# Altered lignans accumulation in a somatic variant of Tempranillo with increased extractability of polyphenols during winemaking

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## Abstract

Vegetative propagation of grapevines can generate spontaneous somatic variations, providing a valuable source for cultivar improvement. In this context, natural variation in the composition of phenolic compounds in grapevine berries and seeds stands as a pivotal factor in crafting wines with diverse oenological profiles from the same cultivar. To deepen on the understanding of the physiological and genetic mechanisms driving somatic variation in grape phenolics, here we characterized a somatic variant from Tempranillo Tinto, the clone VN21, that exhibits an intense reduced berry skin cuticle and increased extractability of phenolic compounds during wine fermentation. Furthermore, VN21 seeds exhibit anomalous development characterized by diminished lignification, substantial anthocyanin accumulation, and an inherent inability to germinate. Transcriptomic analysis identified alterations in the phenylpropanoid biosynthesis pathway, outstanding the down-regulation of a secoisolariciresinol dehydrogenase and the up-regulation of a pinorenisol-lariciresinol reductase genes in the berry skin of VN21 compared to the reference Tempranillo Tinto clone RJ43 at veraison stage. These genes encode enzymes in the lignans branch of the phenylpropanoids pathway that are compounds that can potentially reduce the risk of certain cancers and cardiovascular diseases. Ultra-performance liquid chromatography (UPHLC) analysis in both berry skin and seed confirmed a distinct phenylpropanoid accumulation pattern between VN21 and RJ43, with an overall reduction in the accumulation of lignan compounds in VN21.

The results obtained not only contribute to understand grapevine berry development and phenolic composition but also present opportunities for targeted breeding strategies aimed at enhancing desirable traits for wine production.

**Keywords:** somatic variation, lignans, berry color, UPHLC, RNA-seq.