

# Book of Abstracts

26<sup>th</sup> & 27<sup>th</sup> November, 2020



SI-P42

## IDENTIFICATION OF GENES INVOLVED IN GRAPEVINE REPRODUCTIVE PERFORMANCE VIA ASSOCIATION GENETICS

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Grapevine is the most valuable fruit crop in the world, mainly grown for wine elaboration and to sustain fresh grape and raisin markets. Adverse effects of climate change-derived environmental conditions on viticulture systems predict a decline in fruit quality and crop yield, so understanding the genetic and molecular mechanisms determining crop yield components is essential to develop long-term strategies to increase grapevine resilience. The analysis of a collection of grapevine cultivars of different use (wine, table, multi-purpose) allowed us to evaluate the relationship between various yield components (flowers per inflorescence, fruit set, berries per cluster) and different abnormal reproductive conditions (coulure, millerandage) that may happen during the grapevine developmental cycle. The great phenotypic variation observed for these traits in this grapevine collection has been used for an association study that considered 15,309 single nucleotide polymorphisms (SNPs) detected in the sequence of 289 candidate genes scattered across the 19 grapevine linkage groups. After correcting statistical models for population structure and linkage disequilibrium effects, we identified many SNPs significantly associated with grapevine fruit set and other reproductive performance traits, supporting the polygenic nature and the highly complex genetic determination of these traits. Many of the associated SNPs were found in different putative MADS-box transcription factors, which might play similar functions in grapevine to those reported in other plant species. Within them, some members of the *VviAGL*, *VviAP*, *VviSHP* and *VviSVP* gene subfamilies stood out as firm candidates to test the involvement of their genetic diversity in the variation of fruit set and reproductive performance of the cultivated grapevine. In addition, we observed an additive effect of some of the associated SNPs on the phenotypic value, suggesting that advantageous alleles from different loci could be pyramided to generate superior cultivars with optimized reproductive performance.

Acknowledgements & Funding: This research was funded by the Spanish Ministerio de Economía y Competitividad (MINECO), project AGL2014-59171-R and by the Agencia Estatal de Investigación (AEI), project BIO2017-86375-R, both co-funded by FEDER (UE). JT is funded by a Juan de la Cierva-Incorporación grant (IJC2018-035036-I).