



Comparative QTL mapping of phenology traits in three cross populations of grapevine

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Abstract

Long-term studies on grapevine phenology have clearly demonstrated that global warming is affecting phenological events, leading to an anticipation in their timing, and negatively impacting grape yield and berry quality. Therefore, dissecting the genetic determinants involved in the plant regulation of the phenological stages of budburst, flowering, veraison and ripening can improve our knowledge of the underlying mechanisms and support plant breeding programs and the advancement of vineyard management strategies.

We report here the results of a QTL mapping experiment conducted on three segregating populations obtained from the crossing of 'Cabernet Sauvignon' and 'Corvina', 'Corvina' and the hybrid 'Solaris' and 'Rhine Riesling' and 'Cabernet Sauvignon'. High-density parental and integrated linkage maps were developed by using genotypic information, obtained through hybridization to the Illumina Vitis18KSNP chip, of DNA from 144, 129 and 139 individuals respectively. Each progeny was then evaluated in the field over four seasons. The phenological traits budburst, flowering, veraison as well as technological ripening were assessed, and correlations across years and traits were estimated. A summary of all mapped QTLs in the different years in each population is provided and QTLs reproducible across years and populations as well as potential underlying candidates are discussed.

Keywords: climate change, phenology, cross populations, QTL mapping, candidate genes.