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CHARACTERIZATION OF A GRAPEVINE VARIANT EXHIBITING A MUTANT FLOWER SEX PHENOTYPE

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Grapevine, *Vitis vinifera* L., is mainly cultivated for the production of wine, table grapes, raisins and juices. In 2016, almost 8 million hectares were planted with grapevines worldwide, with a total wine production of more than 270 million liters. *Vitis vinifera* species includes two subspecies: *sylvestris*, the dioecious wild form and *sativa* or *vinifera*, its derived domesticated form. Cultivated, *sativa* varieties normally bear hermaphrodite flowers, although a few ancient varieties with female flowers still exist. Although the molecular basis of sex determination in grapevine is still unknown, a QTL on chromosome 2 has been described as the Sex locus and includes several candidate genes that could play a fundamental role in sex determination. The main objective of this work is the genetic and molecular characterization of a somatic variant line of cultivar Tempranillo Tinto that develops androecium flowers instead of the regular hermaphrodite flowers. Those androecium flowers carry normal stamens and a small gynoecium that, unlike male flowers, still allows fertilization and the development of berries. Phenotyping of the flower sex in a self-progeny of this Tempranillo variant line showed that the mutant phenotype is heritable as a dominant trait appearing in the frequency expected of hermaphrodite flowers. Additionally, genotyping of a microsatellite marker linked to the Sex locus, VVIB23, also supports that the putative causal mutation is fully linked to this locus. We found that a candidate gene within this locus, VviAPT3, encoding an adenine phosphoribosyl transferase that may inactivate cytokinins, is overexpressed in the variant line compared to normal Tempranillo Tinto. In addition, cytokinins applied externally on inflorescences of the variant line were able to induce the development of a gynoecium of normal size. Several experiments following genomics and transcriptomics approaches as well as other focused on VviAPT3 and other candidate genes within the Sex locus are ongoing to identify the causal genetic variation. Understanding this mutant phenotype could help providing molecular genetic evidence on the control of sexual dimorphism in grapevine.

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