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GENOMIC VARIATION AND CLONE GENTOYPING IN *VITIS VINIFERA* L. 'MALBEC'

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Somatic mutations are a major force introducing novel genetic variation; this role becomes enhanced in systems lacking of sexual reproduction. The later is the case of grapevines used in the wine industry. Even though clonal propagation is a normal practice in this industry, a remarkable phenotypic variation has been reported at the intra-cultivar level. However, less is known about the genetic variability among clones. Malbec is the main cultivar for the Argentinean viticulture, showing a notorious phenotypic variation on many traits of technological interest, for example the biochemical composition of berries. Therefore, it turns relevant to develop a formal protocol to discriminate among clones exhibiting different properties. Here we performed a genomic analysis in order to test if the genetic variability is in agreement with the phenotypic variability, and also to develop a genetic-based protocol for clones' discrimination. For this aim we obtained Illumina reads at a 35x depth for four different Malbec clones (MB53, MB59, Cot143 and Cot225). Bioinformatic tools were employed to align these reads to the Pinot noir reference genome (PN40024) and to perform variant calling analysis for single nucleotide variants (SNVs) discovery. Afterwards, strict quality and frequency filters were applied to obtain a set of reliable SNVs. We discovered 2 million of shared SNVs (i.e. all clones shared the same allele); these variants allow distinguishing Malbec from the reference genome. On the other hand, we identified 458 non-shared SNVs (i.e. at least one of the clones has the same allele than the reference); these were of particular interest to us because they allow for clone discrimination. From the latter set we picked 48 SNVs to validate them through Sanger sequencing. After validation these same 48 SNVs were employ to build a chip for the high throughput genotyping platform FLUIDIGM. We genotyped 221 plants, including clones of known origin as well as plants belonging to five different mass selections. We were able to classify all genotyped plants in 10 different haplo-groups; showing that with a small but informative number of SNVs it is possible to discriminate among clones of the same cultivar in an efficient manner.