FPP synthase gene *ispA* with a GPP synthase from *Mentha spicata* and expression of a limonene synthase from *Abies grandis* (23). In each of the

described cases, a plant TPS gene was used from terpene production which is unsurprising because the plant TPS enzymes are better characterized than microbial versions. Since this step of the pathway has been identified as a bottleneck, there remains a need for identification of additional and potentially more efficient terpene synthases.

Fungi are another source of terpenes and the TPS genes that produce them are under explored compared to plants. Current biodiversity estimates suggest that there exist approximately 400,000 plant species compared to between 3 and 5 million fungal species, which represents a tremendous amount of biodiversity that remains largely untapped (29). Only a handful of fungal terpene synthases have been characterized, including aristolochene synthase, trichodiene synthase, presilphiperfolan-8 β -ol synthase and the sesquiterpene synthases of Basidiomycota *Coprinus cinereus*, *Armillaria gallica* and *Omphalotus olearius* (30–36). No fungal monoterpene synthases have been identified to date.

Endophytic fungi are a diverse group of microbes that reside within plant tissues. They have been explored for the production of VOCs and many of them produce an abundance of terpenes (37). Recently, three endophytic fungi in the family Xylariaceae, identified as *Hypoxylon* sp. (isolate CI-4) and related anamorph *Nodulisporium* sp. (isolates EC12 and Ni25-2A), were discovered to produce a series of VOCs that included 1,8-cineole (38–40). Also known as eucalyptol, 1,8-cineole is an oxygenated monoterpene that is the main component of the essential oil of *Eucalyptus globulus*. Cineole is widely used in a number of applications, including medicinally in cough suppressants and mouth wash, and as a flavoring and fragrance additive. It has also been explored as a biofuel with potential as a gasoline additive that may prevent separation in ethanol and petroleum fuel blends, as well as a precursor for commodity chemicals such as p-cresol and benzylic esters (41–44).

Here we have identified 8 new fungal isolates in the family Xylariaceae that produce 1,8-cineole and a variety of other potentially interesting compounds. Through genome sequencing, heterologous gene expression in *E. coli*, and *in vitro* enzymology, we identify the fungal cineole synthase. A mutational analysis of the enzyme

active site reveals a remarkable similarity in the mechanism of the otherwise divergent fungal and plant cineole synthases, for incorporating the oxygen moiety during terpene cyclization and excluding sesquiterpene precursor substrates. Finally we test the yield of cineole production in an overexpression strain to demonstrate the viability of fungal synthases for terpene production.

EXPERIMENTAL PROCEDURES

Fungal isolation and culturing - Plant stem material was collected from various locations in Ecuador as well as Kubah National Park in Sarawak, Malaysia. Stems were stored in clean plastic bags and transported back to Yale University, where they were surface sterilized and plated on isolation media comprised of 1 X potato dextrose agar (PDA) (24 g/L potato dextrose), 0.1 X PDA (2.4 g/L potato dextrose) (EMD Millipore) or water agar (all 15 g/L agar). Several fungi were isolated in the presence of three day-old *Muscodor albus* which was used to enrich for VOC producing isolates, as described previously (45, 46). Isolates observed growing from the stems were transferred to a new 1 X PDA plate. For VOC analysis, agar plugs were inoculated into sealed vials with both 1X PDA and potato dextrose broth (PDB) as described previously (37). Vials were sampled after growth at 23 °C for 4, 8 and 12 days.

GCMS analysis of fungal volatile compounds - Volatile compounds in the headspace of the fungal cultures were sampled by solid phase microextraction (SPME) with a 50/30 μ m divinylbenzene /carboxen/polydimethylsiloxane StableFlex SPME Fiber (Supelco). Compounds were injected into the gas chromatograph (Agilent 7890A) with a ZB-624 column (30 m x 0.25 mm ID x 1.40 μ m film thickness; Phenomenex) paired with a time-of-flight mass spectrometer (GCT Premier, Waters). Electron ionization spectral data were analyzed with the MassLynx Software Suite (Waters) and initial peak identification was carried out by comparison of the EI spectra with the Wiley Registry of Mass Spectral Data, 8th Edition and the National Institute of Standards and Technology (NIST) database. Whenever possible

the compound identification was verified by comparison of retention time and mass spectra with authentic standards (Sigma-Aldrich).

Phylogenetic analysis of fungal isolates - The internal transcribed spacer (ITS) rDNA of the cineole producing fungi was amplified by the colony-PCR method described by van Zeijl et al. using trichoderma lysing enzyme (Sigma) in place of Novozyme 234 (47). The primers used for amplification were ITS1 (TCCGTAGGTGAACCTGCGG) and ITS4 (TCCTCCGCTTATTGATATGC) and the resulting PCR products were sequenced by the W.M. Keck Foundation (48). A phylogenetic tree was constructed comparing the ITS sequence of cineole producing isolates⁵ from this study with previous cineole producers (CI-4, Ni25-2A, EC12) and taxa reported in several recent molecular phylogenetic studies of genera in the family Xylariaceae (Table 1) (49, 50). Sequences were aligned using MUSCLE v3.8.31 and the phylogenetic tree was constructed using Bayesian (MrBayes v3.2.0) and maximum likelihood methods (RAxML v7.2.8) (51, 52).

Genome sequencing of E7406B and terpene synthase gene identification - Genomic DNA from isolate E7406B was obtained from a 7 day-old PDA culture using a Plant DNeasy kit (Qiagen) as described previously (53). This DNA was used for 2x100 paired-end sequencing on an Illumina HiSeq 2000 of both a 180 bp fragment library as well as a 3 kb mate-pair library. The sequencing data were assembled using ALLPATHS-LG into a genome of 45.3 Mbp (54). The assembly yielded 504 scaffolds with a N₅₀ of 855 kbp and genome coverage of 450%. Genome data was submitted to GenBank (Bioproject ID PRJNA244689). Gene models were defined using GeneMark-ES self-training algorithm, identifying 11551 protein coding genes.

Terpene synthase (TPS) genes were identified using Pfam based on similarity to the terpene synthase C-terminal domain family (PF03936). Putative terpene synthase gene identities were also checked using BLAST for similarity to known terpene synthase genes. A total of 13 putative TPS genes were identified and several criteria were used to determine candidates for expression. Alignment of the TPS protein sequences with MUSCLE v3.8.31 was performed to confirm the

presence of the known catalytic motifs DDxx(D/E) and NSE/DTE. Two of the enzymes did not contain the required catalytic residues and were excluded from further analysis, while the remaining 11 enzymes were included in the construction of a phylogenetic tree along with protein sequences of terpene synthases with known products from plants, fungi and bacterial species (Table 2). TPS protein sequences were again aligned using MUSCLE v3.8.31 and the phylogenetic tree was constructed using RAxML v7.2.8.

Cloning and expression of terpene synthase genes in E. coli - Candidate TPS genes were synthesized by GENEWIZ and codon optimized for expression in *E. coli*. These genes were then subcloned into vector pTrc99 between restriction sites NcoI and XmaI, and transformed into *E. coli* DH5 α (22). The bacteria were also co-transformed with pJBEI-2999 which contains the mevalonate pathway optimized for FPP production (22).

Overnight cultures of *E. coli* with terpene synthase plasmids were grown in LB Broth (Sigma) and diluted 1:100 in 50 mL production media (Teknova, EZ-Rich with 1% glucose) as described previously (22). Cultures were induced with 500 μ M IPTG at OD 0.6 and 5 mL was removed for growth in sealed GC/MS vials. Dodecane, which has been shown to trap volatile terpenes and relieve product inhibition while not inhibiting *E. coli* growth, was overlayed on the shaker flask sample at 10% v/v as reported (55). After 48 hr of growth the GC/MS vials were sampled by SPME and the dodecane layer of shaker flask samples was extracted and diluted at 1:10 and 1:100 in ethyl acetate for direct injection into the GC/MS. Both sampling methods were used because SPME is the more sensitive method for detecting minor compounds, while direct injection is less biased toward more volatile compounds, allowing for the determination of relative compound amounts. Production peaks were matched to authentic standards when available for identification, as done for the fungal samples. In addition, retention indices were measured on a DB5-MS column (Agilent) by comparison to an alkane mix (Fluka), and production peaks were compared to known compounds in MassFinder's terpene library and the NIST database. Peak areas in the direct

injection samples were also measured to give a relative amount of each product.

Structural modeling and mutational analysis of Hyp3 enzyme - The protein sequence of Hyp3 was analyzed for subcellular localization signaling motifs using the programs WoLF PSORT and PSORTII online tools (56, 57). The enzyme structure was modeled using the structure of the most closely related TPS enzyme based on phylogeny, *Aspergillus terreus* aristolochene synthase (pdb file 2E4O.pdb) (58), using the Modeller software (<http://toolkit.tuebingen.mpg.de/modeller>) (59). We also aligned this modeled structure with the FPP substrate bound aristolochene synthase (pdb file 4KUX.pdb) and generated the figure using PyMol version 1.7.2.1.

PCR primers matching to the *hyp3* gene in the pTrc99 vector were used to alter the codon at position N136 to produce valine (N136V), isoleucine (N136I), serine (N136S) and alanine (N136A) mutants. These mutants were expressed in *E. coli* DH5 α with pJBEI-2999 as described for other TPS genes and were sampled by SPME after 2 hr induction to ensure that production peaks did not saturate the mass spec detector. GC/MS conditions were the same as described previously for fungal volatile compounds.

Hyp3 protein purification and enzyme assays - The codon optimized *hyp3* gene was PCR amplified from the pTrc99 construct using primers designed for Gibson assembly (forward primer 5'-CAGCAGCGGCCATATCGAAGGTCGTCATA TGGCCCGCCCGATTAC; reverse primer 5' GCTTTGTTAGCAGCCGGATCCTCGAGCATA CTATTAGATAACCGTAAGCC). The *hyp3* gene was cloned using Gibson assembly into a pET16b vector following the His tag (Gibson Assembly Kit, NEB). This Hyp3 expression vector was transformed into *E. coli* BL21 and cells were grown at 37 °C in Terrific Broth (TB) with ampicillin (100 μ g/mL) to an OD of 0.6 – 0.8. When the OD was reached the cells were induced with 1 mM IPTG and transferred to a 30 °C incubator for 4 hours. Cells were lysed using a microfluidizer and clarified by centrifugation. Hyp3 was purified from the clarified lysate using Ni-NTA resin (Qiagen) in wash buffer (20 mM Tris pH 7.5, 10 mM MgCl₂, 200 mM NaCl, 1 mM 2-mercaptoethanol, 10 mM Imidazole), and eluted with elution buffer (20 mM Tris pH 7.5, 10 mM

MgCl₂, 1 mM 2-mercaptoethanol, 300 mM Imidazole). For storage the purified protein was dialyzed into buffer A (20 mM Tris pH 7.5, 10 mM MgCl₂, 1 mM 2-mercaptoethanol, 10% glycerol).

GCMS enzyme activity assays were carried out by incubating a 500 μ L reaction overnight at 30 °C in a 5 mL scintillation vial sealed with parafilm. The reaction contained 100 μ M GPP and 10 μ M Hyp3 enzyme in GCMS assay buffer (buffer A with no glycerol). The reaction vials were sampled by SPME and analyzed by GCMS as described for the bacterial cultures.

Steady-state kinetics of fungal cineole synthase was assayed in a plate reader (Synergy 4, BioTek) by measuring pyrophosphate (PP_i) release via conversion to ATP in an ATP-dependent luminescence assay (PPiLight kit, Lonza). Final concentrations of GPP (Sigma-Aldrich) and (*E,E*)-FPP (Sigma-Aldrich) were varied between 0.25 and 5 μ M. Sample containing no substrate was used as a blank and known concentrations of PP_i were used to obtain the time-dependent calibration curves. Reaction mixtures (total volume 75 μ L) contained 15 μ L of PPiLight solution reconstituted according to the instructions, 10 nM cineole synthase and assay buffer (Buffer A with 50 mM HEPES rather than Tris). Incubation time was 90 min at 30 °C. The activity was determined as the difference of luminescence per minute of the samples with and without the substrate. Concentrations of PP_i released during each assay were calculated from the linear fit equations for each minute of recorded luminescence from the known concentration of PP_i (varied between 0.025 and 10 μ M). The scatter plots of initial rate vs substrate concentration were fitted to the equation

$$V = k_{cat} \times [E]_0 \times x / (K_m + x)$$

from which K_m and k_{cat} values were determined. KaleidaGraph 4.1.3 was used for data analysis.

Quantification of 1,8-cineole production - For cineole quantification, shaker flasks (50 mL) of the fungus in PDA were grown for four days, and *E. coli* DH5 α harboring *hyp3*, with and without pJBEI-2999, were grown for two days in EZ-Rich production media. A 10% dodecane layer was overlaid on each of the samples and an aliquot was removed and sampled after the allotted

growth time as described above, with the inclusion of an internal camphor standard. The amount of cineole in each sample was calculated as compared to a standard cineole curve with a camphor internal standard included.

RESULTS

VOC analysis of fungal isolates - Fungi isolated after collection trips to tropical forests in Ecuador and the Malaysian state of Sarawak were subjected to GC/MS analysis of the volatile compounds produced in the culture headspace. Cultures were grown in sealed vials on PDB media and sampled after 4, 8, or 20 days of growth. We discovered 8 unique isolates producing the monoterpene 1,8-cineole based on comparison to the MS fragmentation pattern in the NIST database. These isolates were identified as E7406B, E6826D, E7015B, E13732D, E13415F, E13615I, and E14012A from locations in Ecuador and B10820A from Kubah National Park in Sarawak. These isolates, along with the originally identified 1,8-cineole producer strain CI4 isolated in the Canary Islands, were then re-tested on both solid PDA and liquid PDB to confirm the production of 1,8-cineole and further catalogue the spectrum of VOCs that they produce. The major VOCs produced by these organisms are presented in Table 3.

The identity of 1,8-cineole was confirmed by comparison to an authentic standard with a match of both the retention time and fragmentation pattern to the fungal product. We also observed a series of other monoterpene compounds produced in a majority of the isolates (Table 3). Authentic standards matched the identity of limonene, p-cymene, γ -terpinene, α -pinene, α -phellandrene, α -terpinene and terpinolene. Other monoterpenes were identified in the spectrum of several of the isolates based on the appearance of a 136 mass peak consistent with compounds with the formula $C_{10}H_{16}$ and comparison with the NIST database, which gave a tentative identification of these compounds as α -pinene, α -phellandrene, α -terpinene and terpinolene.

The cineole producing strains also produced an expansive series of sesquiterpenes. The number observed ranged from 9 compounds in CI4 and E13732D up to 32 in isolate E6826D. The sesquiterpenes were identified by a characteristic 204 Da peak in the mass spectral data and

comparison to the NIST database. These compounds eluted in the range where sesquiterpene standards were observed but with only a single exception, commercially available compounds did not match the product peaks. We were only able to match the compound δ -cadinene in seven of our isolates to the known compound from the extracts of Atlas Cedar and Cade Juniper. We were unable to confirm the identity of the remaining sesquiterpene compounds.

A series of alcohols and acetate derivatives, which are common fungal metabolites, were also among the compounds in the VOC profile of our isolates. The observed compounds included 3-methyl butanol, 2-methyl butanol, produced by all of the strains tested, the related derivatives 3-methyl and 2-methyl butyl acetate in six strains and the shorter chain 2-methyl propanol in six of the strains. Other compounds commonly observed in the tested organisms included dimethylfuran, benzene ethanol, benzene and styrene.

Many of the isolates tested produced an extensive series of volatile polyene compounds with the formula C_7H_{10} and C_9H_{12} . Compounds with these formulas were previously reported as products of isolate CI-4. The previously identified C_7H_{10} compound methyl-1,4-cyclohexadiene was not produced in our cultures based on comparison to an authentic standard, indicating that we may be observing a different subset of these compounds. The largest of the polyene compound peaks was a C_9H_{12} compound that matched the retention time and fragmentation pattern of a compound identified as (3E,5E,7E)-nona-1,3,5,7-tetraene by NMR in a different fungus (manuscript submitted for publication). This is also consistent with the NIST database match for this compound peak. Four smaller peaks eluted immediately after the nonatetraene peak and are likely isomers of this compound, having identical EI fragmentation patterns. The major C_7H_{10} compound produced by our fungi was identified in the database as 1,3,5-heptatriene, which is likely related to the nonatetraene peak.

Phylogenetic analysis of cineole producing fungi - The isolates presented here had a number of VOCs in common, and were typified by the production of 1,8-cineole. We reasoned that these fungi may also be phylogenetically related although they derived from sources around the world. To test this idea, we sequenced the internal

transcribed spacer of our isolates and compared them to the published cineole producing strains CI-4, Ni25-2A, and EC12. These cineole-producing strains all grouped to a clade comprising fungi in the genera *Hypoxylon*, *Annulohypoxylon*, and *Daldinia* within the family Xylariaceae (Fig. 1). This clade is clearly resolved from other genera *Nemania*, *Xylaria*, and *Biscogniauxia* by both Maximum Likelihood and Bayesian phylogenetic approaches. The genera containing cineole producers are closely related and although their phylogenetic relationship was not resolved by ITS sequencing alone in our tree, consistent with previous publications, we can observe to which of these groups our isolates are most closely related (49).

We were largely able to recapitulate the phylogenetic relationships of published strains CI-4, EC12 and Ni25-2A, with EC12 appearing closely related to species of *Daldinia*, Ni25-2A close to *Hypoxylon monticulosum*, and CI-4 close to *Hypoxylon begae* (38–40). Strains E6826D, E13415F and E13732D grouped in a clade containing species of *Annulohypoxylon*, while a second *Annulohypoxylon* clade contained B10820A. Isolates E7015B, E13615I, E7406B and E14012A all appeared closely related to each other and group in a clade containing strains of *Hypoxylon fragiforme*, *Hypoxylon investiens* and *Hypoxylon rubiginosum*. These data suggest that the ability to produce cineole is wide-spread in these genera of Xylariaceae.

Identification and phylogenetic analysis of terpene synthases from isolate E7406B - We wanted to identify the terpene synthase gene responsible for 1,8-cineole production in our fungi. To accomplish this we sequenced the genome of the isolate E7406B. Assembly of the draft genome and gene prediction using ALLPATHS-LG and GeneMark-ES identified 11551 protein coding genes. Thirteen of those were identified as terpene synthase genes using BLAST and Pfam matches but two were excluded from further analysis because they lack the conserved DDxx(D/E) motif required for catalysis. Phylogenetic analysis of the remaining terpene synthases, termed Hyp1-11, revealed that they do not form a monophyletic clade, but are unsurprisingly most closely related to other ascomycete terpene synthases (Fig. 2). In particular, Hyp9 and Hyp10 appear closely related

to a fusicoccadiene synthase while Hyp11 appears related to a TPS producing presilphiperfolan-8- β -ol, a botrydial precursor (33). The plant enzymes in the tree recapitulated the known TPS subfamilies Tpsa, Tpsb and Tpsd. Three known plant 1,8-cineole synthases group amongst the other angiosperm monoterpene synthases (Tpsb) while the recently identified 1,8-cineole synthase from the bacterium *Streptomyces clavuligerus* groups with other bacterial TPS enzymes. None of the TPS enzymes from E7406B appear closely related to these known 1,8-cineole synthases. Since fungal monoterpene synthases have yet to be identified, we reasoned that the 1,8-cineole synthase from Xylariaceae fungi may be divergent from the previously identified ascomycete sesquiterpene synthases. We went on to select TPS genes for heterologous expression to identify their products, prioritizing those which were divergent from known TPS genes.

Identification of fungal 1,8-cineole synthase Hyp3 and other TPS genes - The eight selected genes, *hyp1* – 8, were expressed in *E. coli* DH5 harboring the pJBEI-2999 plasmid for high production of terpene precursors through the mevalonate pathway. The volatile products were measured by GC/MS analysis of both the culture headspace by SPME in sealed vials and direct injection of a dodecane overlay in 50 mL shaker flasks. This analysis revealed that *hyp3* is the gene responsible for 1,8-cineole production in our fungal isolate. *E. coli* expressing Hyp3 produced a major monoterpene product matching the retention time and mass spectrum of a 1,8-cineole standard. Hyp3 appeared specific for monoterpenes, producing 1,8-cineole at about 90% of the product peak area, along with a minor peak of the unoxygenated monoterpene limonene (Table 4). No sesquiterpene products were observed from this enzyme. This result is especially interesting considering that pJBEI-2999 was optimized for production of farnesyl pyrophosphate, the precursor to sesquiterpene biosynthesis. None of the other TPS genes tested exhibited monoterpene specificity.

E. coli expressing pJBEI-2999 with four of the remaining genes produced sesquiterpenes as a majority of their terpene products (Table 4). *Hyp1* appeared to be specific for the oxygenated, uncyclized sesquiterpene trans-nerolidol as identified by comparison to an authentic nerolidol

standard. The other three sesquiterpene synthases appeared to be more promiscuous enzymes, producing a variety of products. The major product of Hyp2 was δ -cadinene, identified by similarity to the known compound from plant extracts, with 22 other minor products, most of which the NIST database identified as containing a naphthalene-like bicyclic ring structure. Products of the other two sesquiterpene synthases, Hyp4 and Hyp5, could not be definitively identified by authentic GC/MS standards. Hyp4 produced unknown compounds tentatively identified in the NIST database as β -caryophyllene and Germacrene A, while Hyp5 produced compounds with an apparent azulene-type bicyclic ring structure, the major components identified as α -bulnesene, β -guaiene and an unknown oxygenated derivative based on comparison of the mass spectra and retention indices. Both of these genes also produced minor monoterpene products at less than 5% of the total peak area. Three of the genes, *hyp6-8*, produced no observed products, despite containing what appeared to be the required catalytic domains. There are a number of reasons this might occur, including misidentified splice sites in the original gene model, low expression of the enzymes in *E. coli*, toxicity of their products, or production of compounds that are not observable with our column and GC/MS conditions including some diterpenes or highly oxygenated sesquiterpenes. Because our goal was to identify the 1,8-cineole synthase we did not explore these non-producing genes further.

Hyp3 enzyme kinetics demonstrate a strong specificity for GPP substrate - We were intrigued by the apparent specificity as well as potential biotechnological applications of the fungal 1,8-cineole synthase. To further explore this enzyme we tested it in *in vitro* activity assays. The purified enzyme was incubated overnight with GPP substrate and products were analyzed by GCMS. This assay confirmed that 1,8-cineole was the major monoterpene product, with no other products observed.

In order to more definitively measure the substrate specificity of Hyp3, steady-state kinetic data with GPP and FPP were compared. Enzymatic activity of the fungal 1,8-cineol synthase was measured with purified enzyme using a luminescence-based pyrophosphate (PPi) detection assay because both GPP and FPP release

PPi prior to cyclization step. Figure 3 clearly shows more specific activity with GPP compared to FPP as expected for a monoterpene synthase, giving k_{cat} value for GPP of $17.7 \pm 2.0 \text{ min}^{-1}$ and an apparent K_m value for of $2.5 \pm 0.6 \text{ }\mu\text{M}$. Measurable activity with the FPP substrate was not observed. This k_{cat} value compares favorably to 1,8-cineole synthases from organisms in other kingdoms; for example those from the sage plant *S. fruticosa* and streptomycete *S. lividans* were measured at 3.2 and 4.7 min^{-1} respectively (16, 60). Substrate affinity, as measured by K_m , varied widely between these enzymes with *S. fruticosa* cineole synthase having about 25-fold weaker affinity, and *S. lividans* about 15-fold tighter. We can also compare activity of the fungal Hyp3 monoterpene synthase to the more phylogenetically related fungal sesquiterpene synthases. The k_{cat}/K_m of $7.0 \text{ min}^{-1} \text{ }\mu\text{M}^{-1}$ for Hyp3 1,8-cineole synthase was similar to the fungal aristolochene synthases, although those enzymes had better affinity for FPP (0.13 μM for *A. terreus* and 0.6 for *P. roqueforti*) and a 7- to 17-fold slower k_{cat} than Hyp3 had for GPP substrate catalysis (61).

Hyp3 enzyme sequence and structural modeling analysis - In plants, monoterpene synthase enzymes contain a signal peptide for plastid localization, while the sesquiterpene synthases are largely cytosolic. A sequence alignment of the Hyp3 enzyme with the related aristolochene synthases showed that Hyp3 contains a slightly expanded N-terminal sequence, 9 amino acids more than *Penicillium roqueforti* aristolochene synthase, but does not contain an obvious signaling sequence. We used several tools for subcellular localization prediction, including WoLF PSORT and PSORT II, to identify any analogous localization signals on the fungal Hyp3 monoterpene synthase. Both of these programs predict that Hyp3 is a cytosolic enzyme (61% cytosolic by PSORT II).

We also created a sequence alignment and structural model of Hyp3 compared to the *Aspergillus terreus* aristolochene synthase, the most closely related terpene synthase in the phylogenetic analysis (Fig. 4A) (58). These models reveal several features in the active site pocket which may influence enzyme specificity and 1,8-cineole catalysis. In substrate bound structures of *Aspergillus terreus* aristolochene

synthase, the FPP substrate C12 and C13 carbons are positioned near the NSE motif containing α -helix (62). Near this position, L209 in the aristolochene synthase is replaced with the bulkier aromatic F267 in Hyp3 which may interfere with the FPP substrate (Fig. 4B). Several other aromatic amino acids, such as F233 and F237, are found near the Hyp3 active site replacing smaller hydrophobic residues and, although they are not predicted to be oriented near the substrate, they may serve to decrease the overall size of the active site pocket. We were most intrigued by an asparagine residue, N136, found in Hyp3 near the DDxx/E active site motif but not observed in the aristolochene synthases (L77 in *Aspergillus terreus* aristolochene synthase) or other Hyp enzymes. In the 1,8-cineole synthase from *Salvia fruticosa* (Sf-CinS1) it was determined that a conserved asparagine residue near the active site was responsible for activating water for attack on the carbocation intermediate (16). The Hyp3 structural model and an alignment of plant cineole synthases with our fungal Hyp3 revealed N136 resides in the same location adjacent to the active site DDxx(D/E) motif (Fig. 5A).

Hyp3 amino acid N136 is critical for cineole oxygen incorporation and monoterpene specificity - We hypothesized that the fungal synthase may use the same mechanism as the plant version to produce 1,8-cineole. To test this hypothesis we made a series of mutations at the N136 position in Hyp3 and tested them in our *E. coli* expression assay. We found that in each of our mutations (N136V, N136I, N136S, and N136A), removing the asparagine eliminated cineole production by the enzyme. In each case, the enzyme was not inactive, but rather produced unoxygenated monoterpenes. The major product of N136V and N136I was limonene, which can be made from the same carbocation intermediate as cineole (Fig. 5B,C,D). When the side-chain at this position is shortened to a serine or alanine, the major monoterpene product becomes the uncyclized myrcene, indicating that the enzyme can no longer catalyze cyclization of the GPP precursor (Fig. 5E,F).

Similar to the plant cineole synthase, this asparagine is also responsible for the specificity of Hyp3 for the monoterpene GPP precursor. Hyp3 normally does not produce sesquiterpene products (Fig. 5B), but when N136 is shortened to serine

sesquiterpene products begin to appear. In the N136A mutant sesquiterpene compounds, which match to farnesene isomers, form the majority of the terpene products from the enzyme.

Expression of Hyp3 in E. coli overexpression strains increases 1,8-cineole titers - Engineered production of terpenes in *E. coli* has been intensely explored recently as an alternative to the natural sources, usually derived from plants. High production titers would be required for microbial production of 1,8-cineole to be a cost-effective alternative to current eucalyptus oil sources. As a first step to test the legitimacy of microbial cineole production we attempted to quantify cineole production from both fungus E7406B and heterologous expression in *E. coli*. The dodecane layer from a four day-old E7406B shake flask culture and two day-old *E. coli* culture was extracted and the amount of cineole produced was quantified in the GC/MS by comparison to an authentic cineole standard curve.

The fungal isolate produced 0.54 ± 0.18 mg/L cineole after four days of growth at 30°C (Fig. 6). When a codon optimized version of the fungal cineole synthase was transferred into *E. coli* DH5 α it initially produced a lower yield than the fungus. The amount produced in *E. coli* was near our limit of detection in our direct injection assay and we only observed the cineole product in one of the three replicates at an amount of 0.09 mg/L. This low amount of production is consistent with previous reports of the monoterpene production capacity of *E. coli* which is limited by low production of the geranyl pyrophosphate precursor (63). When expressed in an *E. coli* strain harboring the mevalonate pathway plasmid pJBEI-2999 the amount of cineole produced increased significantly to 21 ± 11 mg/L. The overexpression strain increased cineole yield at least 230-fold over the *E. coli* alone and about 38-fold over the production level in the fungus.

DISCUSSION

We were intrigued by the capacity of a number of fungal isolates to produce an interesting series of VOCs including terpenes, in particular 1,8-cineole. Endophytic fungi such as these are known to produce an extensive array of terpene molecules, but the enzymes that produce them have been under-studied compared to their plant counterparts. To begin to fill this gap, we set out to

identify the gene responsible for 1,8-cineole biosynthesis in a collection of endophytic fungi within the genera *Hypoxylon*, *Annulohypoxylon* and *Daldinia*. We were able to identify this gene as *hyp3* from the genome of isolate E7406B. This enzyme uses a similar mechanism to produce 1,8-cineole as the plant enzyme, in an apparent example of convergent evolution.

In addition to cineole, these fungi produced a wide variety of volatile compounds. An extensive series of monoterpenoids was observed in each of the isolates except for E7015B, which only produced 1,8-cineole. Several of the commonly produced monoterpenes were identified by authentic standards as D-limonene, p-cymene, α -pinene, α -phellandrene, α - and γ -terpinene and terpinolene. Each of the isolates also produced a series of sesquiterpenes, varying in number from 9 to 32 different species, which were more difficult to identify by GC/MS. The diversity of these molecules produced by these Xylariaceae fungal isolates highlight the large capacity for terpenoid biosynthesis in these fungi.

Only a handful of terpene synthase genes have been identified in ascomycete fungi and, in an effort to identify new terpene synthases including the gene for 1,8-cineole production, we chose to express TPS genes from isolate E7406B that appeared divergent from known synthases. The four sesquiterpene synthase genes identified, *hyp1*, *hyp2*, *hyp4* and *hyp5*, all produced sesquiterpenes with different structures which likely result from different cyclization reactions catalyzed by these enzymes (64). The Hyp1 enzyme produced only the uncyclized trans-nerolidol which is generated by water capture of the nerolidyl cation (65). Hyp2 likely catalyzes a 1,10 ring closure followed by 1,6 ring closure from both farnesyl and nerolidyl cations to produce the bicyclic, cadalane-skeleton compounds δ -cadinene, α -muurolene other minor peaks (66, 67). Products of the Hyp4 and Hyp5 enzymes were not positively identified by standards, but products of Hyp5 were identified in the NIST database as guaienes or the related bulnesene derivatives, which are thought to form by 1,10-closure to form germacrene A followed by 6,2-closure to form the azulenic skeleton (68). The *E. coli* harboring *hyp4* and *hyp5* with pJBEI-2999 also produced minor monoterpene peaks, but since these strains are optimized for the FPP precursor

they should be biased against monoterpene production. More accurate determination of their specificity would require further *in vitro* assays with both GPP and FPP precursors.

The TPS Hyp3 was identified as the cineole synthase in the E7406B fungal genome. 1,8-cineole represented the major product of this terpene synthase at about 90% of the observed peak area with the remainder primarily composed of D-limonene. Unlike the other TPS genes tested, it exclusively produced monoterpenes making it, to our knowledge, the first identified fungal monoterpene synthase. The specificity of this enzyme was confirmed in the *in vitro* enzymatic assay, showing no activity with the FPP substrate, and a k_{cat}/K_m with the GPP substrate that compares favorably to other 1,8-cineole synthases from plants. This monoterpene specificity is intriguing in light of the fact that the overexpression plasmid pJBEI-2999 contains the *ispA* gene which produces the FPP sesquiterpene precursor, and that *E. coli* lack a dedicated GPP synthase which should bias production against monoterpenes. The Hyp3 enzyme is apparently able to bind any GPP substrate not converted to FPP and exclude the 15-carbon substrate.

Hyp3 from the E7406B genome is the first cineole synthase identified from fungi, but plant and bacterial cineole synthases have been characterized structurally and biochemically (16, 60, 69–71). Analysis of cineole synthases in the sage plants *S. officinalis* and *S. fruticosa* (Sf-cin) identified a conserved asparagine (N338) that is critical for activating the water molecule for attack on the α -terpinyl cation, resulting in cineole synthesis. Terpene synthases from plants and fungi are known to diverge greatly at the sequence level, but the overall terpene synthase fold is well conserved in structures of these enzymes. Because of this, we thought it was interesting to note that an asparagine N136 was present in our cineole synthase in the same position as N338 of Sf-cin relative to the DDxx(D/E) motif in the active site (Fig. 5A) (16). We observed that, like in the plant enzyme, mutation of this asparagine abolished cineole production. Both the valine and isoleucine mutants (N136V and N136I) in the Hyp3 enzyme resulted in production of limonene, which results from proton elimination from the α -terpinyl cation rather than carbocation capture by water in the

wild-type (Fig. 5B,C,D, Fig. 7). The serine mutant (N136S) in our enzyme was also unable to activate water for nucleophilic attack. In fact both the serine and alanine mutant (N136A) were unable to catalyze cyclization of the GPP substrate, resulting in production of myrcene (Fig. 5E,F, Fig. 7). These results place the attacking water molecule in the same position within the fungal enzyme as the observed water pocket in the plant version.

In addition, the serine and alanine mutants lost monoterpene specificity and are able to use the FPP substrate for sesquiterpene production. In the case of N136A, the major products are farnesene isomers, which are the sesquiterpene equivalent of the myrcene product. This indicates that, as in the plant cineole synthase, the bulky asparagine side-chain prevents the 15-carbon substrate from fitting into the active site pocket. In the related aristolochene synthase enzymes the residue at this position is a leucine, which is similarly sized to residues that do not support FPP utilization in Hyp3. Clearly other residues that shape the active site pocket are also critical for monoterpene specificity in Hyp3, potentially including aromatic residues that may be positioned near the substrate (F167) or active site pocket (F233 and F237). That we are able to convert Hyp3 from a 1,8-cineole synthase to a limonene, myrcene or farnesene synthase by mutating a single amino acid is yet another example of the plasticity of the active sites in terpene synthase enzymes. Rational conversion of terpene synthases has been achieved previously in a number of studies. Plasticity residues controlling the product profiles of several sesquiterpene synthases were identified through contact mapping and site-directed mutagenesis (13, 15). In the analogous class I active site of diterpene synthases small changes, a single amino acid in some cases, was sufficient to switch the enzyme product specificity (72–74). The ability to convert terpene synthases with a minimal number of mutations to produce different products is thought to be one reason why they seem to diverge so quickly to produce the variety of terpene products seen in nature (15, 75).

Phylogenetic analysis of these terpene synthases suggests that Hyp3 of E7406B is not closely related to the plant or bacterial version of the enzyme, but is more closely related to fungal aristolochene synthases. This would argue against a horizontal gene transfer between the endophytic

fungus and any plant it inhabited, including the *Clarisia racemosa* tree from which it was isolated. Thus, the 1,8-cineole synthase mechanism using an asparagine to activate water in the active site has apparently evolved independently in plants and fungi, an intriguing example of convergent evolution which has been observed for other TPS enzymes and secondary metabolic enzymes in general (76, 77).

ITS-based sequence analysis of the cineole producing isolates reported here, in addition to three previously reported isolates (CI-4, EC-12, and Ni25-2A), placed all of the cineole producers in a clade within the family Xylariaceae, comprising the genera *Daldinia*, *Hypoxydon*, and *Annulohypoxydon*. The phylogenetic relationship between these groups was difficult to resolve based on ITS sequence alone, consistent with previous reports, however they were clearly distinguished from the related genera of *Biscogniauxia*, *Xylaria*, and *Nemania* (49). These results reveal that the capacity to produce 1,8-cineole is common and wide-spread in these genera of fungi. Most of the identified *Daldinia*, *Hypoxydon*, and *Annulohypoxydon* isolates have not been screened for volatile compound production, but it's possible a large fraction of them have cineole production capacity. Considering the close phylogenetic relationship between these cineole producers and the fact that cineole has not been commonly observed in other genera, it seems unlikely that the cineole synthase has arisen completely independently in each of the 11 cineole producing isolates. Rather, it suggests that the gene for cineole synthesis, or a closely related gene that will convert to produce cineole with minimal mutations, evolved in a common ancestor of these isolates. Identification of the 1,8-cineole synthase from additional members of this clade will be required to more thoroughly study its evolution.

There has been interest recently in categorizing terpene synthases in the hope that identifying TPS enzyme phylogenetic relationships will help guide genome mining efforts and predict their terpene product. This has proven difficult in plants, where TPS sequences are dominated by species relationships rather than product, but the addition of a large number of sequenced fungal and bacterial genomes has reignited these efforts (78). Recent work on

terpene synthases from Basidiomycota has attempted to categorize them based on the type of ring-closure catalyzed by the enzymes (34, 35, 79). Most ascomycete terpene synthases in our phylogeny, including those from E7406B, appear distinct from the basidiomycete enzymes as well as plants and bacteria. Efforts to categorize TPS enzymes from Ascomycota in a similar fashion will require the identification of enzymes and products from additional ascomycete genomes.

1,8-cineole is the main component of eucalyptus oil and is a commodity chemical used in non-prescription pharmaceuticals, fragrances, and flavorings and is known to have natural insecticidal and insect repellent properties (80, 81). It has been explored as a potential precursor for synthesis of p-cresol and benzylic esters, which themselves are commodity chemicals used in the production of pharmaceuticals, dyes, fertilizers and agrochemicals (43). Cineole has also been proposed as a biofuel additive in ethanol-gasoline fuel blends (44). On its own, cineole has a heat of combustion of 36 MJ/L, comparable to fossil fuels (32-39 MJ/L) and much higher than ethanol (21 MJ/L). It has an octane rating of 100 and can be used as an additive to raise the octane of gasoline mixtures, giving an octane rating of 95 in a mixture of 8 parts cineole to 1 part gasoline. One hindrance to cineole as a biofuel may come from its high melting point (1.5°C) which would be unsuitable for cold weather use on its own. Other monoterpenes such as limonene (-96.7°C freezing point) have good cold weather properties and could be suitable biofuel additives in mixtures with 1,8-cineole.

For use as a commodity chemical, microbial derived 1,8-cineole would need to be cost-competitive with plant extract sources. Eucalyptus oil production has been estimated at 3000 metric tons annually, so efficient yield from any microbial source would be critical. The cineole yield from a four day-old fungal culture was 0.54 mg/L. By identifying the cineole synthase gene and transferring it to an *E. coli* strain harboring a plasmid for terpene precursor production through the mevalonate pathway, we were able to increase the yield nearly 40-fold to 21 mg/L. The pJBEI-2999 plasmid was optimized for production of the sesquiterpene biofuel target bisabolene and, since it is designed to produce the FPP substrate, it is likely not optimal for production of monoterpenes, such as 1,8-cineole. Thus, only small changes including introduction of a GPP synthase rather than the *ispA* FPP synthase may increase cineole yield substantially. A recent effort to produce limonene in *E. coli* was able to achieve a yield of 400 mg/L indicating that substantial increases in monoterpene yield are possible (23). Furthermore, when terpene pathways are optimized the activity of the terpene cyclase often becomes a bottleneck. Since plant homologues have been used in these efforts to date, screening the tremendous diversity of fungal terpene synthases may reveal enzymes with high activity. Future efforts to correlate the huge variety of fungal terpenes with the genes that produce them may allow production of new terpene derived drugs, commodity chemicals or biofuels.

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FOOTNOTES

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⁴The abbreviations used are: VOC, volatile organic compound; TPS, terpene synthase; GPP, geranyl pyrophosphate; FPP, farnesyl pyrophosphate; GGPP, geranylgeranyl pyrophosphate; PDA, potato dextrose agar; SPME, solid phase microextraction; ITS, internal transcribed spacer; SfCin, *Salvia fruticosa* cineole synthase; SolCin, *Solanum lycopersicum* cineole synthase; NicCin, *Nicotiana suaveolens* cineole synthase

FIGURE LEGENDS

Figure 1. Phylogenetics of cineole producing fungi in the family Xylariaceae. Phylogram of cineole producing fungal isolates (Bold) in the context of members of the family Xylariaceae, genera *Nemania*, *Xylaria*, *Biscogniauxia*, *Hypoxylon*, *Annulohypoxylon* and *Daldinia*. ITS sequences were analyzed by both Bayesian and Maximum Likelihood methods. Nodes are labeled with Bayesian posterior probabilities (top) and maximum likelihood bootstrap values (bottom).

Figure 2. Phylogenetic tree of plant, fungal and bacterial terpene synthases. Gene products of the ascomycete terpene synthases are labeled along with Hyp 1-11 from E7406B. Known 1,8-cineole synthases from bacteria and angiosperm species are also labeled.

Figure 3. Steady-state kinetic analysis of the fungal 1,8-cineol synthase. Comparison of the Hyp3 catalyzed reactions with GPP (dashed line) and FPP (solid line) substrates.

Figure 4. Structural model of Hyp3 based on the *Aspergillus terreus* aristolochene synthase crystal structure. A) Structural model of Hyp3 featuring the DDxxD/E motif (red) N/DxxSxxxE motif (orange) as well as N136 and F267 (cyan with side-chain). B) Aligned model of Hyp3 (blue) with substrate bound aristolochene synthase (yellow). The FPP substrate of the aristolochene synthase is shown colored by element.

Figure 5. Mutational analysis of Hyp3 N136. A) Alignment of Hyp3 sequence near the conserved DDxx(D/E) motif (red box) with plant cineole synthases from *Solanum lycopersicum* (SolCin), *Nicotiana suaveolens* (NicCin), and *Salvia fruticosa* (SfCin). The asparagine (N) critical for plant synthase function is highlighted in red near the catalytic motif. Total ion chromatogram of terpene products of (B) Hyp3 and mutant enzymes (C) N136V, (D) N136I, (E) N136S, and (F) N136A in *E. coli* with pJBEI-2999. The x axis is split to show both monoterpene and sesquiterpene regions of the spectrum. Indicated compounds are 1,8-cineole (1), myrcene (2), limonene (3) and farnesene isomers (4).

Figure 6. Quantification of 1,8-cineole products in producing microbes. Cineole was quantified by comparison to a standard curve of authentic cineole standard and normalized to an internal camphor standard. Error bars represent the standard deviation of three independent culture growths. Compound was only observed in one replicate of *E. coli* DH5 α with the *hyp3* gene.

Figure 7. Schematic of 1,8-cineole product formation by Hyp3 and mutants. Derived from the proposed mechanism of the *Salvia fruticosa* cineole synthase (16). Reaction pathways catalyzed by the wild type, N136I/V, or N136S/A enzymes are indicated.

TABLES

TABLE 1. Summary of organisms used in the *Xylariaceae* phylogenetic tree

Taxon	Strain ID	ITS Accession No.	NCBI Taxon ID
<i>Annulohypoxylon atroroseum</i>	SUT009	DQ223733.1	42309
<i>A. annulatum</i>	H3M	AJ390395	327058
<i>A. cohaerens</i>	F-160,842	AY909025	326618
<i>A. minutellum</i>	H9A	AJ390399	326621
<i>A. multiforme</i>	F160,843	AY909003	326624
<i>A. nitens</i>	ST2313	DQ223751.1	326626
<i>A. stygium</i>	ntu44	FJ205451.1	326628
<i>A. stygium</i>	105F	FJ008986.1	326628
<i>A. stygium</i>	SUT243	DQ223761.1	326628
<i>Biscogniauxia atropunctata</i>	B5A	AJ390411	109358
<i>B. atropunctata</i>	ATCC38987	AF201705	109358
<i>B. bartholomaei</i>	ATCC38992	AF201719	109359
<i>B. marginata</i>	B74A	AJ390417	110534
<i>B. mediterranea</i>	B71C	AJ390413	97377
<i>B. nummularia</i>	B72C	AJ390415	97378
<i>B. repanda</i>	B75A	AJ390418	110535
<i>Daldinia cf. fissa</i>	P.D. Rabenborg (C)	AF176981	103427
<i>D. loculata</i>	HJ 107	AF176969	103429
<i>D. petriniae</i>	HJ103	AF176975	103430
<i>Hypoxylon begae</i>	215 JDR	JN660820.1	326653
<i>H. cinnabarinum</i>	H7R	AJ390398	110541
<i>H. fragiforme</i>	SGLAf55	EU715619.1	63214
<i>H. fragiforme</i>	H12C	AJ390401.1	327061
<i>H. fragiforme</i>	ATCC36662	AF201709	63214
<i>H. fragiforme</i>	H12C	AJ390401	327061
<i>H. fuscum</i>	CBS 113048	AY616699.1	109372
<i>H. fuscum</i>	H16A	AJ390405	109372
<i>H. haematostroma</i>	SUT292	DQ223739.1	152305
<i>H. intermedium</i>	H4A	AJ390396	110540
<i>H. investiens</i>	CBS 118185	FJ185308.1	326663
<i>H. monticulosum</i>	SUT116	DQ223749.1	326669
<i>H. monticulosum</i>	H076	FM209439.1	326669
<i>H. ochraceum</i>	H17R	AJ390406	110544
<i>H. papillatum</i>	ATCC58729	AF201710	58729
<i>H. perforatum</i>	H18R	AJ390407.1	110542
<i>H. perforatum</i>	H18R	AJ390407	110542
<i>H. rickii</i>	H19R	AJ390408	110545
<i>H. rubiginosum</i>	SUT221	DQ223759.1	110542
<i>Nemania aenea var. aureolutea</i>	ATCC 60819	AF201704	109375
<i>N. bipapillata</i>	CL8	AY541610	110536
<i>N. chestersii</i>	N23A	AJ390430	110537
<i>N. serpens</i>	N20A	AJ390431	109381
<i>N. serpens</i>	N112C	AJ390436	109381
<i>Xylaria allantoidea</i>	F-165,173	AY909005	323539
<i>X. arbuscula</i>	WARM	AY183369	114810
<i>X. digitata</i>	CBS 161.22	AY909006	323540
<i>X. globosa</i>	PR7	AY909007	323541
<i>X. hypoxylon</i>	CBS 868.72	AY909011	37992
<i>X. liquidambaris</i>	ATCC 42766	AY909021	323546
<i>X. longipes</i>	CBS 148.73	AY909013	114818
<i>X. multiplex</i>	PR111	AY909019	323545
EC12	EC12	JQ424940	1001832
CI-4	CI-4	GU797135	755336
Ni25-2A	Ni25-2A	JQ968613	1210998
B10820A	YU.101024	KJ412996	1488202
E6826D	YU.101016	KJ412992	1488199
E13415F	YU.101019	KJ412990	1488201
E13732D	YU.101018	KJ412994	1488200
E7015B	YU.101017	KJ412993	1488204
E13615I	YU.101020	KJ412997	1488205
E7406B	YU.101015	KJ412991	1488203
E14012A	YU.101021	KJ412995	1488206

TABLE 2. Summary of TPS enzymes used in the phylogenetic tree

TPS gene	Accession No.	Organism
(-)-4S-limonene synthase	AAB70907.1	<i>Abies grandis</i>
pinene synthase	AAB71085.1	<i>Abies grandis</i>
beta-phellandrene synthase	AAF61453.1	<i>Abies grandis</i>
d-selinene synthase	AAC05727.1	<i>Abies grandis</i>
gamma-humulene synthase	AAC05728.1	<i>Abies grandis</i>
taxadiene synthase	AAC49310.1	<i>Taxus brevifolia</i>
(-)-limonene synthase	AAS47694.1	<i>Picea abies</i>
(-)-alpha/beta-pinene synthase	AAS47692.1	<i>Picea abies</i>
myrcene synthase	AAS47696.1	<i>Picea abies</i>
E,E-alpha-farnesene synthase	AAS47697.1	<i>Picea abies</i>
longifolene synthase	AAS47695.1	<i>Picea abies</i>
E-alpha-bisabolene synthase	AAS47689.1	<i>Picea abies</i>
AtTPS-CIN2	P0DI77.1	<i>Arabidopsis thaliana</i>
cineole synthase	ABH07677.1	<i>Salvia fruticosa</i>
TPS8 cineole synthase	G1JUH5	<i>Solanum lycopersicum</i>
D-cadinene synthase A	Q43714.1	<i>Gossypium arboreum</i>
D-cadinene synthase	P93665.1	<i>Gossypium hirsutum</i>
5-epi-aristolochene synthase	Q40577.3	<i>Nicotiana tabacum</i>
(+)-bornyl diphosphate synthase	AAC26017.1	<i>Salvia officinalis</i>
(+)-sabinene synthase	AAC26018.1	<i>Salvia officinalis</i>
limonene synthase	AAD50304.1	<i>Mentha longifolia</i>
germacrene C synthase	AAC39432.1	<i>Solanum lycopersicum</i>
(E)-B-farnesene synthase	AAB95209.1	<i>Mentha x piperita</i>
2-methylisoborneol synthase	YP_001105919.1	<i>Saccharopolyspora erythraea</i> NRRL 2338
germacradienol synthase	NP_823339.1	<i>Streptomyces avermitilis</i> MA-4680
epi-isozizaene synthase	NP_824208.1	<i>Streptomyces avermitilis</i> MA-4680
pentalenene synthase	NP_824174.1	<i>Streptomyces avermitilis</i> MA-4680
cineole synthase	ZP_05003209.1	<i>Streptomyces clavuligerus</i> ATCC 27064
cadinene synthase	ZP_05004823.1	<i>Streptomyces clavuligerus</i> ATCC 27064
muurolene synthase	ZP_05006242.1	<i>Streptomyces clavuligerus</i> ATCC 27064
linalool synthase	ZP_06776363.1	<i>Streptomyces clavuligerus</i> ATCC 27064
germacrendiol synthase	NP_630182.1	<i>Streptomyces coelicolor</i> A3(2)
2-methylisoborneol synthase	NP_733742.1	<i>Streptomyces coelicolor</i> A3(2)
selinene synthase	YP_001867159.1	<i>Nostoc punctiforme</i> PCC 73102
Pentalenene synthase	Q55012.4	<i>Streptomyces exfoliatus</i>
aristolochene synthase	AAA33694	<i>Penicillium roqueforti</i>
Tri5 Trichodiene synthase	P27679	<i>Fusarium sambucinum</i>
Tri5 Trichodiene synthase	AAN05035	<i>Fusarium sporotrichioides</i>
longiborneol synthase	ACY69978	<i>Gibberella zeae</i>
aristolochene synthase	AAF13264.1	<i>Aspergillus terreus</i>
BOT2 Presilphiperfolan-8-beta-ol synthase	Q6WP50.1	<i>Botryotinia fuckeliana</i>
fusicoccadiene synthase	EEQ31327.1	<i>Arthroderma otae</i> CBS 113480
Omp1 alpha-muurolene synthase	Wawrzyn GT et al., 2012	<i>Omphalotus olearius</i>
Omp2 terpene synthase	Wawrzyn GT et al., 2012	<i>Omphalotus olearius</i>
Omp3 Germacrene A synthase	Wawrzyn GT et al., 2012	<i>Omphalotus olearius</i>
Omp4 delta-cadinene synthase	Wawrzyn GT et al., 2012	<i>Omphalotus olearius</i>
Omp5a gamma-cadinene synthase	Wawrzyn GT et al., 2012	<i>Omphalotus olearius</i>
Omp5b gamma-cadinene synthase	Wawrzyn GT et al., 2012	<i>Omphalotus olearius</i>
Omp6 delta-6 protoilludene synthase	Wawrzyn GT et al., 2012	<i>Omphalotus olearius</i>
Omp7 delta-6 protoilludene synthase	Wawrzyn GT et al., 2012	<i>Omphalotus olearius</i>
Omp8 terpene synthase	Wawrzyn GT et al., 2012	<i>Omphalotus olearius</i>
Omp9 alpha-barbatene synthase	Wawrzyn GT et al., 2012	<i>Omphalotus olearius</i>
Omp10 trans-dauca-4(11),8-diene synthase	Wawrzyn GT et al., 2012	<i>Omphalotus olearius</i>
Cop1 Germacrene A synthase	XP_001832573.2	<i>Coprinopsis cinerea</i> okayama7 (#130)
Cop2 Germacrene A synthase	XP_001836556.1	<i>Coprinopsis cinerea</i> okayama7 (#130)
Cop3 alpha-muurolene synthase	XP_001832925.1	<i>Coprinopsis cinerea</i> okayama7 (#130)
Cop4 delta-cadinene synthase	XP_001836356.1	<i>Coprinopsis cinerea</i> okayama7 (#130)
Cop5 terpene synthase	XP_001834007.1	<i>Coprinopsis cinerea</i> okayama7 (#130)
Cop6 alpha-cuprenene	XP_001832549.1	<i>Coprinopsis cinerea</i> okayama7 (#130)
Hyp1	KJ433269	<i>Hypoxylon</i> sp.
Hyp2	KJ433270	<i>Hypoxylon</i> sp.
Hyp3	KJ433271	<i>Hypoxylon</i> sp.
Hyp4	KJ433272	<i>Hypoxylon</i> sp.
Hyp5	KJ433273	<i>Hypoxylon</i> sp.
Hyp6	KJ433274	<i>Hypoxylon</i> sp.
Hyp7	KJ433275	<i>Hypoxylon</i> sp.
Hyp8	KJ433276	<i>Hypoxylon</i> sp.
Hyp9	KJ433277	<i>Hypoxylon</i> sp.
Hyp10	KJ433278	<i>Hypoxylon</i> sp.
Hyp11	KJ433279	<i>Hypoxylon</i> sp.

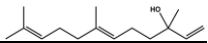
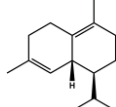
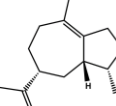
Table 3. Major volatiles produced by fungal isolates

Formula	Compound ID	C14	E7406B	E6826D	E7015B	E13732D	E13415F	E13615I	E14012A	B10820A
Alcohols etc.										
C ₄ H ₁₀ O	2-methyl propanol	X				X	X	X	X	X
C ₅ H ₁₂ O	3-methyl butanol *	X	X	X	X	X	X	X	X	X
C ₅ H ₁₂ O	2-methyl butanol *	X	X	X	X	X	X	X	X	X
C ₇ H ₁₄ O ₂	2-methylbutyl acetate		X	X		X	X			X
Monoterpenoids										
C ₁₀ H ₁₆	α-pinene *					X	X	X	X	X
C ₁₀ H ₁₆	α-phellandrene *					X	X	X		X
C ₁₀ H ₁₆	α-terpinene *			X		X	X	X		X
C ₁₀ H ₁₆	Limonene *	X	X	X		X	X	X	X	X
C ₁₀ H ₁₄	p-cymene *	X		X		X	X	X	X	X
C ₁₀ H ₁₆	phellandrene	X	X	X		X	X	X	X	X
C ₁₀ H ₁₈ O	1,8-cineole *	X	X	X	X	X	X	X	X	X
C ₁₀ H ₁₆	γ-Terpinene *			X		X	X	X		X
C ₁₀ H ₁₆	Terpinolene *	X		X		X	X	X		X
Sesquiterpenoids										
C ₁₅ H ₂₄	Unidentified Sesquiterpenes	x9	x24	x32	x12	x9	x16	x10	x14	x18
Polyenes										
C ₅ H ₈	Pentadiene					X		X		
C ₇ H ₁₀	Heptatriene	X	X	X	X	X	X			
C ₇ H ₁₀	unknown	X	X	X	X		X			
C ₉ H ₁₂	Nonatetraene #*	X	X	X	X	X	X		X	
C ₉ H ₁₂	Nonatetraene Isomer	X	X		X	X	X		X	
C ₉ H ₁₂	Nonatetraene Isomer	X	X		X	X	X		X	
C ₉ H ₁₂	Nonatetraene Isomer	X	X		X	X	X		X	
C ₉ H ₁₂	Nonatetraene Isomer	X	X		X		X			

Verified by NMR

* Verified by authentic GC/MS standard

Table 4. Terpene products of Hyp1-8 in *E. coli* DH5 α with pJBEI-2999

Gene #	Monoterpene	RI	% Peak area	Sesquiterpene	RI	% Peak area	Structure *
Hyp1	none			trans-nerolidol # *		>95	
Hyp2	none			δ -cadinene #*	1521	59	
				Unknown	1661	10	
				21 other peaks			
Hyp3	1,8-cineole #*	1035	90	None			
	D-limonene #	1028	5	None			
Hyp4	D-limonene #	1028	<1	Unknown	1489	78	
	α -terpinene #	1015	<1	Unknown	1483	12	
				12 other peaks			
Hyp5	(E)- β -ocimene #	1047	< 1	Unknown	1663	64	
	sabinene #	989	< 1	α -bulnesene*	1506	27	
				β -guaiene	1494	5	
	unidentified	1037	< 1	6 other peaks			
Hyp6				none observed			
Hyp7				none observed			
Hyp8				none observed			
* Structure of the corresponding product				RI = Retention Index			
# Verified by standard							

FIGURES

Figure 1

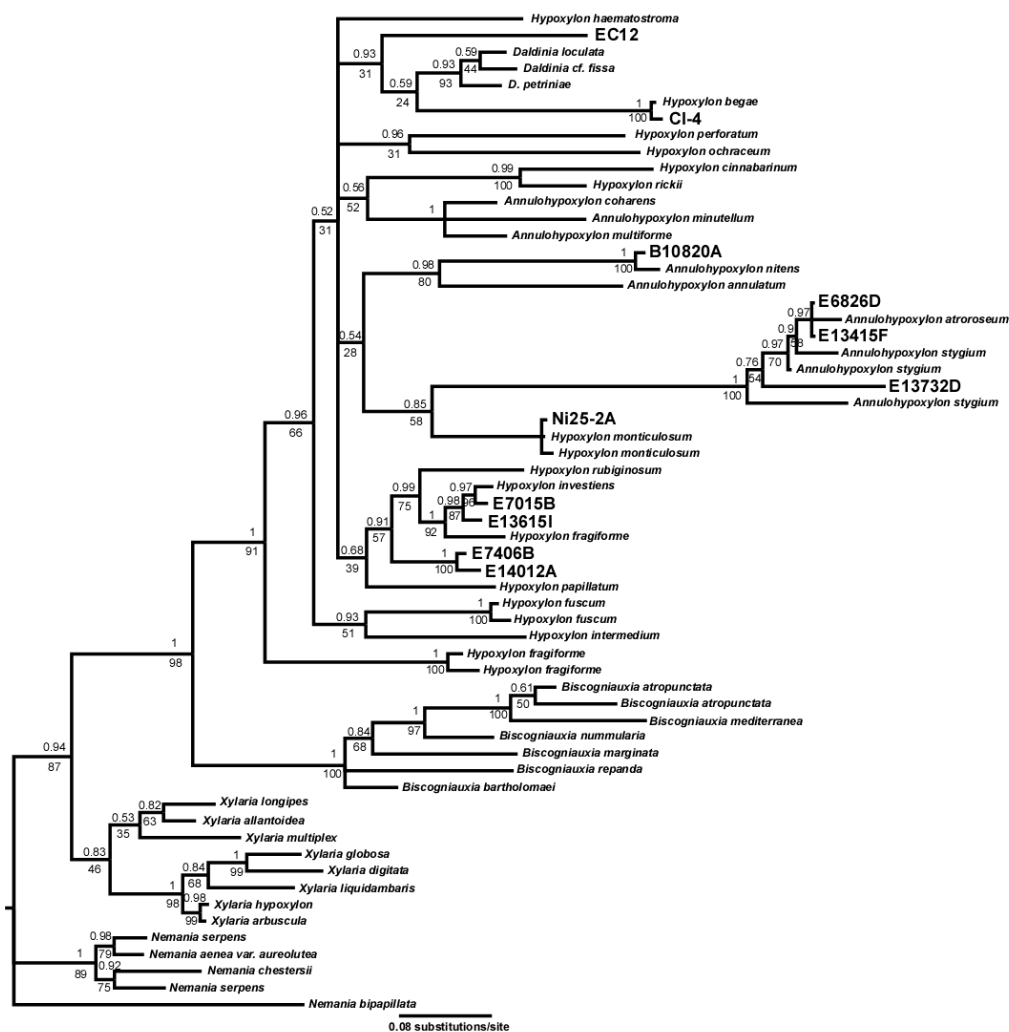


Figure 2

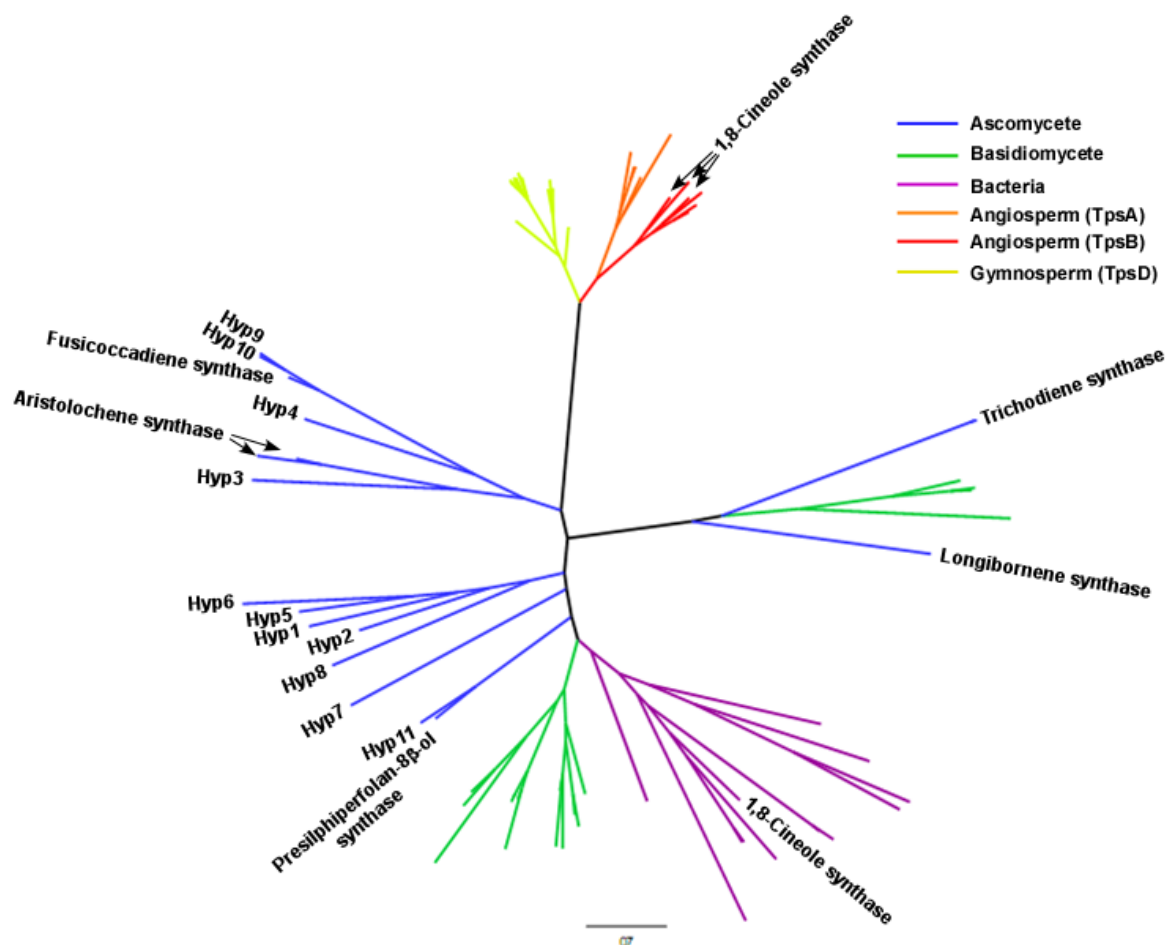


Figure 3

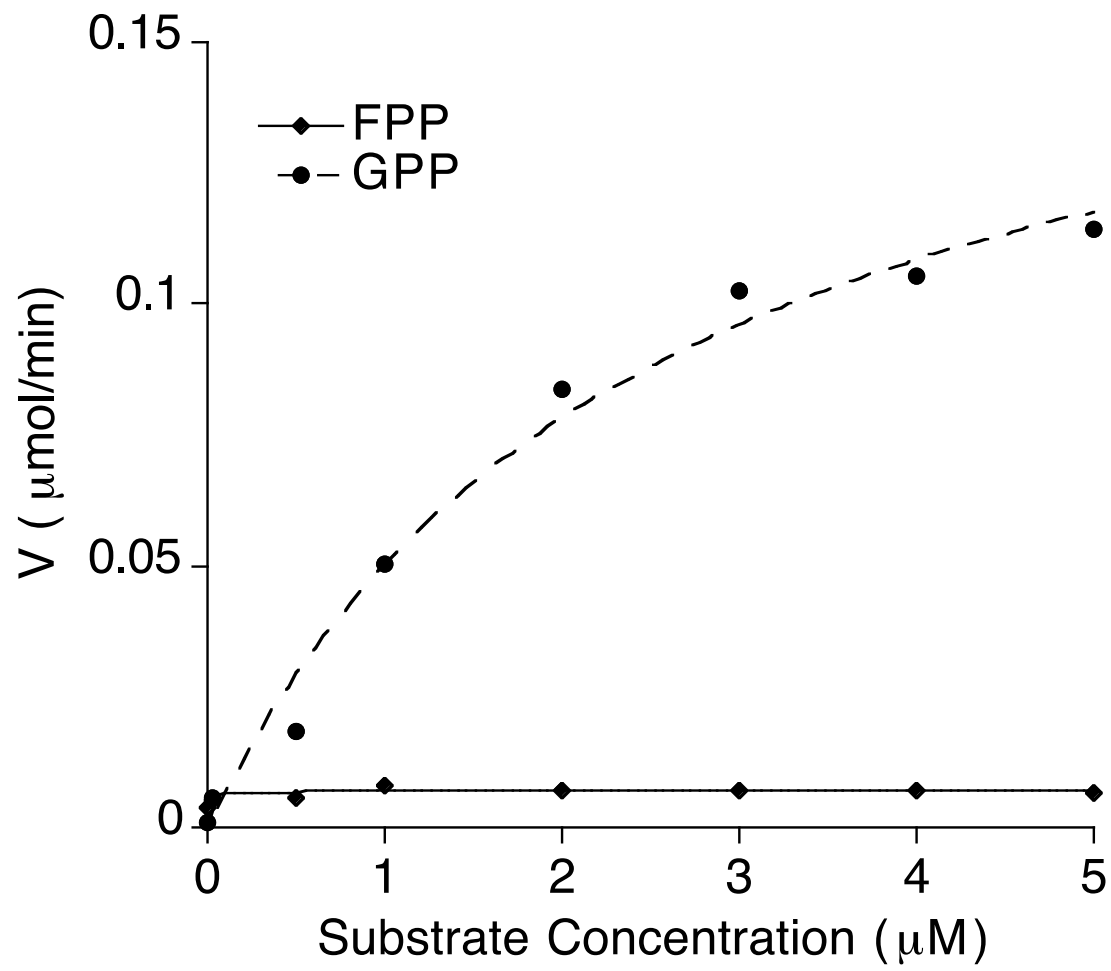


Figure 4

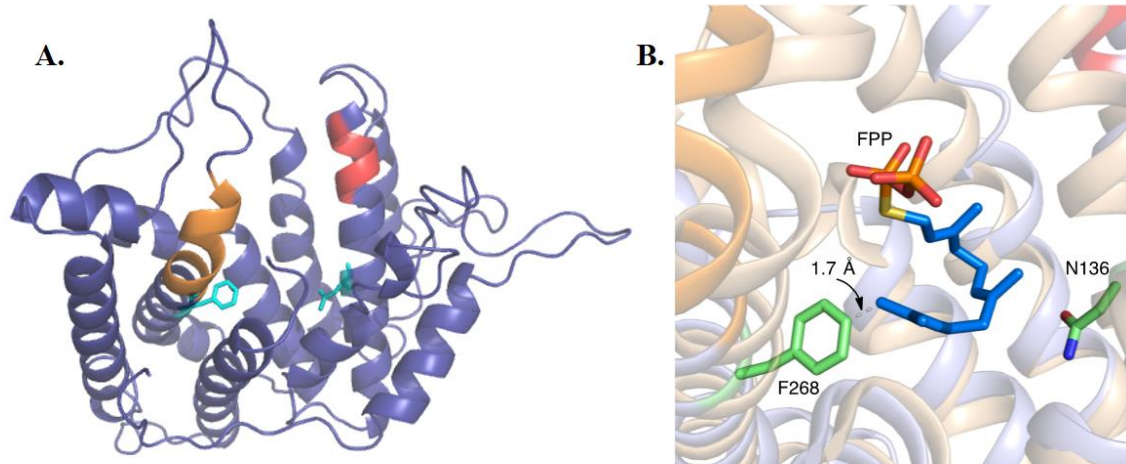


Figure 5

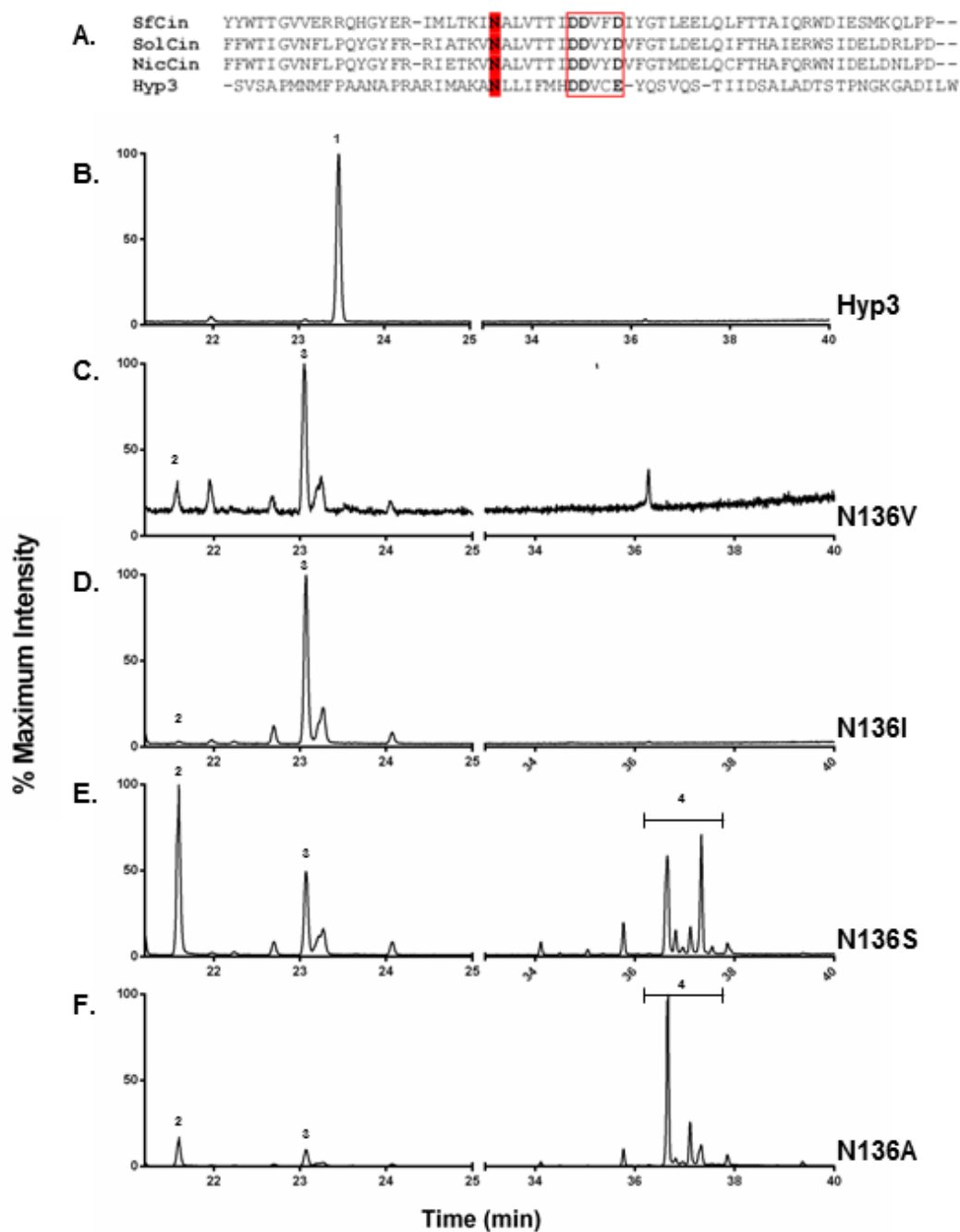


Figure 6

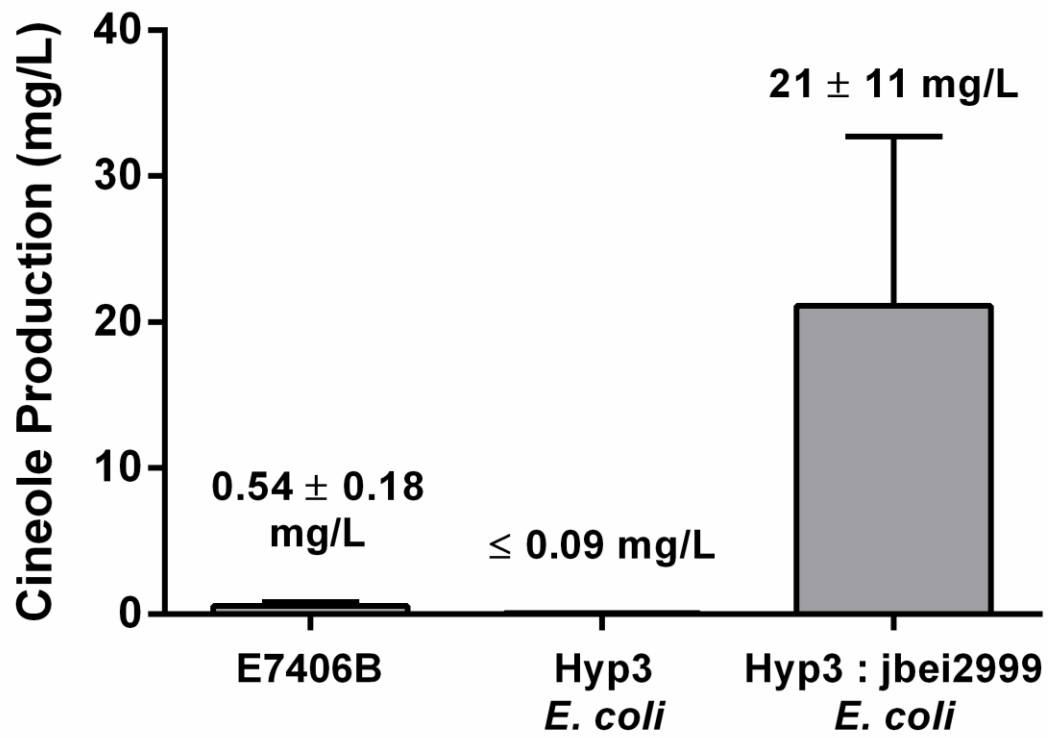
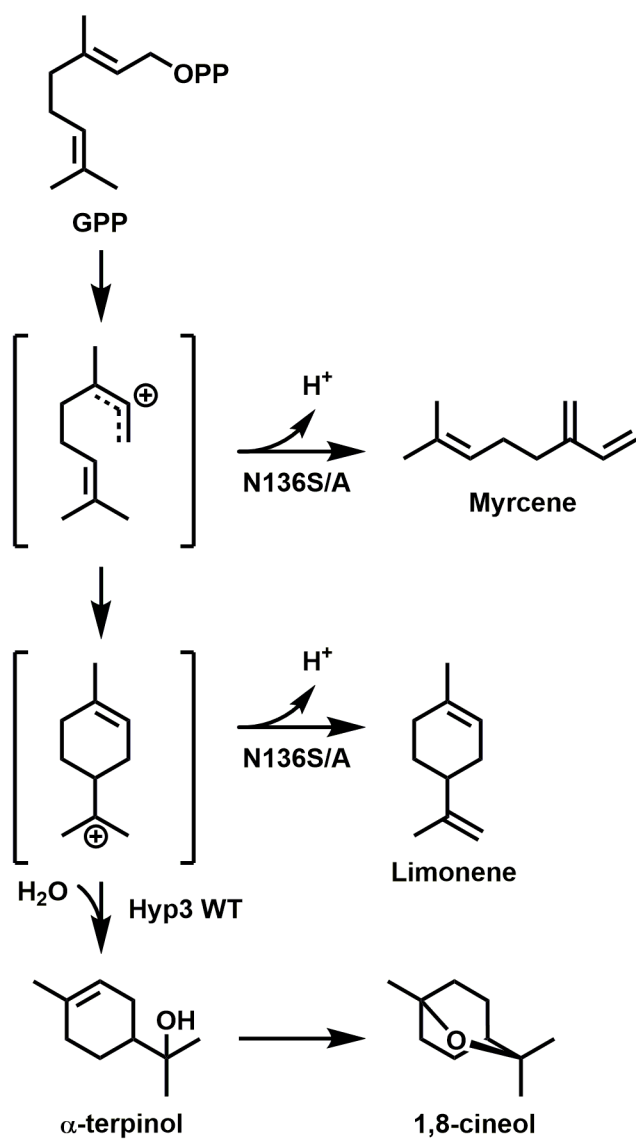


Figure 7



Microbiology:

**Identification of a Fungal 1,8-cineole
Synthase from *Hypoxylon* sp. with
Common Specificity Determinants to the
Plant Synthases**

Jeffrey J. Shaw, Tetyana Berbasova, Tomoaki
Sasaki, Kyra Jefferson-George, Daniel J.
Spakowicz, Brian F. Dunican, Carolina E.
Portero, Alexandra Narvaez-Trujillo and Scott
A. Strobel
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