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Genetic determinism of grapevine development stages as a tool for the adaptation to climate change

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Abstract

A major goal of modern grapevine (*Vitis vinifera* L.) breeding programs is the introgression of resistance genes along with desirable traits for better adaptation to climate change. Developmental stages have an impact on yield components and berry composition and are expected to shift towards earlier dates in the future. We investigated the genetic determinism of phenological stages in the progeny of a cross between two grapevine hybrids, each carrying several quantitative trait loci (QTL) for downy mildew and powdery mildew resistance. The dates of three phenological stages, budbreak, flowering and veraison, were recorded during three consecutive seasons for 209 genotypes in the vineyard. The phenotypic data analysed were the duration of three periods expressed in thermal time (degree-days): 15 February to budbreak, budbreak to flowering and flowering to veraison. High density parental and consensus genetic maps were constructed and used for QTL detection. Several QTL were detected for each period and the corresponding allelic effects were quantified and expressed in degree.days. Two virtual early and late genotypes were created by combining the relevant alleles. Using a previously validated ecophysiological model with simulated climate data for the RCP8.5 IPCC scenario, budbreak, flowering and veraison dates were predicted for the parents, Chardonnay, and the two virtual genotypes for each year up to 2100. Mean temperatures during the ripening period were calculated. The interest of the virtual genotypes in compensating for the expected shift in veraison dates will be discussed.

Keywords: Grapevine, climate change, phenology, QTL, plant breeding.