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Whole genome resequencing and custom genotyping unveil clonal lineages in `Malbec´ grapevines (*Vitis vinifera* L.)

Luciano Calderón[a], Nuria Mauri[b], Claudio Muñoz[c], Pablo Carbonell-Bejerano[d], Laura Bree[e], Cristobal Sola[e], Sebastian Gomez-Talquenca[f], Carolina Royo[b], Javier Ibáñez[b], Jose Miguel Martinez-Zapater[b], Diego Lijavetzky[a]

[a]*Instituto de Biología Agrícola de Mendoza, IBAM-CONICET-UNCuyo, Almirante Brown 500, Chacras de Coria 5505, Argentina*
[b]*Instituto de Ciencias de la Vid y del Vino, CSIC, UR, Gobierno de La Rioja, Logroño, Spain*
[c]*Facultad de Ciencias Agrarias UNCuyo, Almirante Brown 500, Chacras de Coria, Argentina*
[d]*Max Planck Institute for Developmental Biol, Tübingen, Germany*
[e]*Vivero Mercier Argentina, Perdriel, Argentina*
[f]*EEA Mendoza INTA, Luján de Cuyo, Argentina*

***Presenting author:** dlijavetzky@conicet.gov.ar

Grapevine cultivars are clonally propagated to preserve their varietal attributes. However, genetic variations accumulate due to the occurrence of somatic mutations. This process is anthropically influenced through plant transportation, clonal propagation and selection. Malbec is a cultivar that is well-appreciated for the elaboration of red wine. It originated in Southwestern France and was introduced in Argentina during the 1850s. In order to study the clonal genetic diversity of Malbec grapevines, we generated whole-genome resequencing data for four accessions with different clonal propagation records. A stringent variant calling procedure was established to identify reliable polymorphisms among the analyzed accessions. The latter procedure retrieved 941 single nucleotide variants (SNVs). A reduced set of the detected SNVs was corroborated through Sanger sequencing and employed to custom-design a genotyping experiment. We successfully genotyped 214 Malbec accessions using 41 SNVs and identified 14 genotypes that clustered in two genetically divergent clonal lineages. These lineages were associated with the time span of clonal propagation of the analyzed accessions in Argentina and Europe. Our results show the usefulness of this approach for the study of the scarce intra-cultivar genetic diversity in grapevines. We also provide evidence on how human actions might have driven the accumulation of different somatic mutations, ultimately shaping the Malbec genetic diversity pattern.

Keywords: Malbec, genetic diversity, clonal lineages, propagation history, whole genome resequencing