

## Reduced bunch compactness in somatic variants of ‘Tempranillo’ relate to genome structural variation and the sex locus

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### Abstract

Grapevine cultivars are vegetatively propagated to keep their varietal attributes. Still, spontaneous somatic variation that emerges during long cycles of vegetative growth provides the opportunity for natural improvement of traditional grape cultivars. A lower bunch compactness is an advantageous trait for winegrowing as it decreases susceptibility to pests and fungal diseases and enables better adaptation to climate change by enabling a more homogeneous berry ripening. To understand the genetic and molecular mechanisms generating variation in bunch compactness, we studied here two somatic variants of Tempranillo Tinto cultivar that produce looser bunches. One of the somatic variants exhibits a male-like flower phenotype, with an underdeveloped but functional gynoecium (flower sex note 2 according to OIV 151 descriptor), instead of the hermaphroditic flowers regularly developed in this cultivar (note 3). Histological analyses revealed a reduced development of the style and stigma, as well as a remarkable thinning of the gynoecium septum. Genetic analyses of its self-progeny revealed the co-segregation of the male-like phenotype with the hermaphrodite allele of the grape sex locus (*SDR*). A treatment of flower clusters in stages prior to flowering with cytokinins, hormones involved in the gynoecium development, reversed the phenotype in the somatic variant. These findings suggest that some somatic mutation of the hermaphrodite *SDR* allele into male-like could hinder the correct fertilization of the ovules, leading to lower fruit set and looser bunches.

The other somatic variant of Tempranillo Tinto with looser bunches presents a notable reduction in pollen viability, around 50%, compared to the >90% regularly observed in Tempranillo clones. Pollen sterility also segregated in the self-progeny of the somatic variant, suggesting the inheritance of this trait in the progeny. Whole genome DNAseq identified structural variation specific of this clone, concretely a translocation breakpoint between chromosomes 1 and 3 that was confirmed by PCR and Sanger sequencing and was observed also in individuals of the self-progeny with low pollen viability. These findings together with previous reports in other somatic variants such as Tempranillo Blanco suggest that genome structural variation is a recurrent source of low bunch compactness phenotypes by causing deleterious effects on haploid gametes and, ultimately, limiting fruit set.

**Keywords:** bunch compactness, somatic variation, Tempranillo Tinto, flower development, pollen viability.