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PHASED GENOME ASSEMBLY TO TRACK CLONAL IMPROVEMENT IN TEMPRANILLO GRAPEVINE CULTIVAR

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Grapevine cultivars are clonally propagated, in many cases even for centuries, to keep their varietal attributes because they are highly heterozygous. However, upon long periods of propagation, somatic mutations accumulate, which are the base of clonal selection for cultivar innovation. To identify responsible mutations in selected spontaneous somatic variants, here we produced a diploid genome assembly of Tempranillo, the most relevant red wine cultivar in Spain and the third most cultivated worldwide. After PacBio and Oxford Nanopore sequencing, a trio binning approach produced chromosome-arm level and complete assemblies for the two haplo-phases. Based on the *de novo* assembly, we searched for genetic variation in 10 re-sequenced clones of Tempranillo selected for variation in agronomically relevant traits including fruit colour, low fruit sugar accumulation (convenient for quality wine production in warmer climates) or loose bunches that are less prone to fungal diseases. We were able to phase the complex genome rearrangements that originated the white-berried Tempranillo Blanco. Thousands of somatic mutations were detected in each clone, which, combined with gene annotations based on PacBio Iso-seq, identified candidate functional variants related with selected phenotypes. Our results show that trio binning produces high quality genome assemblies that can be exploited to detect genetic variation useful for cultivar improvement and clonal tracking in grapevine.

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