

## Oral presentations

### A large chimeric deletion associates with impairment of cuticle development in a dark berry somatic variant of ‘Tempranillo Tinto’

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#### Abstract

Color intensity is a relevant feature for red wine quality, which depends on the accumulation of anthocyanins during berry ripening and their interaction with other compounds present in the wine. While grape color is a varietal feature, emerging spontaneous somatic variation for this trait can be selected for cultivar improvement. Here we studied the genomic origin of a darker berry clone (VN21) selected in ‘Tempranillo Tinto’ (TT) cultivar, which enables the production of wines with higher color intensity. Using a diploid genome assembly of TT produced following a trio binning approach from PacBio and Nanopore sequencing, and genome re-sequencing data of VN21 compared to other TT clones, we identified a 10 Mb deletion in chromosome 11 that likely affected only the L1 meristem cell layer of VN21. An RNA-seq analysis identified a general down-regulation of genes within the chimeric hemizygous segment in the berry skin of VN21. Down-regulated genes were also enriched in wax biosynthesis functional category genes, including one *CER1* and one *ABCG32* homologs located in the hemizygous segment. SEM images showed that wax accumulation is impaired in the berry cuticle of VN21, which likely leads to the shiny color of VN21 berries. Candidate loss of function polymorphisms remaining hemizygous in VN21 after the chimeric deletion were also detected from TT haplotype comparison. Our findings show that very large hemizygous deletions can stabilize as periclinal chimeras in grapevine clones, giving rise to pleiotropic mutant phenotypes that can be exploited for cultivar innovation.

**Keywords:** berry color, berry wax cuticle, genome structural variation, somatic variation, ‘Tempranillo Tinto’