

Supplementary Information

Microbial-type terpene synthase genes occur widely in nonseed land plants, but not in seed plants

Qidong Jia, Guanglin Li, Tobias G. Köllner, Jianyu Fu, Xinlu Chen, Wangdan Xiong, Barbara Crandall-Stotler, John L. Bowman, David J. Weston, Yong Zhang, Li Chen, Yinlong Xie, Fay-Wei Li, Carl J Rothfels, Anders Larsson, Sean W. Graham, Dennis W. Stevenson, Gane Ka-Shu Wong, Jonathan Gershenzon, and Feng Chen

Materials and Methods

Identification of terpene synthases of the microbial type from transcriptomes and sequenced genomes

The One Thousand Plants Project (OneKP; <https://sites.google.com/a/ualberta.ca/onekp/>) has sequenced transcriptomes for over 1000 non-model plant species spanning almost all major plant clades (from green algae to flowering plants) (1). All transcriptomes were pre-assembled with the SOAPdenovo-Trans (2) assembler. Transcriptomes of 1103 representative species (Table S1) were analyzed in this study. For all the assembled contigs, the longest regions without stop codons were annotated and translated using the getorf program from the EMBOSS package (3) with a minimum length of 150 amino acids. The resulting peptides were searched against the Pfam-A database locally using HMMER 3.0 hmmsearch (4) with an E-value of $1e^{-5}$. Only sequences with best hits from the following four HMM profiles were considered as putative terpene synthases:

Terpene_synth_C (PF03936) and Terpene synthase N-terminal domain (PF01397), TRI5 (PF06330) and SmMTPSLs (a profile created by using 48 microbial type TPSs identified from *S. moellendorffii*). For sequences from the same species that had 100% identity, only the longest one was retained, to reduce redundancy. All the putative TPS sequences were subjected to a BLASTP search against the NCBI's non-redundant database using default parameters. A TPS was annotated as “Microbial TPS-like protein” (MTPSL) if all the top ten best hits were from bacteria and/or fungi or identical/highly similar to SmMTPSLs.

Assembly of hornwort *Anthoceros punctatus* genome and identification of *MTPSL* genes

For *Anthoceros punctatus*, the Illumina paired-end whole genome sequencing data (access number: SRR1278954) (5) were retrieved from NCBI's Sequence Read Archive (SRA) database. The reads were assembled using SPAdes-3.1.1 (6) and the resulting contigs and singletons were further assembled by CAP3 (7). The final CAP3 assembly contains 34448 sequences (16272 contigs and 18176 singletons) a total length of 97Mb, of which 15596 sequences have a minimum length of 500 bp. The N50 contig length based on these 15596 sequences is 12,462 bp. The assemblies were searched for occurrences of terpene synthases using homology-based methods and *ab initio* predictors. A TBLASTN search was performed with an E-value cutoff of $1e^{-30}$ using the 716 *MTPSL* genes identified from OneKP transcriptomes. We also ran SNAP (8) trained for *Arabidopsis thaliana* on the assembly. The resulting protein sequences of predicted genes were subsequently subjected to a HMMER search against four HMM profiles (PF03936, PF01397, PF06330 and SmMTPSLs generated by using 48 microbial type TPSs from *S. moellendorffii*).

Phylogenetic analyses of terpene synthases.

Bacterial and fungal terpene synthases were obtained from Pfam (version 27.0). Considering that certain MTPSLs from plants may contain a transit peptide that is absent in bacterial and fungal TPSs and certain fungal TPSs contain an extended N-terminal domain, to reduce ambiguities in sequence alignment, only the terpene synthase C terminal domains were included. Sequences were aligned using MAFFT (linsi) (9) with 1000 iterations of improvement. ProtTest (10) was used to select the most appropriate protein evolution model for the protein alignment under the Akaike Information Criterion. For the maximum likelihood analyses, we used RAxML (11) with 1000 bootstrap replicates under the best substitution model (LG+G+F) selected by ProtTest.

Plant material, genomic DNA isolation and PCR

Scapania nemorea, *Anthoceros punctatus* and *Sphagnum fallax* were cultured axenically in Hatcher's medium (12), Knop medium (13) and BCD medium (14), respectively.

Genomic DNA from each species was isolated using the VIOGENE plant genomic DNA isolation kit (Viogene BioTek Corp., Taiwan) and used for PCR with primers listed in Table S9. PCR products were cloned into the pGEM®-T Easy Vector (Promega, USA) and fully sequenced.

Reagents

(*E*)-GPP, (*E,E*)-FPP, (*Z,Z*)-FPP and (*E,E,E*)-GGPP were purchased from Echelon Biosciences (Salt Lake City). (*Z,E*)-FPP was kindly provided by Nathalie Gatto and Wilhelm Boland from Max Planck Institute for Chemical Ecology, Jena, Germany. [1-³H](*E,E*)-FPP was a product of American Radiolabeled Chemicals (St. Louis).

Terpene synthase enzyme assays and kinetic measurements

Representative members from each of the four groups of *MTPSL* genes were selected for gene synthesis. The synthesized cDNAs were cloned into a protein expression vector pEXP5/CT-TOPO (Thermo Fisher Scientific, USA). Protein expression in *E. coli* and terpene synthase enzyme assays were performed as previously described (15). To determine the kinetic properties of Mon-UJTT-MTPSL4, its cDNA was first amplified via PCR using a pair of primers listed in Table S9. The PCR product was cloned into pET32a, in which the Mon-UJTT-MTPSL4 coding sequence was fused to the his-tag coding sequence at its N-terminal. *E. coli*-expressed recombinant Mon-UJTT-MTPSL4 was purified through the his-tag using the HisTrap HP column (GE Lifesciences, USA). The purified Mon-UJTT-MTPSL4 was used for kinetic measurements using [1-³H](*E,E*)-FPP as substrate via a radiochemical method as previously described (16).

References

1. Matasci N, *et al.* (2014) Data access for the 1,000 Plants (1KP) project. *Gigascience* **3**:17.
2. Xie Y, *et al.* (2014) SOAPdenovo-Trans: de novo transcriptome assembly with short RNA-Seq reads. *Bioinformatics* **30**(12):1660-1666.
3. Rice P, Longden I, Bleasby A (2000) EMBOSS: the European Molecular Biology Open Software Suite. *Trends Genet* **16**(6):276-277.
4. Finn RD, Clements J, Eddy SR (2011) HMMER web server: interactive sequence similarity searching. *Nucleic Acids Res* **39**(Web Server issue):W29-37.
5. Li FW, *et al.* (2014) Horizontal transfer of an adaptive chimeric photoreceptor from bryophytes to ferns. *Proc Natl Acad Sci U S A* **111**(18):6672-6677.
6. Bankevich A, *et al.* (2012) SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* **19**(5):455-477.
7. Huang X, Madan A (1999) CAP3: A DNA sequence assembly program. *Genome Res* **9**(9):868-877.
8. Korf I (2004) Gene finding in novel genomes. *BMC Bioinformatics* **5**:59.
9. Katoh K, Misawa K, Kuma K, Miyata T (2002) MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. *Nucleic Acids Res* **30**(14):3059-3066.
10. Darriba D, Taboada GL, Doallo R, Posada D (2011) ProtTest 3: fast selection of best-fit models of protein evolution. *Bioinformatics* **27**(8):1164-1165.
11. Stamatakis A (2014) RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics* **30**(9):1312-1313.
12. Hatcher RE (1965) Towards the establishment of a pure culture collection of hepaticae. *The Bryologist* **68**(2):227-231.
13. Reski R, Abel WO (1985) Induction of budding on chloronemata and caulonemata of the moss, *Physcomitrella patens*, using isopentenyladenine. *Planta* **165**(3):354-358.
14. Ashton NW, Cove DJ (1977) The isolation and preliminary characterisation of auxotrophic and analogue resistant mutants of the moss, *Physcomitrella patens*. *Mol Gen Genet* **154**(1):87-95.
15. Li G, *et al.* (2012) Nonseed plant *Selaginella moellendorffii* has both seed plant and microbial types of terpene synthases. *Proc Natl Acad Sci USA* **109**(36):14711-14715.
16. Tholl D, Chen F, Petri J, Gershenzon J, Pichersky E (2005) Two sesquiterpene synthases are responsible for the complex mixture of sesquiterpenes emitted from *Arabidopsis* flowers. *Plant J* **42**(5):757-771.
17. Hanssen HP, Sprecher E, Abraham WR (1986) 6-Protoilludene, the major molatile metabolite from *ceratocystis piceae* liquid cultures. *Phytochemistry* **25**(8):1979-1980.

Table S2. Summary statistics of *MTPSLs* in 9 plant lineages.

Lineage	Species Count	MTPSL Count	Mean	Median	St. Dev.	Min	Max
Angiosperms	699	5	0.01	0	0.16	0	4
Gymnosperms	80	0	0	0	0	0	0
Monilophytes	70	353	5.04	4.50	3.81	0	20
Lycophytes	22	83	3.77	3	2.65	0	10
Hornworts	7	14	2	0	3.32	0	9
Mosses	41	79	1.93	1	1.82	0	7
Liverworts	26	177	6.81	8	4.15	0	16
Charophytes	47	1	0.02	0	0.15	0	1
Chlorophytes	111	0	0	0	0	0	0

Table S3. 22 MTPSL genes designated as Unclassified and their top hits from Non redundant (NR) database of NCBI

MTPSL_id	Lineages	NR_top_hit	evaluate	bit_score	Scientific_name	Kingdom
(RXRQ_WCZB)_MTPSL7	Hornworts	gi 751680917 gb KIM31075.1	0	1019	Serendipita vermifera MAFF 305830	Fungi
(RXRQ_WCZB)_MTPSL8	Hornworts	gi 353240956 emb CCA72799.1	0	981	Piriformospora indica DSM 11827	Fungi
(RXRQ_WCZB)_MTPSL9	Hornworts	gi 353240956 emb CCA72799.1	7E-130	391	Piriformospora indica DSM 11827	Fungi
MCHJ_MTPSL1	Charophytes	gi 913451420 ref WP_050430829.1	0.001	50.8	Chondromyces crocatus	Bacteria
MRKX_MTPSL1	Angiosperms	gi 588255974 ref XP_006957163.1	0	558	Wallemia mellicola CBS 633.66	Fungi
QAIR_MTPSL1	Angiosperms	gi 751178290 gb KIL64254.1	5E-177	508	Amanita muscaria Koide BX008	Fungi
QAIR_MTPSL2	Angiosperms	gi 751175026 gb KIL61028.1	0	620	Amanita muscaria Koide BX008	Fungi
QAIR_MTPSL3	Angiosperms	gi 751174784 gb KIL60790.1	7E-143	427	Amanita muscaria Koide BX008	Fungi
QAIR_MTPSL4	Angiosperms	gi 751181225 gb KIL67171.1	0	691	Amanita muscaria Koide BX008	Fungi
JKAA_MTPSL1	Lycophytes	gi 927407765 ref XP_013949969.1	0	541	Trichoderma virens Gv29-8	Fungi
ZYCD_MTPSL1	Lycophytes	gi 238496645 ref XP_002379558.1	1E-130	390	Aspergillus flavus NRRL3357	Fungi
AEXY_MTPSL1	Liverworts	gi 389636521 ref XP_003715910.1	6E-178	513	Magnaporthe oryzae 70-15	Fungi
IRBN_MTPSL6	Liverworts	gi 751680917 gb KIM31075.1	0	934	Serendipita vermifera MAFF 305830	Fungi
JHFI_MTPSL16	Liverworts	gi 751680917 gb KIM31075.1	6E-101	313	Serendipita vermifera MAFF 305830	Fungi
LGOW_MTPSL3	Liverworts	gi 629725325 ref XP_007822988.1	7E-56	196	Metarhizium robertsii	Fungi
NWQC_MTPSL8	Liverworts	gi 629725325 ref XP_007822988.1	6E-36	144	Metarhizium robertsii	Fungi
OFTV_MTPSL7	Liverworts	gi 751680917 gb KIM31075.1	0	931	Serendipita vermifera MAFF 305830	Fungi
RTMU_MTPSL4	Liverworts	gi 667838359 ref XP_007783348.1	3E-128	386	Coniosporium apollinis CBS 100218	Fungi
WJLO_MTPSL3	Liverworts	gi 549052256 emb CCX30236.1	4E-68	231	Pyronema omphalodes CBS 100304	Fungi
WJLO_MTPSL4	Liverworts	gi 549052256 emb CCX30236.1	1E-71	240	Pyronema omphalodes CBS 100304	Fungi
YBQN_MTPSL8	Liverworts	gi 648165817 gb KDR79494.1	0	596	Galerina marginata CBS 339.88	Fungi
QIAD_MTPSL2	Monilophytes	gi 629662947 ref XP_007805277.1	2E-77	251	Endocarpon pusillum Z07020	Fungi

Table S4. Eight MTPSLs identified from the transcriptome of the liverwort *Scapania nemorea*

Gene	Group
Liv-IRBN-MTPSL1	I
Liv-IRBN-MTPSL2	I
Liv-IRBN-MTPSL3	I
Liv-IRBN-MTPSL4	I
Liv-IRBN-MTPSL5	I
Liv-IRBN-MTPSL6	II
Liv-IRBN-MTPSL7	III
Liv-IRBN-MTPSL8	U^a

^aunclassified

Table S5. *MTPSL* genes from the genome of the hornwort *Anthoceros punctatus*

Gene	Protein	Group
ApMTPSL1	408	II
ApMTPSL2	430	III
ApMTPSL3	436	II
ApMTPSL4	401	III
ApMTPSL5	413	III
ApMTPSL6	421	III
ApMTPSL7	427	III

Table S6. *MTPSL* genes from the genome of the moss *Sphagnum fallax*

Gene	Protein size	Group
SfMTPSL1	472	
SfMTPSL2	341	
SfMTPSL3	328	
SfMTPSL4	482	
SfMTPSL5	489	
SfMTPSL6	477	
SfMTPSL7	481	
SfMTPSL8	484	
SfMTPSL9	377	
SfMTPSL10	481	
SfMTPSL11	440	
SfMTPSL12	487	
SfMTPSL13	455	
SfMTPSL14	456	
SfMTPSL15	472	
SfMTPSL16	472	
SfMTPSL17	341	
SfMTPSL18	457	
SfMTPSL19	453	
SfMTPSL20	455	
SfMTPSL21	455	

Table S7. A list of sequenced genomes searched for *MTPSL* genes

Species	Data version
<i>Amaranthus hypochondriacus</i>	v1.0
<i>Amborella trichopoda</i>	v1.0
<i>Ananas comosus</i>	v3
<i>Aquilegia coerulea</i>	v1.1
<i>Aquilegia coerulea</i>	v3.1
<i>Arabidopsis halleri</i>	v1.1
<i>Arabidopsis lyrata</i>	v1.0
<i>Arabidopsis thaliana</i>	TAIR10
<i>Boechera stricta</i>	v1.2
<i>Brachypodium distachyon</i>	v3.1
<i>Brachypodium stacei</i>	v1.1
<i>Brassica rapa</i>	FPsc v1.3
<i>Capsella grandiflora</i>	v1.1
<i>Capsella rubella</i>	v1.0
<i>Carica papaya</i>	ASGPBv0.4
<i>Chlamydomonas reinhardtii</i>	v5.5
<i>Citrus clementina</i>	v1.0
<i>Citrus sinensis</i>	v1.1
<i>Coccomyxa subellipsoidea C-169</i>	v2.0
<i>Cucumis sativus</i>	v1.0
<i>Eucalyptus grandis</i>	v2.0
<i>Eutrema salsugineum</i>	v1.0
<i>Fragaria vesca</i>	v1.1
<i>Glycine max</i>	Wm82.a2.v1
<i>Gossypium raimondii</i>	v2.1
<i>Kalanchoe marnieriana</i>	v1.1
<i>Klebsormidium flaccidum</i>	v1.0
<i>Linum usitatissimum</i>	v1.0
<i>Malus domestica</i>	v1.0
<i>Manihot esculenta</i>	v6.1
<i>Medicago truncatula</i>	Mt4.0v1
<i>Micromonas pusilla CCMP1545</i>	v3.0
<i>Micromonas</i> sp. RCC299	v3.0
<i>Mimulus guttatus</i>	v2.0
<i>Musa acuminata</i>	v1
<i>Oryza sativa</i>	v7_JGI
<i>Ostreococcus lucimarinus</i>	v2.0
<i>Panicum hallii</i>	v2.0
<i>Panicum virgatum</i>	v1.1
<i>Phaseolus vulgaris</i>	v1.0
<i>Physcomitrella patens</i>	v3.3
<i>Populus trichocarpa</i>	v3.0
<i>Prunus persica</i>	v2.1
<i>Ricinus communis</i>	v0.1
<i>Salix purpurea</i>	v1.0
<i>Selaginella moellendorffii</i>	v1.0
<i>Setaria italica</i>	v2.2
<i>Setaria viridis</i>	v1.1
<i>Solanum lycopersicum</i>	iTAG2.3
<i>Solanum tuberosum</i>	v3.4
<i>Sorghum bicolor</i>	v3.1
<i>Sphagnum fallax</i>	v0.5
<i>Spirodela polyrhiza</i>	v2
<i>Theobroma cacao</i>	v1.1
<i>Triticum aestivum</i>	v2.2
<i>Vitis vinifera</i>	Genoscope.12X
<i>Volvox carteri</i>	v2.1
<i>Zea mays</i>	6a
<i>Zostera marina</i>	v2.2

Table S8. A list of representative *MTPSL* genes experimentally studied.

Sequence ID	Lineage	Species	Group
Liv-IRBN-MTPSL2	Liverworts	<i>Scapania nemorea</i>	I
Liv-IRBN-MTPSL4	Liverworts	<i>Scapania nemorea</i>	I
Mos-GOWD-MTPSL2	Mosses	<i>Sphagnum lescurii</i>	I
Mos-QKQO-MTPSL3	Mosses	<i>Pseudotaxiphyllum elegans</i>	II
Mos-VBMM-MTPSL3	Mosses	<i>Anomodon rostratus</i>	II
Hon-ApMTPSL7	Hornworts	<i>Anthoceros punctatus</i>	III
Mon-GSXD-MTPSL3	Monilophytes	<i>Myriopteris eatonii</i>	IV
Mon-UJTT-MTPSL4	Monilophytes	<i>Pityrogramma trifoliata</i>	IV
Mon-YJJY-MTPSL1	Monilophytes	<i>Woodsia scopulina</i>	IV

Table S9. Primers used in this study

Region amplified	Primer	DNA sequences
ApMTPSL1 and its neighboring gene	Forward	5'-CACTACTGCGTCGGCTTCATG-3'
	Reverse	5'-CGCACAGCATTCAACAATTCACCT-3'
ApMTPSL2 and its neighboring gene	Forward	5'-CAGGTAGGAGCCCCGCGATTT-3'
	Reverse	5'-AGGGAAAAGGAGGGTGGTG-3'
SfMTPSL1 and its neighboring gene	Forward	5'-CAGAAGCAAAGTATCGGTCTCTTAC -3'
	Reverse	5'-CACTGTTAGCAGGGTATGGTGAAC-3'
Liv-IRBN-MTPSL1	Forward	5'-TTCTGAGGACGAGCGTATTCTTC-3'
	Reverse	5'-GCAAAACGTCAACTAAACGAGAAG-3'
Liv-IRBN-MTPSL2	Forward	5'-TCATACTCGCCTCCATATCCTGTG-3'
	Reverse	5'-GATTTGAAATGTCAGTCATGTGTGC-3'
Liv-IRBN-MTPSL3	Forward	5'-GATGCCAACGCAGCCATACAGAC-3'
	Reverse	5'-GCCTGATACCCAGTTTCTGACGG-3'
Liv-IRBN-MTPSL4	Forward	5'-CAGTATGTGTGAACTCCTCTGGGTC-3'
	Reverse	5'-GCACTCCTTTTCTGTACCGACTGG-3'
Liv-IRBN-MTPSL5	Forward	5'-TCAAAGGCATCACCTGAAGTCTG-3'
	Reverse	5'-ATATTATCGGTGTCCAATCCTCC-3'
Liv-IRBN-MTPSL6	Forward	5'-AATGCTTGGTGTGTGTTTCGTCTC-3'
	Reverse	5'-CCTCCATGTGATTTTCGCAAAGTAG-3'
Liv-IRBN-MTPSL7	Forward	5'-CTGGCAGATGATTTAGATGAGATAGC-3'
	Reverse	5'-CAGAAACAACCCGCAAACCATTC-3'
Liv-IRBN-MTPSL8	Forward	5'-TCTCCCTGTTGCCACTGCTTTCC-3'
	Reverse	5'-GTTGGTCCTGGTACGGCGACTGA-3'
Mon-UJTT-MTPSL4-pET32a	Forward	5'-CATGCCATGGCATCCATTATATTAGGAAGCTC-3'
	Reverse	5'-CCCAAGCTTAGTTAAAGGCCATCATGACAC-3'

```

*           20           *           40           *           60
Liv-IRBN-MTPSL8 : MA--SPATIRLPDILSAMDRFELRTHPDEREVTRASNEWFNSYNMMPAPIFEKFKCDFG : 58
gi|751680917   : MASPSPATIRLPDILSAMDKFELRTHPDEREVTRASNEWFNSYNMMPAPIFEKFKCEFG : 60
MA SPATIRLPDILSAM4FELRTHPDEREVTRASNEWFNSYNMMPAPIFEKFKVFC FG

*           80           *           100          *           120
Liv-IRBN-MTPSL8 : LMTAMSYPDTDATRLRITADYMSILFAYDDLMDLPSSDLMHDRIASSKAAKIMMQVLTHP : 118
gi|751680917   : LMTAMSYPDTDATRLRITADYMSILFAYDDLMDLPSSDLMHDRIASSKAAKIMMQVLTHP : 120
LMTAMSYPDTDATRLRITADYMSILFAYDDLMDLPSSDLMHDRIASSKAAKIMMQVLTHP

*           140          *           160          *           180
Liv-IRBN-MTPSL8 : HKFKPVPGLPVATAFHDFWTRFCATSTPSMQKRFTETTYEYVMAVKNQVGNRASSVCPSI : 178
gi|751680917   : HKFKPVPGLPVATAFHDFWTRFCATSTKSMQKRFTETTYEYVMAVKNQVGNRQSSVCPSI : 180
HKFKPVPGLPVATAFHDFWTRFCATST SMQKRFTETTYEYVMAVKNQVGNR SSVCPSSI

*           200          *           220          *           240
Liv-IRBN-MTPSL8 : EEYVSLRRDTSIAKVTYACIEYCLNIDCPDEAFYHPSLALQEAGNDILSWANDVYSFDN : 238
gi|751680917   : EEYVSLRRDTSIAKVTYACIEYCLNIDVPDEAFYHPSLALQEAGNDILSWANDVYSFDN : 240
EEYVSLRRDTSIAKVTYACIEYCLNID PDEAFYHPSLALQEAGNDILSWANDVYSFDN

*           260          *           280          *           300
Liv-IRBN-MTPSL8 : EQCSGDCHNLIAVVAINKNITVQAAMEYAMGMIDSAINRFFEECSNVPSFGPDVDPKVQA : 298
gi|751680917   : EQCSGDCHNLIAVVAINKNITVQAAMEYAMGMIDSAIARFFEECANVPSFGPDVDPKVQA : 300
EQCSGDCHNLIAVVAINKNITVQAAMEYAMGMIDSAI RFFEEC NVPSFGPDVDPKVQA

*           320          *           340          *           360
Liv-IRBN-MTPSL8 : YIKGVELYLSGSVFWHLESERYFGPRVKHVKDTLMVELRPLDEGAKPAFDLIYKLP SNLT : 358
gi|751680917   : YIKGVELYLSGSVYVWHLESERYFGPRVKHVKDTLMVELRPLDEGAKPAFNLIYKLP SNLT : 360
YIKGVELYLSGSV5VWHLESERYFGPRVKHVKDTLMVELRPLDEGAKPAF1LIYKLP SNLT

*           380          *           400          *           420
Liv-IRBN-MTPSL8 : SNVLAAVSNRTPTP-PAPVEAAP-AAPSPPPRTTRGTPT-----PAHHAPEIHAPVPIS : 410
gi|751680917   : SNVLAAVTPTTKTPEVPVAAAPTVAAPSPPRCSSNSSTGTVRASPVQH--EIHAPTPIIS : 418
SNVLAAV3 T TP P PV AAP APSPPR 3 3 T P H EIHAP PIS

*           440          *           460          *           480
Liv-IRBN-MTPSL8 : PFNPNFPTVSPVPPPSYEHQRAFAQYMAAQLDEKMRAEQYVYVQAPQYYSAPQSPYQDQ : 470
gi|751680917   : PFNPNFPTSNPNMPPPSYEQQRVFAQFMAAQLDEKMRAEQW-QVPQYYSAPQSPYQDQ : 477
PFNPNFPT P 6PPPSYE QR FAQ5MAAQL KMRAEQ 5 Q PQYYSAPQSPYQ Q

*           500          *           520          *           540
Liv-IRBN-MTPSL8 : QQ---KLRQNSLMEVLLSRPTSELTNILVIASVLMASSPLALVPFVPLLVLVLLFPEAPA : 526
gi|751680917   : QQQQLTKARQNSLMEALLNRPTSELTNILVIASVLMASSPLALIPFVPLLVLVLLYPEAPA : 537
QQ K RQNSLME 6L RPTSELTNILVIASVLMASSPLAL6PFVPLLVLVLL5PEAPA

Liv-IRBN-MTPSL8 : VLLS : 530
gi|751680917   : VLLA : 541
VLL

```

Fig. S1. Sequence alignment of IRBN_MTPSL6 identified from the transcriptome of the liverwort *Scapania nemorea* with its top hit in nr database at NCBI. “gi:751680917” is putative terpene synthase gene identified in the fungus *Serendipita vermifera*. The two sequences are 91% identical.

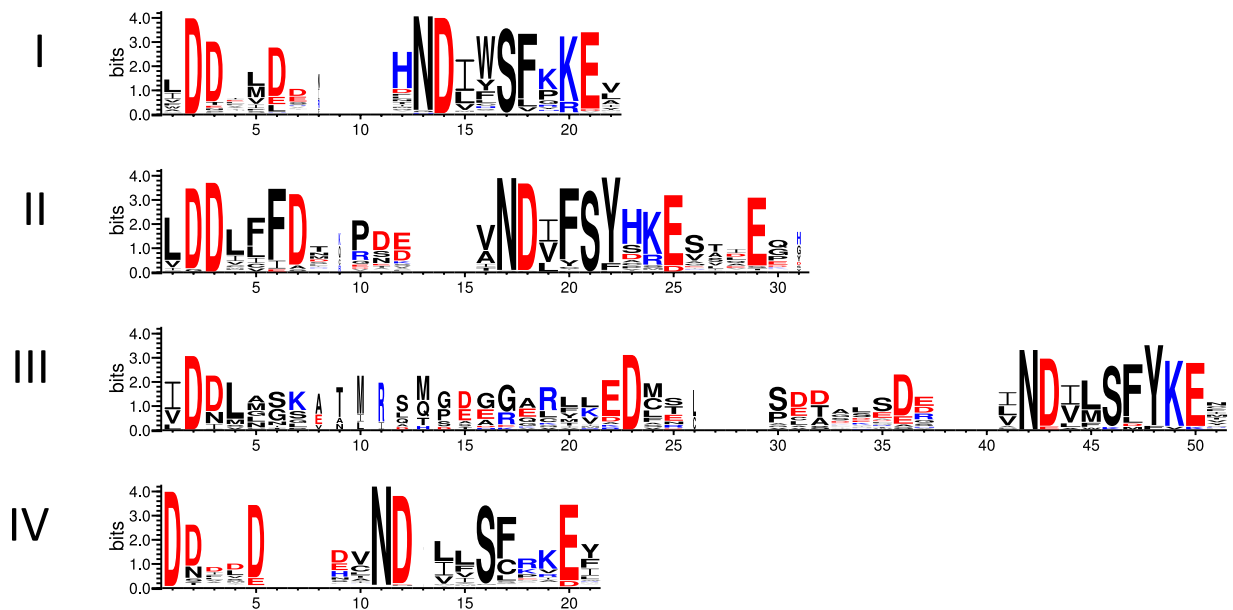


Fig. S2. Identification of conserved motifs among the four groups (I, II, III and IV) of microbial type (MTPSL) terpene synthases. The ‘NDxxSxxxD/E’ motif is highly conserved among all MTPSLs. The canonical ‘DDxxD’ motif was present in group I and IV proteins, but group II proteins displayed a conserved ‘DDxxxD’ motif, whereas in the group III enzymes only the first two aspartates (‘DD’) are conserved. Sequence motif logos made using weblogo 3.0, showing the conserved motifs found in each group of terpene synthase genes of microbial type.

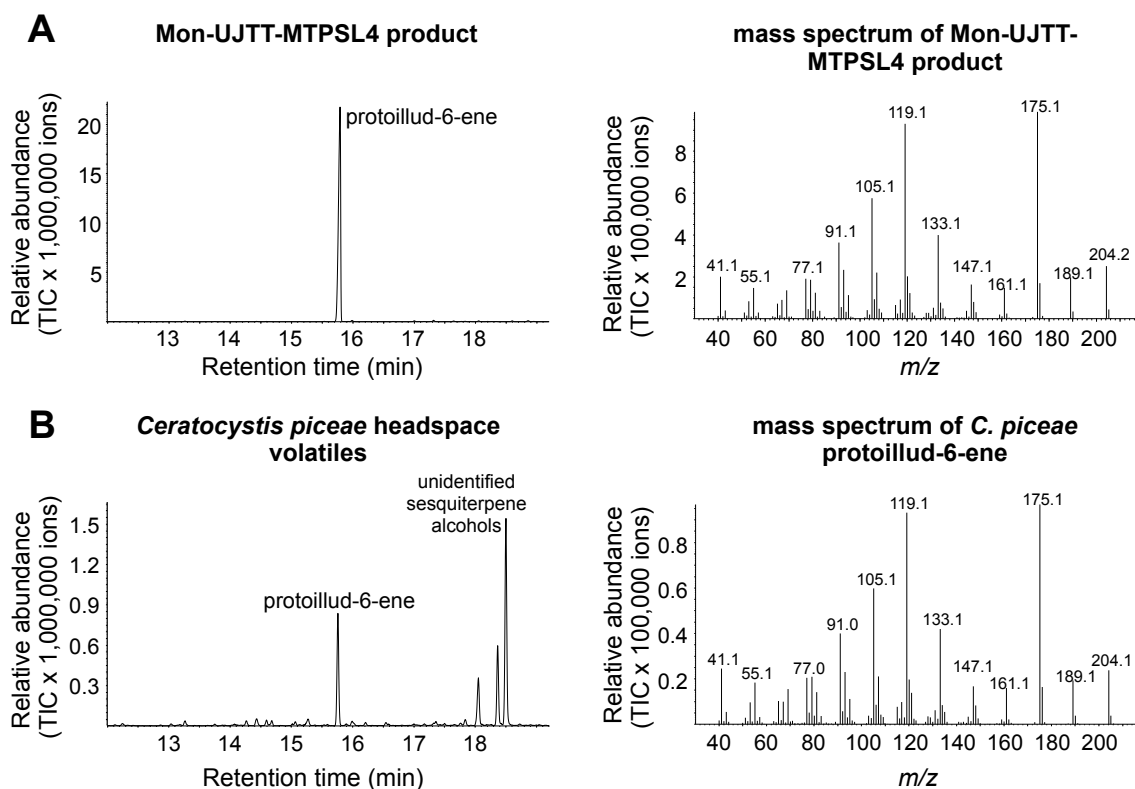
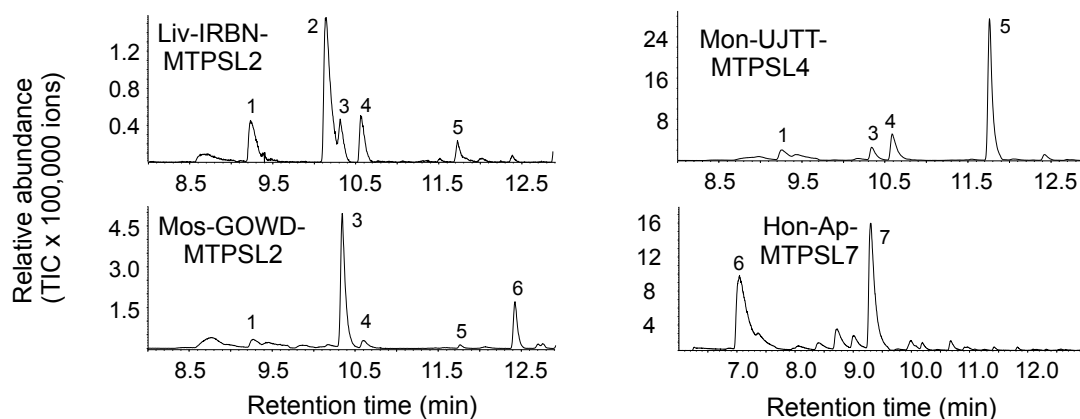


Fig. S3. Product identification of Mon-UJTT-MTPSL4. (A) The gene was heterologously expressed in *Escherichia coli* and the crude bacterial protein extract was incubated with FPP. The enzyme product was collected using solid phase micro extraction (SPME) and analyzed with gas chromatography/mass spectrometry (GC-MS). (B) Volatiles from the headspace of a liquid culture of *Ceratocystis piceae* were collected using SPME and analyzed with GC-MS. *C. piceae* has been reported to produce protoillud-6-ene as main sesquiterpene hydrocarbon (17).

A Monoterpene synthase activity



B Diterpene synthase activity

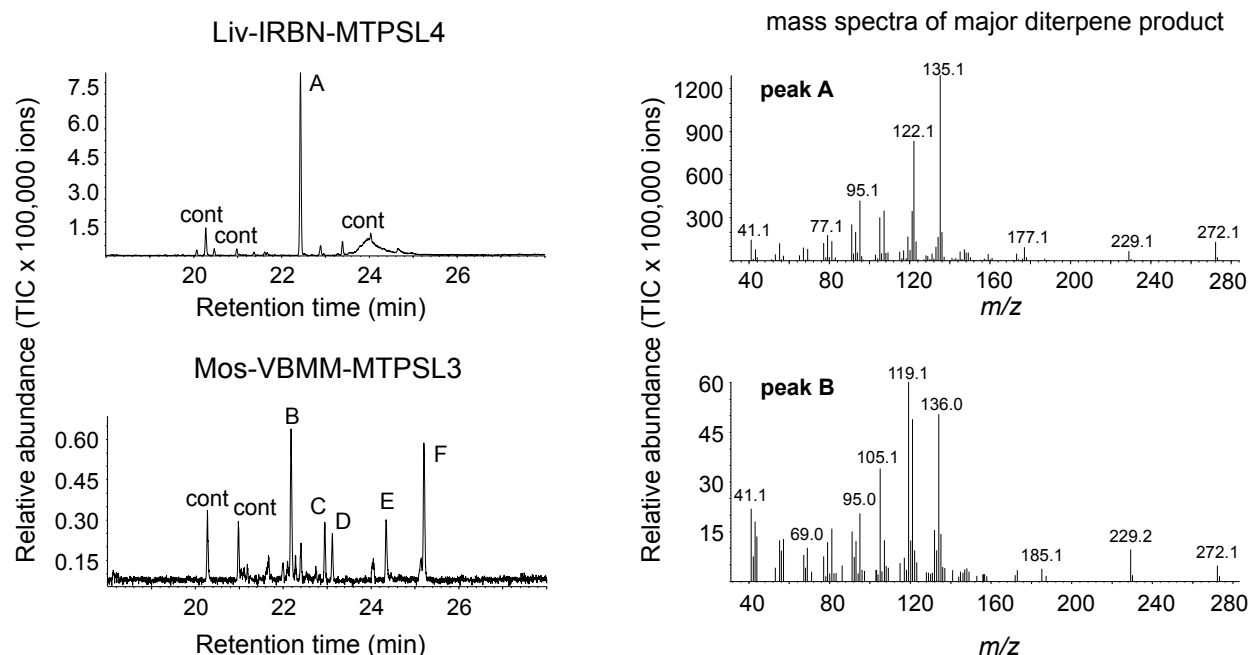


Fig. S4. Monoterpene synthase and diterpene synthase activities of MTPSLs. *MTPSL* genes were heterologously expressed in *Escherichia coli* and crude protein extracts were incubated with the potential substrates GPP (A) and GGPP (B), respectively. Monoterpene products were collected using solid-phase micro-extraction and diterpene products were extracted with hexane. Products were analyzed using gas chromatography/mass spectrometry. 1, myrcene*; 2, limonene*; 3, (*Z*)- β -ocimene; 4, (*E*)- β -ocimene*; 5, linalool*; 6, allo-ocimene; 6, α -pinene; 7, β -phellandrene. A-F, unidentified diterpenes. Compounds marked with an asterisk (*) were identified using authentic standards.

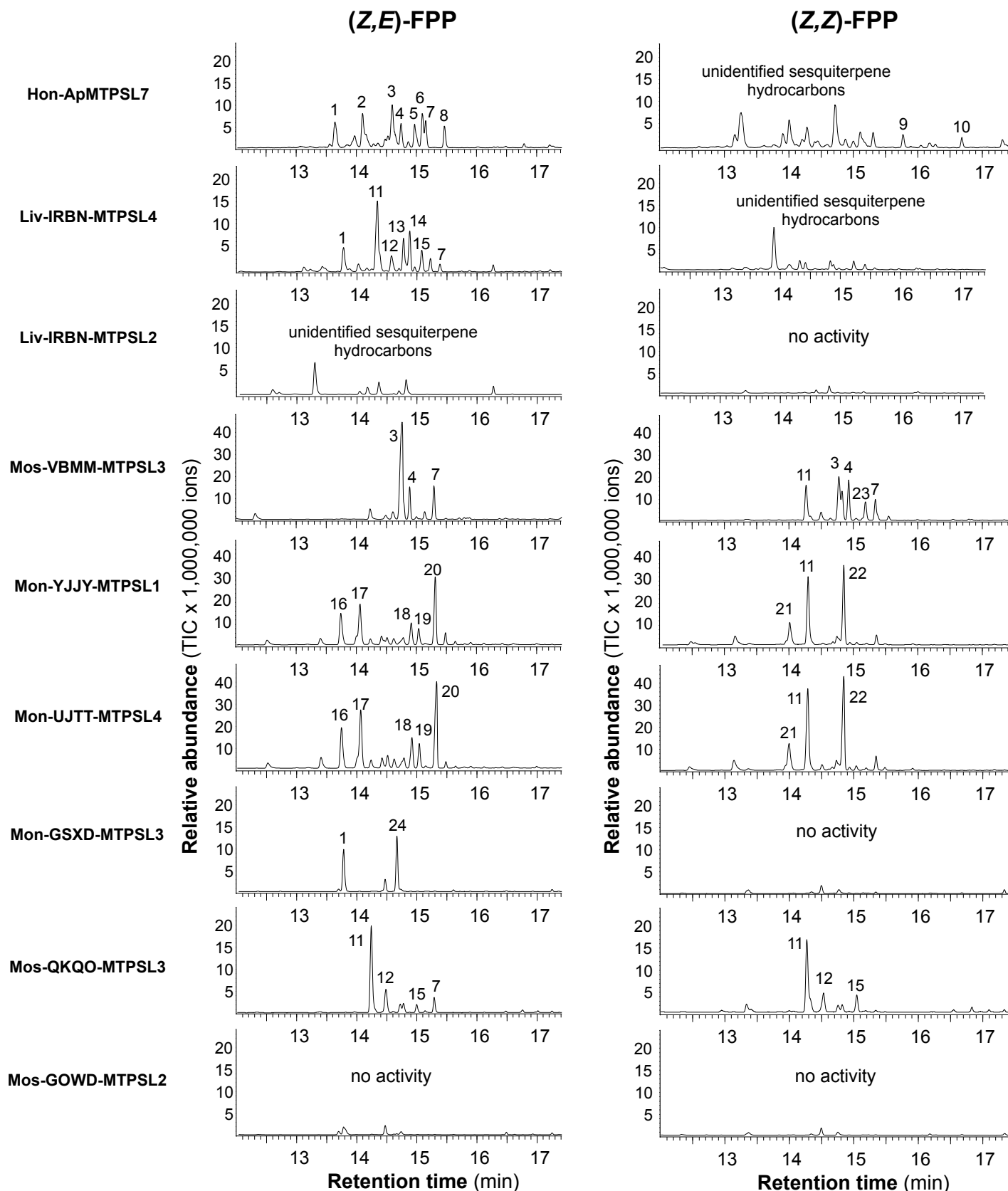


Fig. S5. Sesquiterpene synthase activity of representative MTPSLs with (Z,E)-FPP and (Z,Z)-FPP. MTPSL genes were heterologously expressed in *Escherichia coli* and crude protein extracts were incubated with the potential substrates (Z,E)-FPP and (Z,Z)-FPP. Enzyme products were collected using solid-phase micro-extraction and analyzed with gas chromatography/mass spectrometry. 1, (*E*)- β -farnesene; 2, β -acoradiene; 3, β -bisabolene; 4, (*Z*)- γ -bisabolene; 5, unidentified ST; 6, unidentified ST; 7, (*Z*)- α -bisabolene; 8, nerolidol; 9, unidentified oxygenated ST; 10, unidentified oxygenated ST; 11, γ -curcumene; 12, zingiberene; 13, unidentified ST; 14, unidentified ST; 15, β -sesquiphellandrene; 16, unidentified ST; 17, *epi*-bicyclosesquiphellandrene; 18, γ -cadinene; 19, δ -cadinene; 20, α -cadinene; 21, unidentified ST; 22, unidentified ST; 23, (*E*)- γ -bisabolene; 24, (*E,E*)- α -farnesene. ST, sesquiterpene.