

**Supplementary Information:**

**Evolution of isoprenyl diphosphate synthase-like terpene synthases in fungi**

Guo Wei, Franziska Eberl, Xinlu Chen, Chi Zhang, Sybille B. Unsicker, Tobias G. Köllner,  
Jonathan Gershenzon and Feng Chen

**Table S1.** GGDPSs identified in 6 species the class of Pucciniomycetes

Species	Gene ID	Gene name
<i>Cronartium quercuum</i>	fgenesh1_pm.202_#_11	CqGGDPS1
<i>Puccinia coronata</i>	PCA_SD_04467-T1	PcGGDPS1
	PCA_SD_09689-T1	PcGGDPS2
<i>Puccinia graminis</i>	PGTG_12321T0	PgGGDPS1
	PGTG_19831T0	PgGGDPS2
<i>Puccinia striiformis</i>	maker-PST130_10993-snap-gene-0.3-mRNA-1	PsGGDPS1
<i>Puccinia triticina</i>	PTTG_02381T0	PtGGDPS1
	PTTG_02381T1	PtGGDPS2
<i>Septobasidium PNB30-8B</i>	estExt_fgenesh1_pm.C_60078	SsGGDPS1
	estExt_fgenesh1_pg.C_50169	SsGGDPS2

**Table S2.** Kovats retention index of (*E*)- $\beta$ -ocimene and (*E,E*)- $\alpha$ -farnesene.

Identified terpenes	Retention indices <sup>1</sup>	Reference retention indices <sup>2</sup>
( <i>E</i> )- $\beta$ -ocimene	1050.3	1050
( <i>E,E</i> )- $\alpha$ -farnesene	1504.9	1505

<sup>1</sup>Retention indices relative to C<sub>7</sub>-C<sub>40</sub> saturated alkanes in this study.

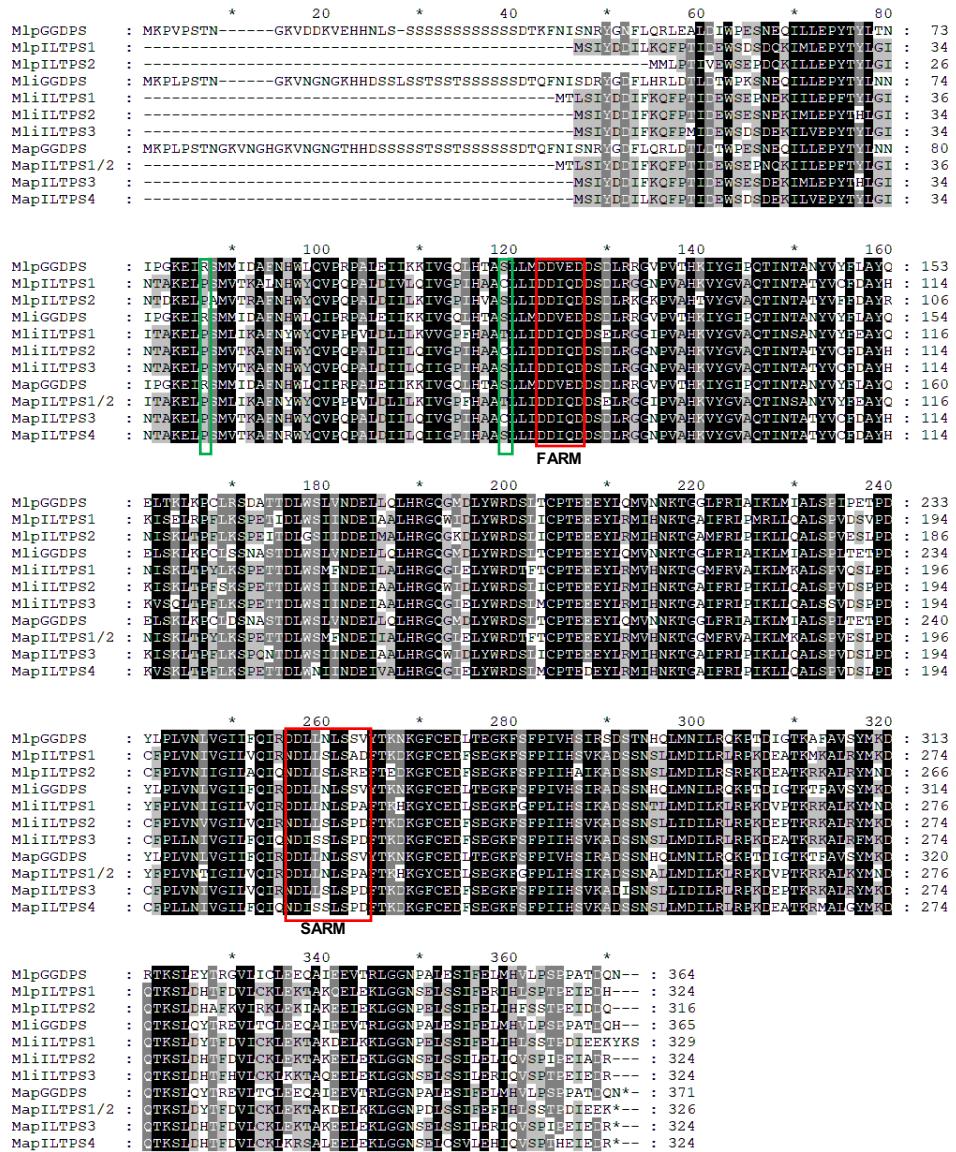
<sup>2</sup>Reference retention indices were obtained by Sparkman.

Sparkman, O. D. Identification of essential oil components by gas chromatography/mass spectroscopy Robert P. Adams. *J Am Soc Mass Spectr* **8**, 671-672, doi:10.1021/jasms.8b01049 (1997).

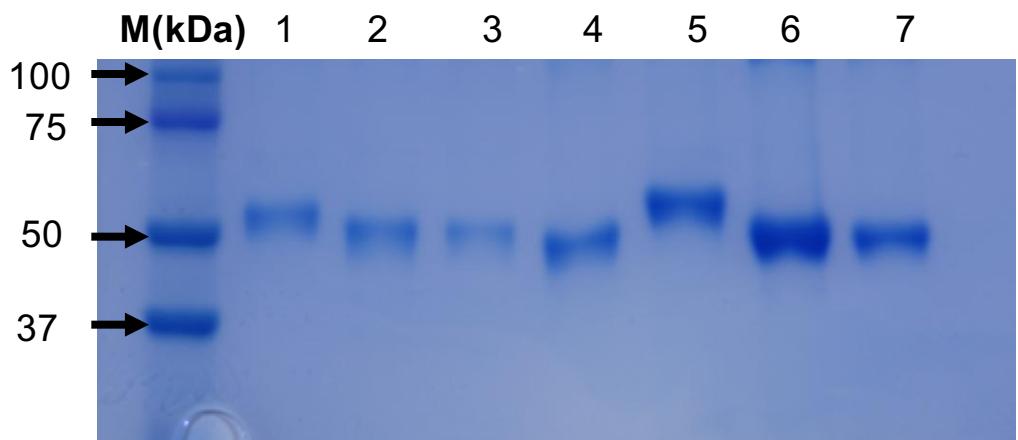
**Table S3.** Primers used in this study.

Primer name	Sequence (5' to 3')
<b>For gene cloning and expression (pET-32a vector)</b>	
MliGP for	<u>GGATCCATGAAACCTTACCTCAACAAATGG</u>
MliGP rev	<u>AAGCTTCATGTTGATCTGTTGCAGGTGG</u>
MliILTPS1 for	<u>GAATTCATGACTCTCAGTATCTATGACGACA</u>
MliILTPS1 rev	<u>CTCGAGCTAGCTTGATTCTTCTTCAATA</u>
MliILTPS2 for	<u>GAATTCATGAGTATCTATGATGACATCTCAA</u>
MliILTPS2 rev	<u>CTCGAGCTATCGGTCTGCGATCTCAGGAATT</u>
MliILTPS3 for	<u>GGATCCATGAGTATCTATGATGACATTTC</u>
MliILTPS3 rev	<u>AAGCTTCTATCGGTCTTCAATCTCAGGAGTT</u>
MlpGP for	<u>GGATCCATGAAACCTGTACCTCAACAAATGG</u>
MlpGP rev	<u>AAGCTTCATTTGATCTGTTGCAGGTGG</u>
MlpILTPS1 for	<u>GGATCCATGAGTATCTATGATGACATTTC</u>
MlpILTPS1 rev	<u>AAGCTTCTAATGGTCTTCAATCTCAGGAG</u>
MlpILTPS2 for	<u>GGATCCATGATGCTCCCTACTATTGTTG</u>
MlpILTPS2 rev	<u>AAGCTTCTATTGGTCATCAATTTCAGG</u>
<b>For RT-qPCR</b>	
qMlpGP for	CAACAACAAAACCGGGGGAC
qMlpGP rev	TCAGGGGTCTCAGGTATCGG
qMlpILTPS1 for	ACCATAAACACAGCCACTTACG
qMlpILTPS1 rev	GTGCCGCAATCTCATCGTTG
qMlpILTPS2 for	ACAAACACCTCCCTACTATTGTTG
qMlpILTPS2 rev	ATGATTGAAAGCCCTGGTGAC
<b>For site-directed mutagenesis</b>	
R81P for	CCCTGGGAAAGAAATCCCCTCGATGATGATCGATG
R81P rev	CATCGATCATCATCGAGGGGATTCTTCCAGGG
250254 for	CATCTTCAAATCAGAAACGATCTCTGAGCCTTCTGTTACAC
250254 rev	GTGTAAACAGAGGAAAGGCTCAAGAGATCGTTCTGATTGAAAGATG
S73C for	GGACCAATACATGCTGCCTGTCTTACTCGACGACATC
S73C rev	GATGTCGTCGAGTAATAGACAGGCAGCAGTATTGGTCC

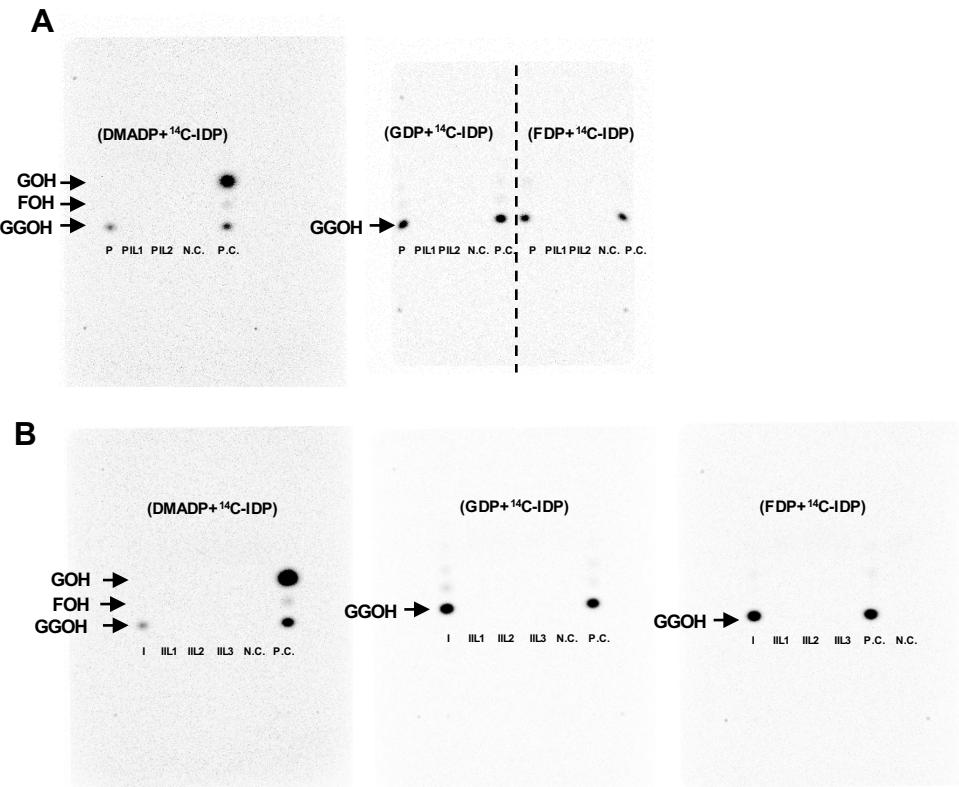
“for” and “rev” stand for forward primer and reverse primer, respectively.



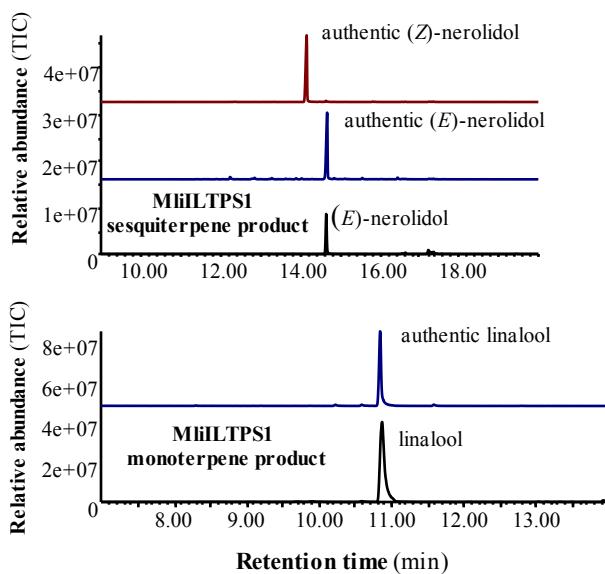
**Fig. S1.** Multiple sequence alignment of *Melampsora* GGDPS proteins. Each GGDPSs sequences from *Melampsora larici-populina*, *Melampsora lini*, and *Melampsora allii-populina* were selected. The first highly conserved domains ‘DD<sub>XX</sub>D’(FARM), and second less conserved motif“NSE/DTE” (SARM) were indicated in red boxes. Green boxes mark sequences were selected for site directed mutagenesis. Mlp, *Melampsora larici-populina*; Mli: *Melampsora lini*; Map, *Melampsora allii-populina*.



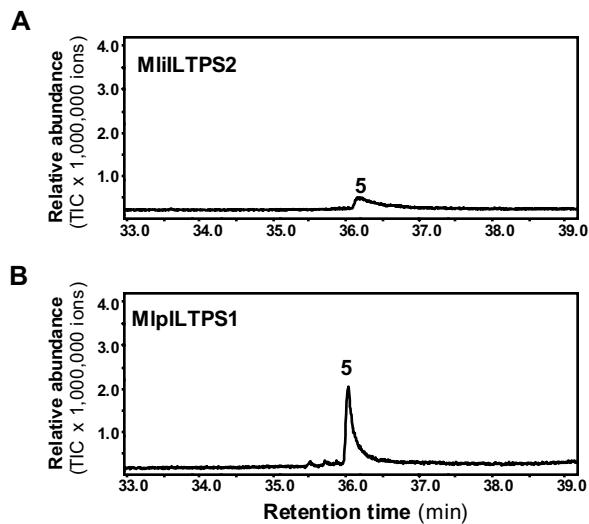
**Fig. S2.** SDS-PAGE analysis of purified His-tagged proteins. 1: MliGGPPS; 2: MliILTPS1; 3: MliILTPS2; 4: MliILTPS3; 5: MlpGGPPS; 6: MlpILTPS1; 7: MlpILTPS2.



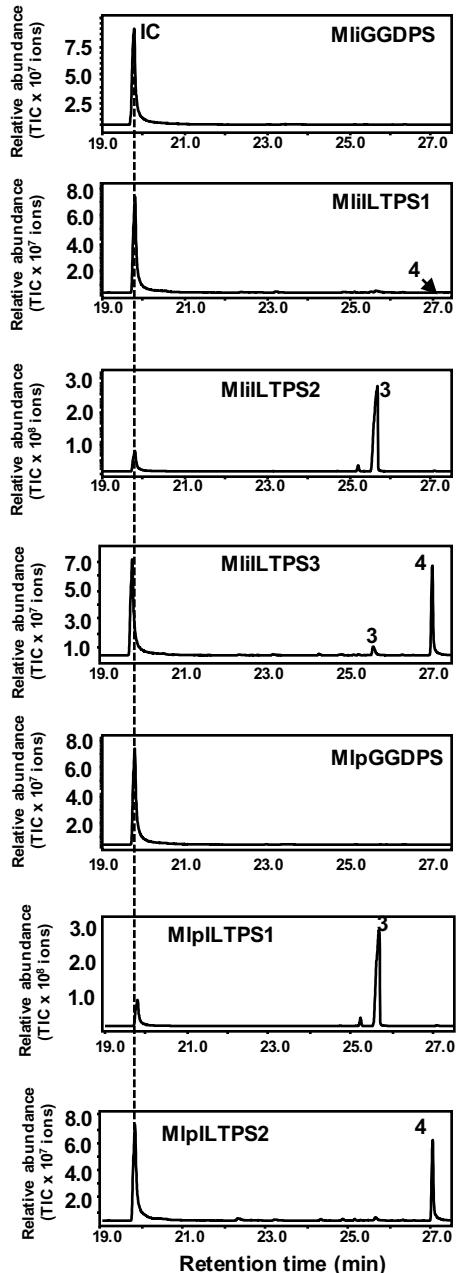
**Fig. S3.** The original full-length blots presented in Figure 2. All descriptions are the same as in Figure 2. *In vitro* IDS enzymatic assays of the GGDPSs and ILTPSs. (A) Assays of MlpGGDPS (P), MlpILTPS1 (PIL1), MlpILTPS2 (PIL2) from *Melampsora larici-populina* using DMADP, GDP, and FDP together with [ $1-^{14}\text{C}$ ]-IDP as substrates. (B) Assays of MliGGDPS (I), MliILTPS1 (III1), MliILTPS2 (III2) and MliILTPS3 (III3) from *Melampsora lini* using DMADP, GDP, and FDP together with [ $1-^{14}\text{C}$ ]-IDP as substrates.



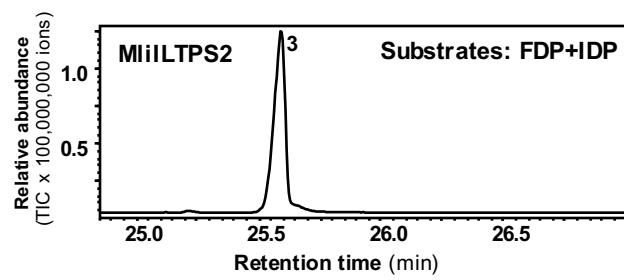
**Fig S4. Identification of monoterpene and sesquiterpene products of MliILTPS1.** Enzyme products were extracted from the assays with hexane and analyzed using GC-MS. Authentic standards diluted in hexane were used for identification.



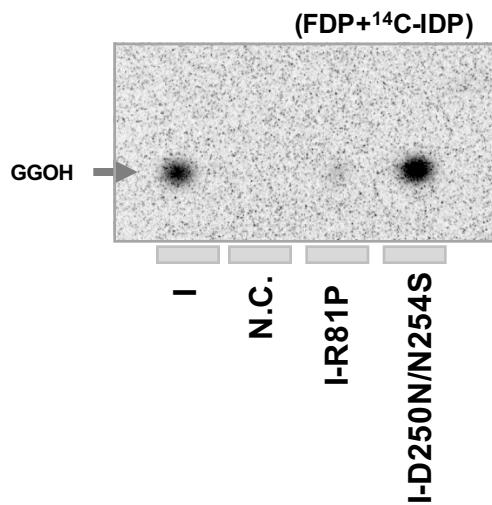
**Fig. S5.** GC chromatograms of the diterpene products of MliILTPS2 (A) and MlpILTPS1 (B). Recombinant proteins were incubated with GGDP as substrate and reaction products were extracted with hexane and analyzed using GC-MS. The total ion chromatograms (TICs) are shown. 5, (*E,E,E*)- $\alpha$ -springene.



**Fig. S6.** Sesquiterpene volatile profiles of *E. coli* BL21-DE3-Star expressing different recombinant enzymes. Volatiles were collected from the headspace of the induced bacterial cultures using SPME and analyzed using GC-MS. 3. (*E,E*)- $\alpha$ -farnesene; 4, (*E*)-nerolidol. “IC” stands for an internal compound indole.



**Fig. S7.** GC chromatogram of sesquiterpene product of MiILTPS2 using FDP in the presence of IDP. Reaction products were captured and analyzed using GC-MS. The total ion chromatograms (TICs) are shown. 3, (*E,E*)- $\alpha$ -farnesene.



**Fig. S8.** *In vitro* IDS enzymatic assays of the MliGGDPS and two mutants. Assays of MliGGDPS (I), boiled MliGGDPS (N.C.), MliGGDPS R81P (I-R81P) and MliGGDPS D250N/N254S (I-D250N/N254S) from *Melampsora lini* using FDP together with [ $1-^{14}\text{C}$ ]-IDP as substrates. The reaction products were separated via thin-layer chromatography (TLC). GGOH, geranylgeraniol.