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ABSTRACT BOOK
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Characterization of deletions causing berry color variation in Garnacha and Tempranillo

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Gray and white somatic variants that can be the base of new cultivars occasionally appear in some black-berried grapevine cultivars. Genetic and molecular studies have associated color loss to the emergence of deletions at the grape color locus located on chromosome 2 in heterozygous colored cultivars carrying a functional and a null allele. Depending on the size of the deletions, side-effects adding to the loss of pigmentation capability may appear in these variants. In this study, we developed a SNP-based chip to evaluate along chromosome 2 the extension of hemizygous deletions in grape color variants through loss of heterozygosity analysis. These markers were used to characterize white and gray isolates originated from Garnacha Tinta and Tempranillo Tinto and collected along the Ebro valley (NE Spain). Two main deletion classes were detected in Garnacha Blanca correlating with the geographical origin of the accessions, while Tempranillo gray berry variants showed higher variation. Comparative genomics of Garnacha variants after whole-genome re-sequencing was addressed to understand the mutational mechanisms generating color variation. The results show that these deletions are generally associated with more complex genome rearrangements. Additional structural variation between independent lines of Garnacha Blanca likely emerged in different ancestral clonal lines of Garnacha Tinta. These results can be exploited for the selection of color variants best suited for the development of new cultivars and can help to detect rearrangement hotspots in the grapevine genome.

Keywords: berry color, color locus, deletions, genome structural variation, heterozygosity loss, somatic variation