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Towards genome-wide association studies under abiotic stress in *Vitis vinifera*

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Genome-wide association studies have proven their efficiency to decipher the genetic determinism of traits of agronomic interest in several plant species. In order to perform such studies in grapevine, we first designed an association panel of 279 *V. vinifera* cultivars from the French National Grapevine Germplasm Collection (Domaine de Vassal, INRA, France). It is composed of three subgroups of 93 cultivars representing the three main genetic pools, which differ in use and geographical origin: wine West, wine East, table East. This panel exhibited a good genetic and phenotypic representativeness of the whole collection. Linkage disequilibrium extent was quite small, 43 Kb for a corrected r^2 predicted value of 0.2, emphasizing the need for several dozen thousands markers to achieve powerful genome wide association studies. The second step consisted in dense genotyping of this panel using a 18K SNP Infinium chip and genotyping by sequencing (GBS). While the first method provided useful genotypes at 12K SNPs, about 100K SNPs are expected using GBS with *ApeK*I. Data processing is in progress and this resource will be made available to the scientific community. The third step consists in phenotyping this panel for traits of interest. Vines were planted in a randomized block design at Le Chapitre Research Vineyard (Montpellier SupAgro, France). Traits related to yield (cluster and berry weights) and phenology (maturity date) were measured in three years within the DLVitis program. Then within the Innovine program, grass was used as a cover crop between rows in the whole trial and part of the design was irrigated to obtain two levels of water availability. In addition to yield and phenology traits, berry composition (sugars, acids, anthocyanins, tannins and aromas), pruning weight and adaptation to drought (delta C13) have been measured during two growing seasons under both water availability conditions. This association panel, together with the accumulated data, represent highly valuable resources for genetic studies in grapevine. We are calling for an international collaborative effort to use such a panel in field and greenhouse trials to address questions on adaptation to changing environments.

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