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Uncover the genetic basis of drought response in grapevine rootstocks

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Consequences of global climate change are becoming more evident, since abiotic stresses including drought, flooding and extreme temperatures severely impact viticulture in all wine-producing regions. Breeding grape rootstocks for resilience to water deficit is an achievable strategy; however, little information is available about the genetic control of grape tolerance to drought. A Genome Wide Association Study and a Candidate Gene approach were adopted in our study to investigate the genetic basis of drought response in an *ad hoc* core-collection consisting of different genotypes of *Vitis spp.* and hybrids. Grape accessions were characterized using the 20K SNP genotyping array and by resequencing four candidate genes. The effect of water stress experiment on pot-grown plants was evaluated under semi-climate controlled conditions in the greenhouse and phenotypic differences in stomatal conductance were assessed by means of thermal infrared imaging. A significant genetic association was found for stomata closure under severe drought therefore some representative rootstock genotypes (101.14, SO4, Riparia Gloire de Montpellier and 110R) were chosen for a deeper characterization. Plant transpiration and photosynthesis parameters were evaluated in additional drought stress experiments in greenhouse and in a hydroponic system. Differences in stomatal sensitivities and plant stress index were observed both among studied genotypes and the two experimental settings. These results represent a step forward in the dissection of grapevine rootstocks mechanisms of drought resilience.

Keywords: abiotic stress, GWAS, phenotyping, polymorphism, rootstocks, single-nucleotide