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Characterization of a cv. Tempranillo Tinto variant exhibiting a male-like flower phenotype

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Domesticated grapevine (*Vitis vinifera* L.) is used for wine, fresh fruit, raisins and juice production. Two subspecies can be identified within this species: *V. vinifera* ssp. vinifera, the cultivated form comprising mostly hermaphrodite and some female cultivars and *V. vinifera* ssp. *sylvestris*, the suggested wild dioecious ancestor. Studies dealing with this trait identified a major QTL on chromosome 2 as the grapevine Sex Determining Region (SDR), which harbours several proposed candidate genes. The aim of this work is the genetic and molecular characterization of a Tempranillo Tinto somatic variant that shows an androgenized flower phenotype. Whilst flowers in this somatic variant develop normal stamens, they present a reduced gynoecium that, unlike canonical male flowers of *V. vinifera* ssp. *sylvestris*, still enable fruit setting and ripening. Phenotyping results of a self-cross progeny of this variant line (more than 100 offspring) indicated that the mutant flower phenotype is inheritable. Furthermore, genotyping results of the microsatellite marker VVIB23, linked to the SDR, showed that the putative mutation co-localizes with this locus. One of the proposed female development inhibitor genes underlying the SDR locus is VviAPT3, which encodes an adenine phosphoribosyl transferase that may inactivate cytokinins by using them as substrate. The inactivation of these hormones, which promote gynoecium development in wild male vines if applied exogenously, could explain the mutant phenotype. RT-qPCR and RNA-seq expression analyses during flower development demonstrated the overexpression of VviAPT3 in the mutant line compared to a normal flower Tempranillo Tinto line used as control. Several experiments are ongoing to identify the genetic variation that causes this male-like phenotype, such as the comparison of the whole genome sequences of the variant and a control Tempranillo line, or the genotyping of VviAPT3 and other candidate genes through Sanger sequencing.

Keywords: Grapevine, flower mutant, sex determination