

Reduced berry skin epi-cuticular wax and cutin accumulation associates with a genomic deletion and increased polyphenols extractability in a clone of Tempranillo Tinto

Carolina Royo^{1*}, Yolanda Ferradás^{1,2}, Robin Bosman³, Fernando Alba-Elías⁴, Javier Ibáñez¹, Justin Lashbrooke³, José Miguel Martínez-Zapater¹, Pablo Carbonell-Bejerano¹

¹ Instituto de Ciencias de la Vid y del Vino, Finca La Grajera, Ctra. de Burgos Km. 6, 26007 Logroño. Spain

² Current address: Facultad de Biología, Universidad de Santiago de Compostela, 15872 Santiago de Compostela. Spain

³ South African Grape and Wine Research Institute, Stellenbosch University, Stellenbosch, South Africa.

⁴ Universidad de La Rioja, Departamento de Ingeniería Mecánica, Logroño, Spain.

*Corresponding author: carolina.royo@icvv.es

Abstract

Tempranillo Tinto (TT) is the third-most planted red wine variety in the world, and it is mostly grown in the Iberian Peninsula. Spontaneous somatic variation appearing during vegetative propagation can be exploited to improve elite varieties as Tempranillo Tinto, including the selection of new phenotypes enhancing berry quality. We described previously that a somatic variant of TT with darker fruit color, the clone VN21, exhibits increased extractability of polyphenols during the winemaking process. To unravel the molecular mechanism underlying this phenomenon, we performed whole-genome resequencing to compare VN21 to other TT clones, revealing a 10 Mb deletion in chromosome 11 that likely affected only the L1 meristem cell layer of VN21 and tissues derived from it, such as external cell layers of berry skin. A putative loss-of-function allele of an *ABCG32* gene (homologous to cuticle biogenesis transporters), was left hemizygous in this segment after the deletion in VN21. Scanning electron microscopy images suggested a lower content epi-cuticular wax in the berry cuticle of VN21, which likely leads to the shiny colour of VN21 berries. A GC-MS analysis of epi-cuticular waxes and cutins extracted from berry skin and leaves confirmed a general decrease in the accumulation of cuticle constituent compounds in VN21, supporting a role for the mutated *ABCG32* transporter in the phenotype. Our findings show that somatic mutations altering berry cuticle biogenesis can have an effect on the extractability of polyphenols from the berry skin, which could be exploited for varietal wine innovation.

Keywords: somatic variation, whole genome resequencing, deletion, waxes, GC-MS.