

Genomic characterization of terpene biosynthetic genes in seven *Vitis vinifera* L. varieties

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Abstract (250 words)

Grapes (*Vitis vinifera* L.) are a fruit crop of high economic significance globally. Each grapevine cultivar is characterized by its distinctive grape aroma, affecting the wine quality. In several cultivars, the aroma is shaped by terpenoid (mono- and sesqui-terpenoids). Their profile is controlled by terpene synthases (TPS), which are part of a largely expanded gene family. How the variation in TPS copy number and sequence among cultivars determines terpenoid profiles of grapes remains largely unexplored. We annotated TPS in the haplotypes of seven genomes (Riesling, Albariño, Fiano, Gewürztraminer, Pinot Noir, Cabernet Sauvignon, and Viognier) using BLAST, GMAP, PFAM, and phylogenetic analyses. Further, TPS expression patterns and terpenoid accumulation during berry development and ripening were characterized using RNA-Seq and SPME/GC-MS platforms, respectively. Variation in TPS copy number exists among cultivars. Specifically, the TPS counts span a range of 251 to 150 for Riesling and Fiano, respectively, when considering combined haplotypes within each cultivar. Total terpenoid accumulation patterns throughout development were consistent among the five aromatic cultivars, marked by high concentrations in flowers, followed by a decline and subsequent rise during berry development and ripening, respectively. Conversely, non-aromatic cultivars exhibited no substantial increase in terpenoid concentration during ripening. Transcriptome and network analyses are currently employed to determine which TPS are expressed in the berry and determine the terpenoid profile of the specific cultivar. These findings shed light on the genomic determinants of grape aroma in major cultivars, and allow future studies focused on cultivar-specific responses of terpenoid biosynthesis to environmental stresses.

Keywords: aroma, grapes, transcriptomics, metabolomics, development