9. 
Title: One amino acid makes the difference: The formation of escin-kaurene and 15a-hydroxy-ent-kaurene in poplar
Abstract: 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. The recently sequenced genome of Populus trichocarpa possesses two putative cysAliphosphophoryl synthase genes (PTPS17, PTPS18) and two putative kaurene synthase genes (PTPS17, PTPS20), most likely arisen through a genome duplication and a recent tandem gene duplication, respectively. We could show that PTPS17 and PTPS19 mediated the production of escinophyllophonate (ext-ACP) and escin, respectively, the precursors for gibberellic biosynthesis. Despite high sequence similarity to PTPS19, the kauren synthase-like enzyme PTPS20 converted ext-ACP into the diterpene alcohol 15α-hydroxy-ent-kaurene. Living homology-based structure modeling and site-directed mutagenesis we could demonstrate that one amino acid side chain determined the different product specificity of PTPS19 and PTPS20. The biological role of 15α-hydroxy-ent-kaurene in poplar is not known yet. However, the high expression of ext-ACP and escinophyllolactone synthase (ESO) genes points towards an important role of this diterpene in poplar.

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10. 
Title: Biochemical and molecular analysis of Coffea arabica to identify candidate genes related to diterpenoid biosynthesis
Abstract: Coffee is consumed by more than 600 million people in the world daily. It is known that two diterpene alcohols, 15α-hydroxy-ent-kaurene and 15α-hydroxy-ent-kaurene, are the diterpenoids found exclusively in the Coffea genus. It has been suggested that CAF-KAH are initially produced in the pericarp of the developing fruit, and after maturation they accumulate in the endosperm. Several nontargeted effects on human health are described for CAF-KAH, such as antioxidant, anti-inflammatory and anti-microbial 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 GTIPS and F450 genes responsible for CAF-KAH biosynthesis in Coffea arabica. The expression of several class II GTIPS and F450 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.

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11. 
Title: Next-generation sequencing and transcriptome analysis-based isolation of terpene synthases in Piper nigrum
Abstract: Black pepper is one of the most popular spices in the world used for its pungency. It has been used in cooking and traditional medicine for its antiseptic, anti-inflammatory and anti-inflammatory properties. RNA was isolated from unripe fruit of pepper corn and was submitted to transcriptome analysis by Illumina next-generation sequencing. Fifty-five million reads of 101 bases-pair resulted in assembly of 119,354 contigs, the contigs yielded 65,787 unigenes and functional annotation was done through KEGG (Anakloplia). Using NOCBL and BLASTx with published terpene synthase query, we found ten unigenes annotated as sesquiterpene synthases, among which two were obtained by PCR. The genes were expressed in engineered yeast and identified by GC-MS and GC-MS-TOF, respectively, as the main product. The genome database thus provides the molecular basis of identifying genes involved in the biosynthesis of sesquiterpenoids in black pepper.

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12. 
Title: Draft genome sequences of three conifer species have recently been released
Abstract: Draft genome sequences of three conifer species have recently been released. Although genome assembly is far from being optimal in these 20-28 gigabase genomes, they have permitted the genome-wide examination of the terpene synthase and cycloartenol P450 gene families. Using a combination of available transcriptome and genome sequence resources in white pine (Pinus glauca), 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 polyketoid, and 307 P450s, including 43 putative polyketoid, TPSs in hemiterpene, monoterpenes, 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.

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