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# Understanding the expression of gene families involved in anthocyanin biosynthesis during berry ripening: Tannat as a case study.

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## Abstract (250 words)

The quality of wine is assessed, among other things, by its color, which is mainly due to its anthocyanin content. These pigments are polyphenols that give red, purple and blue hues depending on the relative proportion of anthocyanins produced by the action of flavonoid 3'5' hydroxylase (delphinidin-3-glucoside, petunidin-3-glucoside, malvidin-3-glucoside) or flavonoid 3' hydroxylase (cyanidin-3-glucoside, peonidin-3-glucoside). To study the genes involved in this biosynthetic pathway, we focused on Vitis vinifera cv. Tannat, known for producing wines with higher anthocyanin content and darker purple color compared to most red grape varieties. In this work, we have performed RNA-Seq analysis of skins during berry development, taking green and red berries at 50% veraison as separate samples, as an experimental strategy to focus on the differential expression of genes of interest. Several novel (not previously annotated in the Pinot noir reference genome PN40024 12X) and varietal (not in the reference genome) genes showed differential expression associated with color change during veraison. Expression of a novel F3'5'H gene and a varietal F3'H gene was confirmed by RT-qPCR in the same samples used for RNA-Seq and in another growing season. This work establishes the specific expression fingerprint for gene families (CHS, CHI, F3H, F3'H, F3'5'H, DFR, LDOX, 3GT, OMT, MYBA1, MYBA2, MYBA3) directly involved in anthocyanin biosynthesis and regulation during Tannat veraison.

**Keywords:** Anthocyanins, *Vitis vinifera*, Tannat, RNA-Seq.