BMC Genomics Genome wide identification and characterization of the TPS gene family in wheat (Triticum aestivum L.) and expression analysis in response to aphid damage

Download this article in PDF format | Export citation

Citations (1) References (61) Cited by

Genome wide identification and characterization of the TPS gene family in wheat (Triticum aestivum L.) and expression analysis in response to aphid damage

Views 0 | Citations 0

April 2021 · Arab Proceedings Paradoxical · 2020

DOI: 10.21744/ap.v1i1.1000 · Cite this paper

Lei Zhao · Guoqing Zhao · Frédéric Francis · Yong Liu

Abstract and Keywords

Terpene synthase (TPS) gene family in Hexaploid wheat and plays an important role in regulating various biological processes in plants, especially in pathogen and herbivore defense. However, the TPS family members in wheat have not yet been fully identified. In this study, we identified 32 TPS genes were identified and classified into three subfamilies based on phylogenetic analysis. Gene structure and motif analysis showed that the TPS genes exhibited conserved gene structure and motif distribution patterns. Gene duplication and synteny analysis revealed that tandem and dispersed duplications were the most important sources of the TPS family expansion in wheat. Cis-acting elements in the promoter region of the TPS genes were enriched in hormone and stress response, suggesting that the TPS genes may be involved in various biological processes. Expression profiles derived from transcriptomic data and qRT-PCR analysis showed that most TPS genes were expressed in different tissues and organs and TPS-mediated pathways in wheat responses to aphid damage. Our results provide a comprehensive understanding of the TPS family in wheat growth and development. TaTPS-7D gene contained at least two cis-acting elements in its promoter region and was significantly induced by aphid infestation and methyl jasmonate pathways. This study can provide valuable resources for functional genomics research and genetic improvement of wheat. The TPS genes with aphid-induced expression patterns may be related to wheat development, particularly to plant pest interactions and further breeding for aphid resistance in wheat.

Figure contents uploaded by Yong Liu · Author content

Discover the world's research

Join ResearchGate to find the people and research you need to help your work.

Sign up for free

Already have an account? Log in

Keywords: Terpene synthase · Transport · Biological stress · Expression analysis · Aphid resistance gene

Introduction

Terpenoids are known as compounds are synthesized from isoprenoid units and are the largest and most diverse group of biomolecules (Wallrabe, 1999; Bohlmann and Keeling, 2008; Chen et al., 2011). Terpenoids are the secondary metabolites and have been studied for years (Bohlmann et al., 2000), and plant terpenoids have been reported to have various functions in plant growth and development, such as photosynthesis, hormones, and defense against herbivores and pathogens (Tholl, 2015; Chen et al., 2011). Terpenoids can be classified into primary or secondary metabolites according to their physiological functions. Primary metabolites are directly involved in the growth and development of plants, such as photosynthesis, respiration, and hormones, which are essential for the survival of plants. Secondary metabolites are not directly involved in the growth and development of plants, but they can enhance the plant fitness of wheat to pest and pathogen attacks (Chen et al., 2011). Terpenoids are the most diverse and abundant plant secondary metabolites, which are used to attract pollinators and defend against herbivores and pathogens (Tholl, 2015; Wallrabe et al., 2021). Terpene synthase (TPS) gene family is the key enzyme in the biosynthesis of terpenoids, which catalyze the conversion of linear precursors into various terpenoid products (Chen et al., 2011). Terpenoids are synthesized through two pathways, the mevalonate (MVA) pathway and the methylerythritol phosphate (MEP) pathway, which are located in different cellular compartments, the MVA pathway in the cytosol and the MEP pathway in the plastid (Tholl, 2015; Wallrabe et al., 2021). Terpenoids are synthesized through

et al. 2007). TPS-a subfamily covered all sesquiterpene synthetases of angiosperms (Bohlmann et al. 1998), with RRx8W found in almost all TPS-a and most of TPS-e/f subfamilies. It was suggested that monoterpene and diterpene synthetases usually contain an N-terminal plasmid targeting peptide located in the upstream region of the conserved or modified RRx8W (Bohlmann et al. 1998). However, although the TPS-g subfamily lacked the common RRx8W sequence of monoterpene synthetase, some studies in other species showed that the enzymes encoded by TPS-g subfamily can catalyze monoterpene, sesquiterpene and diterpene (Richter et al. 2016; Li et al. 2017). The terpenoid products in plants depend on their subcellular location (Chen et al. 2011; Arimura et al. 2008). Also, TaTPS protein of TPS-g subfamily was found to potentially regulate the production of many terpenes. Only three predicted TaTPS (TaTPS106, TaTPS134, TaTPS118) lacked the exact DDxxD motif feature of TPS, which catalyzed the reaction initiated by the diphosphate group cleavage of isoprene phosphate substrate. The TPS-c subfamily protein contained not only the conserved motif DDxxD, but also the conserved motif DxDD, which play a major role in the activation mechanism of TPS protonation (Prisic et al. 2007). In addition to the conserved domain DDXXD, NSE/DTE was the second important conserved domain of C-terminal domain (Christianson 2006; Degenhardt et al. 2009). The conserved domain NSE/DTE was found in the proteins of TPS-a, TPS-b, TPS-g and TPS-e/f subfamily.

The expression of 42 *TaTPS* genes was found to have significant changes, 30 *TaTPS* genes of which were up-regulated after aphid damage. It was suggested that the *TaTPS* genes plays a key role in pest plant defense. Although the defense effect of *TaTPS* gene has not been studied, the were identified in *TPS* gene of wheat by bioinformatics analysis. These *TPS* genes were focused to be the key factors for wheat growth and defense in specific signaling pathways. In this study, Many CREs are related to abiotic stress responses, such as light (G-box, Sp1, Box 4 and others), damage (box S, W-box, WUN-motif, JERE), anaerobic conditions (ARE), drought (MBS) and other stress responses. Light cycle-related elements (32) were distributed in almost all transcripts. In addition, a large number of transcripts had identified elements related to hormone and biological stress response, such as abscisic acid, gibberellin, MeJA, salicylic acid, auxin and others. Abscisic acid response element (ABRE) was distributed in 142 transcripts of *TaTPS* genes, the largest proportion. In addition, MeJA response element (TGACG-motif and CGTCA-motif) was distributed in 139 transcripts of *TaTPS* genes. Other CREs may be involved in the regulation of wheat growth and development and other aspects. Among them, six transcripts of *TaTPS* genes contain MBS1 (MYB binding site involved in the regulation of flavonoid biosynthesis gene), showed that these six genes may be involved in the metabolism of flavonoids. All *TaTPS* genes contained at least three CREs, indicating the availability and diversity of gene expression regulation.

Previous studies have shown that *TaTPS* gene may be involved in a variety of abiotic stresses. A variety of other CREs that may be related to wheat biological process were also found. The induced defense of insect pests depends on the hormone signaling pathway (such as SA, MeJA and others). Therefore, the important CREs of hormone pathway also become the important CREs of insect defense. We analyzed the CREs of *TaTPS* genes after infected of aphid. The CREs involved in screening for plant defense responses and hormone signaling pathway were analyzed and displayed

in Fig. 8, which contains the TGACG-motif, W-box, CGTCA-motif, as-1, TCA-element, ABRE, ERE, GARE-motif, TATC-box, TC-rich repeats, H-box. All *TaTPS* genes transcripts contain more than two defense-related or hormone-related CREs. Among them, ABRE, CGTCA-motif, TGACG-motif and as-1 are the most frequent CREs in the promoter region of *TaTPS* genes transcripts. This demonstrates that *TaTPS* genes may participate in the response of plants to a variety of hormones. TC-rich repeats, H-box and W-box are CREs of defense and stress response. H-box only exists in the promoter region of *TaTPS126*, *TaTPS130* and *TaTPS139*. TC-rich repeats are distributed in TPS-b and TPS-e/f subfamilies. While W-box is distributed in each subfamily, only one gene of TPS-b subfamily contains W-box, and the number of W-box of TPS-g subfamily is large and widely distributed. In addition, the TATC-box exists in the promoter region of *TaTPS102*, *TaTPS135* and *TaTPS43*. Aphid-induced *TaTPS* genes promoter contains abundant CREs, it is suggested that *TaTPS* gene may play an important role in other metabolic regulation besides defensive effect on aphid. This was similar to the study of other plant species (Tuskan et al. 2006; Nieuwenhuizen et al. 2013). Terpenes produced by insect-induced defense depend on signal pathways such as jasmonic acid and salicylic acid (Ozawa et al. 2000; Irmisch et al. 2014a, b). In addition, terpenes also participate in the direct defense response of plants (Gershenzon and Dudareva 2007). Hormone and defense-related CREs exist in almost all transcripts of *TaTPS* gene. This suggests that some related genes of *TaTPS* may be involved in the defense of wheat pests.

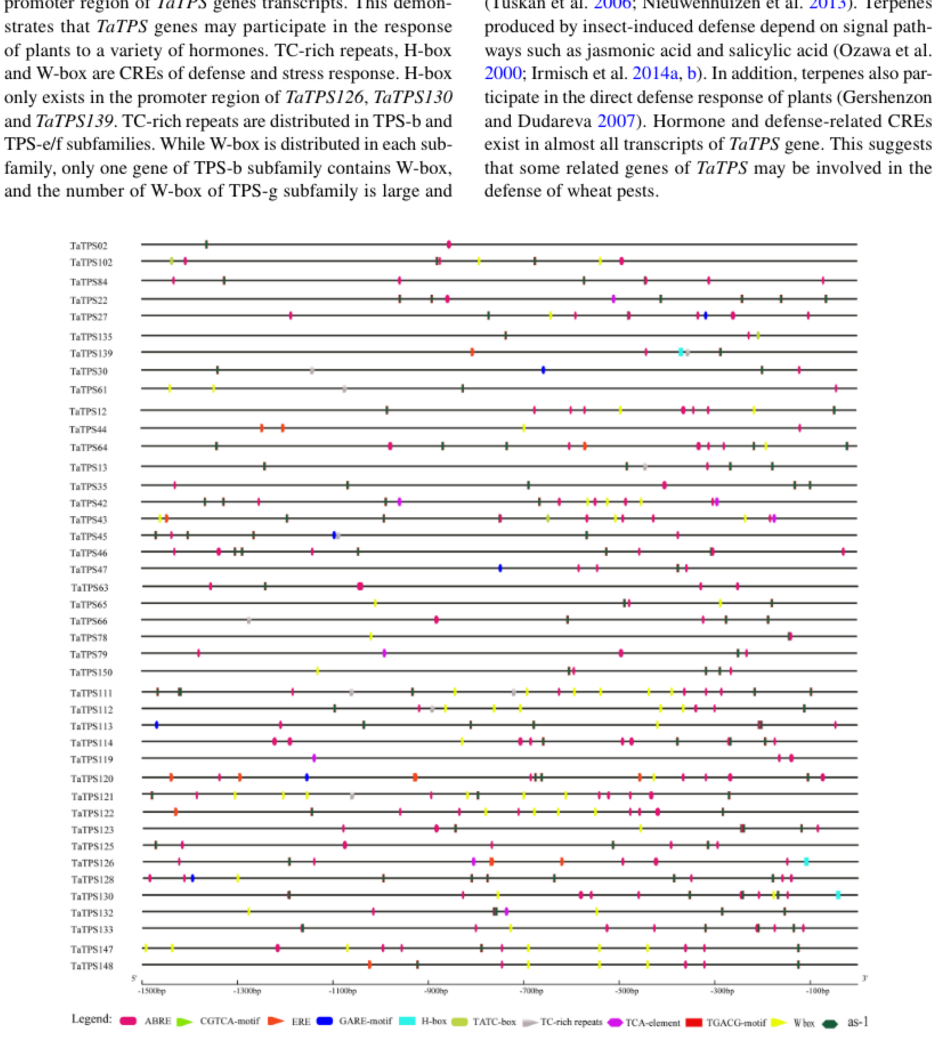

Fig. 8 The hormone or defense-related *cis*-regulatory elements of *TaTPS* gene, whose expression changed significantly after aphid damage was analyzed. Based on the scale at the bottom, the upstream length of the translation starting point can be inferred

Here, the genome-wide analysis of wheat *TPS* gene family was carried out. 153 *TaTPS* genes were identified and divided into six subgroups. The *TPS* gene family is highly conserved in species. *TaTPS* gene plays an important role in wheat pest defense, which is expressed in response to aphid damage. This study not only has a comprehensive understanding of the *TaTPS* gene family, but also provides precious resources for insight into the biological role of the *TaTPS* gene. Although the specific role of the *TaTPS* gene still needs a lot of experimental verification, the results of this study provide some new information for the defense function of the *TaTPS* gene. It could play an important role in breeding new wheat varieties with aphid resistance.

Author contribution statement LZ and YL conceived and designed the experiments; LZ and XZ performed the experiments and analyzed the data; LZ and YL wrote the manuscript; FF helped to draft the manuscript. All authors read and approved the manuscript to the final submission.

Supplementary Information The online version contains supplementary material available at https://doi.org/10.1007/s11738-021-03236-y.

Acknowledgements This study was supported by the National Key R&D Program of China (2017YFD0201705), and the Funds of Shandong 'Double Tops' Program (SYL2017XTTD11). The funding agent only provided the financial support and did not involve in the design of the experiment, collection, interpretation and analysis of data and in the drafting of the manuscript.

Data availability The raw data of RNA-seq analysis come from SRA (SRX4372399 and SRX4372400) database in NCBI. Others of the datasets supporting the results of this article are included within the article and its Supplementary Material.

Declarations

Conflict of interest The authors declare that they have no conflict of interest.

References

Abbas F, Yu R (2017) Volatile terpenoids: multiple functions, biosynthesis, modulation and manipulation by genetic engineering. Planta 246:1–14. https://doi.org/10.1007/s00425-017-2749-x
Altschul SF, Madden TL, Schäffer AA, Zhang JH, Zhang Z, Miller W, Lipman DJ (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res 25:3389–3402. https://doi.org/10.1093/nar/25.17.3389
Arimura GI, Garms S, Maffei M et al (2008) Herbivore-induced terpenoid emission in *Medicago truncatula*: concerted action of jasmonate, ethylene and calcium signaling. Planta 227:453–464. https://doi.org/10.1007/s00425-007-0631-y
Aubourg S, Lecharny A, Bohlmann J (2002) Genomic analysis of the terpenoid synthase (AtTPS) gene family of *Arabidopsis thaliana*. Mol Genet Genom 267:730–745. https://doi.org/10.1007/s00438-002-0709-y
Bai JF, Wang YK, Wang P et al (2018) Genome-wide identification and analysis of the COI gene family in wheat (*Triticum aestivum* L.). BMC Genom 19:754. https://doi.org/10.1186/s12864-018-5116-9
Bailey TL, Boden M, Buske FA et al (2009) MEME Suite: tools for motif discovery and searching. Nucleic Acids Res. https://doi.org/10.1093/nar/gkp335
Betsiashvili M, Ahern KR, Jander G (2015) Additive effects of two quantitative trait loci that confer *Rhopalosiphum maidis* (corn leaf aphid) resistance in maize inbred line Mo17. J Exp Bot 66:571–578. https://doi.org/10.1093/jxb/eru379
Block AK, Vaughan MM, Schmelz EA, Christensen SA (2018) Biosynthesis and function of terpenoid defense compounds in maize (*Zea mays*). Planta 249:21–30. https://doi.org/10.1007/s00425-018-2999-2
Bohlmann J, Keeling CI (2010) Terpenoid biomaterials. Plant J 54:656–669. https://doi.org/10.1111/j.1365-313X.2008.03449.x
Bohlmann J, Meyer-Gauen G, Croteau R (1998) Plant terpenoid synthases: molecular biology and phylogenetic analysis. Proc Natl Acad Sci USA 95:4126–4133. https://doi.org/10.1073/pnas.95.8.4126
Brillada C, Nishihara M, Shimoda T, Garms S, Boland W, Maffei ME, Arimura G (2013) Metabolic engineering of the C16 homoterpene TMTT in *Lotus japonicus* through overexpression of (E,E)-geranyllinalool synthase attracts generalist and specialist predators in different manners. New Phytol 200:1200–1211. https://doi.org/10.1111/nph.12442
Chen F, Tholl D, Bohlmann J, Pichersky E (2011) The family of terpene synthases in plants: a mid-size family of genes for specialized metabolism that is highly diversified throughout the kingdom. Plant J 66:212–229. https://doi.org/10.1111/j.1365-313x.2011.04520.x
Christianson DW (2006) Structural biology and chemistry of the terpenoid cyclases. Chem Rev 106:3412–3442. https://doi.org/10.1021/cr050286w
Degenhardt J, Köllner TG, Gershenzon J (2009) Monoterpene and sesquiterpene synthases and the origin of terpene skeletal diversity in plants. Phytochemistry 70:1621–1637. https://doi.org/10.1016/j.phytochem.2009.07.030
Dudareva N (2003) (E)-beta-ocimene and myrcene synthase genes of floral scent biosynthesis in snapdragon: function and expression of three terpene synthase genes of a new terpene synthase subfamily. Plant Cell 15:1227–1241. https://doi.org/10.1105/tpc.011015
Falara V, Akhtar TA, Nguyen TT et al (2011) The tomato terpene synthase gene family. Plant Physiol 157:770–789. https://doi.org/10.1104/pp.111.179648
Finn RD, Tate J, Mistry J et al (2008) The Pfam protein families database. Nucleic Acids Res 32:D138. https://doi.org/10.1093/nar/gkh121
Gershenzon J, Dudareva N (2007) The function of terpene natural products in the natural world. Nat Chem Biol 3:408–414. https://doi.org/10.1038/nchembio.2007.5
Glover NM, Daron J, Pingault L, Vandepoele K, Paux E, Feuillet C, Choulet F (2015) Small-scale gene duplications played a major role in the recent evolution of wheat chromosome 3B. Genome Biol 16:188. https://doi.org/10.1186/s13059-015-0754-6
Goff SA, Ricke D, Lan TH et al (2002) A draft sequence of the rice genome (*Oryza sativa* L. ssp. Japonica). Science 296:92–100.https://www.jstor.org/stable/3076391
Guo AY, Zhu QH, Chen X, Luo JC (2007) GSDS: a gene structure display server. Hereditas (Beijing) 29:1023–1026. https://doi.org/10.1360/yc-007-1023
Harborne JB (1991) Recent advances in the ecological chemistry of plant terpenoids. In: Harborne JB, Tomas-Barberan FA (eds)

Ecological chemistry and biochemistry of plant terpenoids. Clarendon Press, Oxford, pp 399–426
Holub EB (2001) The arms race is ancient history in *Arabidopsis*, the wildflower. Nat Rev Genet 2:516–527. https://doi.org/10.1038/35080508
Hu B, Jin JP, Guo AY, Zhang H, Luo JC, Gao G (2014) GSDS 2.0: an upgraded gene feature visualization server. Bioinformatics 31:1296. https://doi.org/10.1093/bioinformatics/btu817
Huang XS, Li KQ, Xu XY, Yao ZH, Jin C, Zhang SL (2015) Genome-wide analysis of WRKY transcription factors in white pear (*Pyrus bretschneideri*) reveals evolution and patterns under drought stress. BMC Genom 16:1104. https://doi.org/10.1186/s12864-015-2233-6
Huang XZ, Xiao YT, Köllner TG et al (2018) The terpene synthase gene family in *Gossypium hirsutum* harbors a linalool synthase GhTPS12 implicated in direct defence responses against herbivores. Plant Cell Environ 41:261–274. https://doi.org/10.1111/pce.13088
Hyatt DC, Youn B, Zhao Y, Santhamma B, Coates RM, Croteau RB, Kang C (2007) Structure of limonene synthase, a simple model for terpenoid cyclase catalysis. Proc Natl Acad Sci USA 104:5360–5365. https://doi.org/10.1073/pnas.0700915104
Irmisch S, Krause ST, Kunert G, Gershenzon J, Degenhardt J, Köllner TG (2012) The organ-specific expression of terpene synthase genes contributes to the terpene hydrocarbon composition of chamomile essential oils. BMC Plant Biol 12:84. https://doi.org/10.1186/1471-2229-12-84
Irmisch S, Mccormick AC, Günther J et al (2014a) Herbivore-induced poplar cytochrome P450 enzymes of the CYP71 family convert aldoximes to nitriles which repel a generalist caterpillar. Plant J 80:1095–1107. https://doi.org/10.1111/tpj.12711
Irmisch S, Jiang Y, Chen F, Gershenzon J, Köllner TG (2014b) Terpene synthases and their contribution to herbivore-induced volatile emission in western balsam poplar (*Populus trichocarpa*). BMC Plant Biol 4:270. https://doi.org/10.1186/s12870-014-0270-y
Keeling CI, Bohlmann J (2006) Genes, enzymes and chemicals of terpenoid diversity in the constitutive and induced defence of conifers against insects and pathogens*. New Phytol 170:657–675. https://doi.org/10.1111/j.1469-8137.2006.01716.x
Keeling CI, Weisshaar S, Ralph SG, Jancsik S, Hamberger B, Dullat HK, Bohlmann J (2011) Transcriptome mining, functional characterization, and phylogeny of a large terpene synthase gene family in spruce (*Picea* spp.). BMC Plant Biol 11:43. https://doi.org/10.1186/1471-2229-11-43
Kessler A (2001) Defensive function of herbivore-induced plant volatile emissions in nature. Science 291:2141–2144. https://doi.org/10.1126/science.291.5511.2141
Kiryu M, Hamanaka M, Yoshitomi K, Mochizuki S, Akimitsu K, Gomi K (2018) Rice terpene synthase 18 (OsTPS18) encodes a sesquiterpene synthase that produces an antibacterial (E)-nerolidol against a bacterial pathogen of rice. J Gen Plant Pathol 84:221–229. https://doi.org/10.1007/s10327-018-0774-7
Köllner TG, Schnee C, Gershenzon J, Degenhardt J (2004) The variability of sesquiterpenes emitted from two *Zea mays* cultivars is controlled by allelic variation of two terpene synthase genes encoding stereoselective multiple product enzymes. Plant Cell 16:1115–1131. https://doi.org/10.1105/tpc.019877
Köllner TG, Held M, Lenk C, Hiltpold I, Turlings TCJ, Gershenzon J, Degenhardt J (2008) A maize (E)-beta-caryophyllene synthase implicated in indirect defense responses against herbivores is not expressed in most American maize varieties. Plant Cell 20:482–494. https://doi.org/10.1105/tpc.107.051672
Krzywinski M, Schein J, Birol I (2009) Circos: an information aesthetic for comparative genomics. Genome Res 19:1639–1645. https://doi.org/10.1101/gr.092759.109
Lescot M, Déhais P, Thijs G et al (2002) PlantCARE, a database of plant *cis*-acting regulatory elements and a portal to tools for in silico analysis of promoter sequences. Nucleic Acids Res 30:325–327. https://doi.org/10.1093/nar/30.1.325
Li FQ, Li W, Lin YJ, Pickett JA, Birkett MA, Wu K, Wang G, Zhou JJ (2017) Expression of lima bean terpene synthases in rice enhances recruitment of a beneficial enemy of a major rice pest. Plant Cell Environ 41:111–120. https://doi.org/10.1111/pce.12959
Liu D, Huang X, Jing W et al (2017) Identification and functional analysis of two P450 enzymes of *Gossypium hirsutum*, involved in DMNT and TMTT biosynthesis. Plant Biotechnol J. https://doi.org/10.1111/pbi.12797
Lynch M, Conery JS (2000) The evolutionary fate and consequences of duplicate genes. Science 290:1151–1155. https://doi.org/10.1126/science.290.5494.1151
Ma R, Chen JL, Cheng DF, Sun JR (2010) Activation of defense mechanism in wheat by polyphenol oxidase from aphid saliva. J Agric Food Chem 58:2410–2418. https://doi.org/10.1021/jf9037248
Ma J, Yang YJ, Wei L et al (2017) Genome-wide identification and analysis of the MADS-box gene family in bread wheat (*Triticum aestivum* L.). PLoS ONE 12:e0181443. https://doi.org/10.1371/journal.pone.0181443
Martin DM, Fäldt J, Bohlmann J (2004) Functional characterization of nine Norway spruce TPS genes and evolution of gymnosperm terpene synthases of the TPS-d subfamily. Plant Physiol 135:1908–1927. https://doi.org/10.1104/pp.104.042028
Martin DM, Aubourg S, Schouwey MB et al (2010) Functional annotation, genome organization and phylogeny of the grapevine (*Vitis vinifera*) terpene synthase gene family based on genome assembly, FLcDNA cloning, and enzyme assays. BMC Plant Biol 10:226. https://doi.org/10.1186/1471-2229-10-226
Mccormick AC, Unsicker SB, Gershenzon J (2012) The specificity of herbivore-induced plant volatiles in attracting herbivore enemies. Trends Plant Sci 17:303–310. https://doi.org/10.1016/j.tplants.2012.03.012
Miller DJ, Allemann RK (2012) Sesquiterpene synthases: passive catalysts or active players? Nat Prod Rep 29:60–71. https://doi.org/10.1039/C1NP00060H
Moore RC, Purugganan MD (2005) The evolutionary dynamics of plant duplicate genes. Curr Opin Plant Biol 8:122–128. https://doi.org/10.1016/j.pbi.2004.12.001
Nieuwenhuizen NJ, Green SA, Chen X, Bailleul EJ, Matich AJ, Wang MY, Atkinson RG (2013) Functional genomics reveals that a compact terpene synthase gene family can account for terpene volatile production in apple. Plant Physiol 161:787–804. https://doi.org/10.1104/pp.112.208249
Ning P, Liu CC, Kang JQ (2017) Genome-wide analysis of WRKY transcription factors in wheat (*Triticum aestivum* L.) and differential expression under water deficit condition. PeerJ 5:e3232. https://doi.org/10.7717/peerj.3232
O'Maille PE, Malone A, Dellas N et al (2008) Quantitative exploration of the catalytic landscape separating divergent plant sesquiterpene synthases. Nat Chem Biol 4:617–623. https://doi.org/10.1038/nchembio.113
Ozawa R, Arimura G, Takabayashi J, Shimoda T, Nishioka T (2000) Involvement of jasmonate- and salicylate-related signaling pathways for the production of specific herbivore-induced volatiles in plants. Plant Cell Physiol 41:391–398. https://doi.org/10.1093/pcp/41.4.391
Paterson AH, Bowers JE, Bruggmann R et al (2009) The *Sorghum bicolor* genome and the diversification of grasses. Nature 457:551–556. https://doi.org/10.1038/nature07723
Pichersky E, Gershenzon J (2002) The formation and function of plant volatiles: perfumes for pollinator attraction and defense. Curr Opin Plant Biol 5:237–243. https://doi.org/10.1016/S1369-5266(02)00251-0

Pichersky E, Noel JP, Dudareva N (2006) Biosynthesis of plant volatiles: nature's diversity and ingenuity. Science 311:808–811. https://doi.org/10.1126/science.1118510
Popper ZA, Michel G, Hervé C et al (2011) Evolution and diversity of plant cell walls: from algae to flowering plants. Annu Rev Plant Biol 62:567–590. https://doi.org/10.1146/annurev-arplant-042110-103809
Prisic S, Xu J, Coates RM, Peters RJ (2007) Probing the role of the DXDD motif in Class II diterpene cyclases. ChemBioChem 8:869–874. https://doi.org/10.1002/cbic.200700045
Richter A, Seidl-Adams I, Köllner TG, Schaff C, Tumlinson JH, Degenhardt J (2015) A small, differentially regulated family of farnesyl diphosphate synthases in maize (*Zea mays*) provides farnesyl diphosphate for the biosynthesis of herbivore-induced sesquiterpenes. Planta 241:1351–1361. https://doi.org/10.1007/s00425-015-2254-z
Richter A, Schaff C, Zhang Z et al (2016) Characterization of biosynthetic pathways for the production of the volatile homoterpenes DMNT and TMTT in *Zea mays*. Plant Cell. https://doi.org/10.1105/tpc.15.00919
Starks CM, Back K, Chappell J, Noel JP (2010) Structural basis for cyclic terpene biosynthesis by tobacco 5-epi-aristolochene synthase. Science 29:1815–1820. https://doi.org/10.1002/chin.199804171
Sun Y, Huang XZ, Ning YS et al (2017) TPS46, a rice terpene synthase conferring natural resistance to bird cherry-oat aphid, *Rhopalosiphum padi* (Linnaeus). Front Plant Sci. https://doi.org/10.3389/fpls.2017.00110
Tholl D (2006) Terpene synthases and the regulation, diversity and biological roles of terpene metabolism. Curr Opin Plant Biol 9:297–304. https://doi.org/10.1016/j.pbi.2006.03.014
Trapp SC, Croteau RB (2001) Genomic organization of plant terpene synthases and molecular evolutionary implications. Genetics 158:811–832. https://doi.org/10.0000/PMID11404343
Tuskan GA, Difazio S, Jansson S et al (2006) The genome of black cottonwood, *Populus trichocarpa* (Torr. & Gray). Sci 313:1596–1604. https://doi.org/10.1126/science.1128691
Voorrips RE (2002) MapChart: software for the graphical presentation of linkage maps and QTLs. J Hered 93:77–78. https://doi.org/10.1093/jhered/93.1.77
Wang XY, Shi XL, Hao BL, Ge S, Luo JC (2005) Duplication and DNA segmental loss in the rice genome: implications for diploidization. New Phytol 165:937–946. https://doi.org/10.1111/j.1469-8137.2004.01293.x
Wang YP, Tang HB, Debarry JD et al (2012) MCScanX: a toolkit for detection and evolutionary analysis of gene synteny and collinearity. Nucleic Acids Res 40:e49. https://doi.org/10.1093/nar/gkr1293
Warren RL, Keeling CI, Yuen MMS et al (2015) Improved white spruce (*Picea glauca*) genome assemblies and annotation of large gene families of conifer terpenoid and phenolic defense metabolism. Plant J 83:189–212. https://doi.org/10.1111/tpj.12886
Yoshikuni Y, Ferrin TE, Keasling JD (2006) Designed divergent evolution of enzyme function. Nature 440:1078–1082. https://doi.org/10.1038/nature04607
Zebelo S, Song YY, Kloepper JW, Fadamiro H (2016) Rhizobacteria activates (+)-δ-cadinene synthase genes and induces systemic resistance in cotton against beet armyworm (*Spodoptera exigua*). Plant Cell Environ 39:935–943. https://doi.org/10.1111/pce.12704
Zhan HS, Hong Y, Zhao X, Wang M, Weining S, Nie XJ (2017) Genome-wide identification and analysis of MAPK and MAPKK gene families in bread wheat (*Triticum aestivum* L.). Genes. https://doi.org/10.3390/genes8100284
Zhang Y, Li ZX, Yu XD et al (2015) Molecular characterization of two isoforms of a farnesyl pyrophosphate synthase gene in wheat and their roles in sesquiterpene synthesis and inducible defence against aphid infestation. New Phytol 206:1101–1115. https://doi.org/10.1111/nph.13302
Zhang Y, Hu L, Yu D et al (2019) Integrative analysis of the wheat *PHT1* gene family reveals a novel member involved in arbuscular mycorrhizal phosphate transport and immunity. Cells. https://doi.org/10.3390/cells8050490
Zhu Y, Wu NN, Song WL, Yin GJ, Qin YJ, Yan YM, Hu YK (2014) Soybean (*Glycine max*) expansin gene superfamily origins: segmental and tandem duplication events followed by divergent selection among subfamilies. BMC Plant Biol 14:93. https://doi.org/10.1186/1471-2229-14-93
Zimin AV, Puiu D, Hall R, Kingan S, Clavijo BJ, Salzberg SL (2017) The first near-complete assembly of the hexaploid bread wheat genome, *Triticum aestivum*. GigaScience 6:1–7. https://doi.org/10.1093/gigascience/gix097

Publisher's Note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Similar research

The terpene synthase gene family in Gossypium hirsutum harbors a linalool synthase GhTPS12 implicated in direct defense responses against herbivores
Article · Full-text available · October 2017 · 500 Reads · 82 Citations
Plant Cell and Environment
XinZheng Huang · Yutao Xiao · Tobias Köllner · [...] · Yu-yuan Guo
Herbivore-induced terpenes have been reported to function as ecological signals in plant-insect interactions. Here we showed that insect-induced cotton volatile blends contained 16 terpenoid compounds with a relatively high level of linalool. The high diversity of terpene...
Read more
View

Terpene Synthase Gene OtLIS Confers Wheat Resistance to Sitobion avenae by Regulating Linalool Emission
Article · November 2021 · 55 Reads · 6 Citations
Journal of Agricultural and Food Chemistry
Yidi Zhan · Lei Zhao · Xiaojing Zhao · [...] · Yong Liu
View

Genome-wide analysis of terpene synthases in soybean: Functional characterization of GmTPS3
Article · July 2014 · 197 Reads · 37 Citations
Gene
Jianyu Liu · Fang Huang · Xia Wang · [...] · Deyue Yu
Terpenes (terpenoids or isoprenoids) constitute a large class of plant natural products and play numerous functional roles in primary and secondary metabolism as well as inecological interactions. This study presents a genomic analysis of 23 putative soybean (Glycine max)...
Read more
View

Genome-wide identification and characterization of terpene synthase genes in Gossypium hirsutum
Article · April 2022 · 23 Reads · 10 Citations
Gene
Cui-Ping Zhang · Jin-Li Zhang · Zheng-Ran Sun · [...] · Daohua He
Terpenoids are widely distributed in plants and play important roles in the regulation of plant growth and development and in the interactions between plants and both the environment and other organisms. However, terpene synthase (TPS) genes have not been systematically...
Read more
View

Functional characterization of (E)-β-caryophyllene synthase from lima bean and its up-regulation by spider mites and alamethicin
Article · April 2017 · 122 Reads · 7 Citations
Journal of Integrative Agriculture
Fengqi li · Ningning Fu · Jing-Jiang Zhou · Guirong Wang
E)-β-Caryophyllene is a sesquiterpene compound widely distributed in plants and functions in plant defence. However, little is known about the sequence and function of (E)-β-caryophyllene synthase in lima bean (Phaseolus lunatus). Here, we report a new full-length...
Read more
View

AHF analysentechnik AG
Quality Monitoring in Fluorescence Imaging
Check and correct your fluorescence imaging system with Argolight monitoring tools.
Learn more

ResearchGate
Company: About us · Blog · Careers
Resources: Help Center · Contact us
Business Solutions: Marketing Solutions · Scientific Recruitment · Publisher Solutions
Download on the App Store · GET IT ON Google Play

© 2008-2025 ResearchGate GmbH. All rights reserved.
Terms · Privacy · Copyright · Imprint · Consent preferences