

## High quality phased assembly of grape genome offer new opportunities in chimera detection

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### Abstract

In perennial plants and especially those propagated through cuttings, several genotypes can coexist in a single individual, thus leading to chimeras. When the variant induces a noticeable phenotype modification, it can lead to a new cultivar. Viticulture already took economic advantage of this natural phenomenon: for instance, the berry skin of cv. 'Pinot Gris' derived from cv. 'Pinot Noir' by the selection of a chimera. Chimeras could also impact other crucial traits without being visually identified. Periclinal chimera where the variant has entirely colonised a cell layer is the most stable and can be propagated through cuttings. In grapevine, two functional cell layers are present in leaves, L1 and L2. However, lateral roots are formed from the L2 cell layer only. Thus, comparing DNA sequences of roots and leaves could allow chimera detection. In this study we used new generation Hifi long reads sequencing and recent bioinformatics tools applied to 'Merlot' grape cultivar to detect periclinal chimeras. Sequencing of cv. 'Magdeleine Noire des Charentes' and 'Cabernet Franc', the parents of cv. 'Merlot', allowed haplotype resolved assembly. Pseudomolecules were built with few contigs, in some occasions only one per chromosome. This high resolution allowed haplotype comparison. Annotation from PN40024 was transferred to all pseudomolecules. Through variant detection, periclinal chimeras were found on both haplotypes. These results open new perspectives on chimera detection which is an important resource to improve cultivars through clonal selection or breed new ones. Detailed results will be presented and the validation of these positions will be discussed.

**Keywords:** Chimera, Hifi Sequencing, trio-binning, phased assembly, Whole genome