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P0822 Investigating the novel sesquiterpene biosynthesis pathway in *Copaifera officinalis*, 'the diesel tree,' through next-generation de novo transcriptome sequencing and functional genomics

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Trees in the genus *Copaifera* produce a sesquiterpene-rich oleoresin that has been used as traditional medicine, food and cosmetics, and even as a biofuel, leading to the common name 'diesel trees.' While sesquiterpene biosynthesis is common in plants, these unique trees can produce liters of sesquiterpenes. Investigating the entire sesquiterpene biosynthesis pathway and associated precursor pathways present in *Copaifera* trees could lead to a greater understanding of this unique phenotype. In specific, it is unclear if these trees respond to biotic stress or wounding by up-regulating terpenoid biosynthesis; or whether the large quantities of sesquiterpenes are a result of specialized storage and/or unique biosynthesis characteristics. Solexa (Illumina) next-generation transcriptome sequencing was performed on mRNA isolated from *C. officinalis* leaf and stem tissue. Reads were assembled using either the CLC bio genomics or Velvet, and annotated using the Kyoto Encyclopedia of Genes and Genomes (KEGG) and Gene Ontology (GO). Six putative terpene synthase transcripts were identified by BLAST similarity to known sesquiterpene synthases and conserved domain motifs (CDD NCBI), cloned, and expressed in recombinant *Escherichia coli* for functional characterization. As *C. officinalis* oleoresin and tissues contain primarily sesquiterpenes, putative mevalonic acid (MVA), sesquiterpene precursor biosynthesis, and 2-C-methyl-D-erythritol 4-phosphate (MEP) transcripts were assembled and transcripts present in tissues were quantified using qPCR. In conclusion, *de novo* transcriptome sequencing allowed for rapid identification and characterization of genes associated with two metabolic pathways. We can now test hypotheses associated with the entire terpene metabolic pathway in *C. officinalis* instead of single genes.

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