

TERPNET 2015 Poster Abstracts

Poster Number	Title	Abstract	Topic	Author	Author Company	Co-Authors
9	One amino acid makes the difference: The formation of ent-kaurene and 16 α -hydroxy-ent-kaurene in poplar	<p>Labdane-related diterpenoids form the largest group among the diterpenes and fulfill important functions in primary as well as in secondary metabolism. The biosynthesis of labdane-related diterpenes is mediated through the action of class II and class I terpene synthases. Although terpene synthases have been well investigated in poplar, little is known about diterpene formation in this woody perennial plant species.</p> <p>The recently sequenced genome of <i>Populus trichocarpa</i> possesses two putative copalylidiphosphate synthase genes (PtTPS17, PtTPS18) and two putative kaurene synthase genes (PtTPS19, PtTPS20), most likely arisen through a genome duplication and a recent tandem gene duplication, respectively. We could show that PtTPS17 and PtTPS19 mediated the production of ent-copalylidiphosphate (ent-CPP) and ent-kaurene, respectively, the precursors for gibberellin biosynthesis. Despite high sequence similarity to PtTPS19, the kaurene synthase-like enzyme PtTPS20 converted ent-CPP into the diterpene alcohol 16α-hydroxy-ent-kaurene. Using homology-based structure modeling and site-directed mutagenesis we could demonstrate that one amino acid side chain determined the different product specificity of PtTPS19 and PtTPS20. The biological role of 16α-hydroxy-ent-kaurene in poplar is not known yet. However, the high expression levels of PtTPS20 and PtTPS17 in developing fruits suggest an important</p>	Biosynthesis: Central Steps	Irmisch, Sandra	Max Planck Institute for Chemical Ecology	Müller, Andrea T.; Schmidt, Lydia; Gershenzon, Jonathan; Köllner, Tobias G.
10	Biochemical and molecular analysis of <i>Coffea arabica</i> to identify candidate genes related to diterpenes biosynthesis	<p>Coffee is consumed by more than 800 million people who enjoy its taste, flavor, and health benefits. Cafestol (CAF) and kahweol (KAH) are two diterpenes found exclusively in the <i>Coffea</i> genus. It has been suggested that CAF/KAH are initially produced in the perisperm of the developing fruit, and after maturation they accumulate in the endosperm. Several nutraceutical effects on human health are described for CAF/KAH, such as antioxidant, anticarcinogenic and anti-inflammatory properties. However, studies also suggest that CAF may also increase cholesterol levels in blood, highlighting the importance of understanding their biosynthesis and functions. We used an integrated analysis of CAF/KAH metabolite accumulation and gene expression analyses during fruit development to identify the dTPS and P450 genes responsible for CAF/KAH biosynthesis in <i>Coffea arabica</i>. The expression of several class II dTPS and P450 families showed a strong correlation with CAF/KAH profiles and were selected for cloning, and functional characterization. This study aims to unravel the genes involved in CAF/KAH biosynthesis and provide the tools for manipulating CAF/KAH levels in coffee beans. It will also open the possibility to develop plants with desirable CAF/KAH content and improve beverage quality focusing on human health.</p>	Biosynthesis: Central Steps	Ivamoto, Suzana	University of British Columbia/Universidade Estadual de Londrina	Celedón, José; Yuen, Macaire; Domingues, Douglas; Pereira, Luiz; Bohlmann, Jörg
11	Next-generation sequencing and transcriptome analysis-based isolation of terpene synthases in <i>Piper nigrum</i>	<p>Black pepper is one of the most popular spices in the world used from antiquity. It has been used in cooking and traditional medicine for its antioxidative, anticancer, and anti-inflammatory activities. RNA was isolated from unripen fruit of pepper corn and was submitted to transcriptome analysis utilizing Illumina next-generation sequencing. Fifty five million readings of 90 base-pair resulted in assembly of 119,354 contigs. The contigs yielded of 66,787 unigenes and functional annotation was done against TAIR10 (<i>Arabidopsis</i>). Using NCBI Local tBLASTn with published terpene synthase as query, we found twenty unigenes annotated as sesquiterpene synthases, among which two clones were obtained by PCR. The genes were expressed in the engineered yeast to produce caryophyllene and cadina-4,11-diene, respectively, as the main product. These transcriptome data thus provided the molecular basis of identifying genes involved in the biosynthesis of sesquiterpenoids in black pepper.</p> <p>Keywords: transcriptome, <i>Piper nigrum</i>, sesquiterpene synthase</p> <p>Acknowledgement: This work was supported by a grant from the Next-Generation BioGreen 21 Program (Systems and Synthetic Agrobiotech Center Grant No. PJ011055012015), Rural Development Administration, Republic of Korea.</p>	Biosynthesis: Central Steps	Jin, Zhehao	Seoul National University	Lee, Ah-Reum; Kwon, Moonhyuk; Ro, Dae-Kyun; Kim, Soo-Un
12	White spruce draft genome reveals the diversity of terpene synthase and cytochrome P450 gene families	<p>Draft genome sequences of three conifer species have recently been released*. Although genome assembly contiguity is far from being optimal in these 20 gigabase genomes, they have permitted the genome-wide examination of the terpene synthase and cytochrome P450 gene families. Using a combination of available transcriptomic and genomic sequence resources in white spruce (<i>Picea glauca</i>), we obtained a manually-curated set of non-redundant genes with at least 400 amino acids of coding sequence in these gene families. We annotated 83 TPSs, including 28 putative pseudogenes, and 307 P450s, including 43 putative pseudogenes. TPSs in hemiterpene, monoterpene, sesquiterpene, and diterpene biosynthesis were identified but monoterpene and sesquiterpene synthases were most numerous. Many of these, particularly the sesquiterpene synthases, have not previously been functionally characterized in conifers. Over 10% of the P450s identified are predicted to be involved in the functionalization of terpenoids in general and specialized metabolism. Together, these annotations provide a valuable resource for understanding the evolution of functional diversity of terpenoids in conifers.</p> <p>*Birol I, et al. (2013) <i>Bioinformatics</i> 29(12):1492-1497. Nystedt B, et al. (2013) <i>Nature</i> 497(7451):579-584. Neale DB, et al. (2014) <i>Genome Biol.</i> 15(3):R59. Warren RL, et al. (2015) <i>Plant J.</i> submitted.</p>	Biosynthesis: Central Steps	Keeling, Christopher	University of British Columbia	Yuen, Macaire; Nelson, David; Bohlmann, Joerg