Open Conference on
Grapevine Physiology
and Biotechnology
LOGROÑO - LA RIOJA
7-11 July 2024

Tracking the origin of Tempranillo Tinto through whole genome resequencing and high-throughput genotyping

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Abstract

Grapevine cultivars are vegetatively propagated to maintain their varietal characteristics. This process of multiplication leads to spontaneous somatic mutations that can eventually generate a variant phenotype, of potential interest for cultivar improvement and innovation. However, regardless their phenotypic effect, somatic mutations stack in the genome, and they can be used to reveal the origin and dissemination history of ancient cultivars. Here, a stringent somatic variant calling over whole genome resequencing data from 35 'Tempranillo Tinto' clones or old vines from seven Iberian winemaking regions revealed 135 single nucleotide variations (SNVs) shared by some of the clonal lines. Among them, we selected 56 highly informative SNVs to custom-design a high-throughput genotyping chip for this cultivar, which was validated and further tested in 94 'Tempranillo Tinto' vines from highly diverse regions. Phylogenetic analyses revealed that 'Tempranillo Tinto' samples grouped in three major clonal lineages, a clustering that reflected the geographic origin of the samples. After combining these results with genome re-sequencing data from the two 'Tempranillo Tinto' parents, we found the Ebro River Valley as the most likely region of origin for 'Tempranillo Tinto'. Results also revealed one major historical dissemination route that likely progressed westwards from this original site, towards the main winemaking regions found across the Duero River Valley and to the South in Portugal. Collectively, the results obtained in this study shed light on the origin and historical dispersal of 'Tempranillo Tinto' in the Iberian Peninsula, and released highly informative SNVs for the differentiation of intra-cultivar lineages.

Keywords: clonal lineage, grapevine, Iberian Peninsula, phylogenomics, SNV