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

Reduced bunch compactness in a clone of Tempranillo associates with a complex reciprocal translocation detected by long-read sequencing genomics

Pablo Carbonell-Bejerano[1*], Noelia Alañón[1], Yolanda Ferradás[1,2], Nuria Mauri[1,3], José Miguel Martínez-Zapater[1], Javier Ibáñez[1*].

[1] Instituto de Ciencias de la Vid y del Vino (ICVV, CSIC-CAR-UR), Departamento de Viticultura, Logroño, Spain
[2] Departamento de Biología Funcional, Universidad de Santiago de Compostela, Santiago de Compostela, Spain
[3] Centre for Research in Agricultural Genomics (CSIC-IRTA-UAB-UB), Cerdanyola del Vallès, Barcelona, Spain

[*]Corresponding author: pablo.carbonell@icvv.es and javier.ibanez@icvv.es

Abstract

Grapevine cultivars are vegetatively propagated to maintain their varietal attributes. However, spontaneous somatic variation emerges during prolonged periods of vegetative growth, providing an opportunity for the natural improvement of traditional grapevine cultivars. Notably, reduction in bunch compactness is a favorable trait in viticulture, offering advantages such as decreased susceptibility to bunch fungal diseases, and a more uniform ripening of berries. To unravel the genetic and developmental mechanisms behind bunch compactness variation, we examined a somatic variant of Tempranillo Tinto cultivar with loose bunches. We found that the mutant clone exhibits a ~50% reduction in pollen viability compared to typical Tempranillo clones. By aligning Illumina and Nanopore whole-genome sequencing reads to a diploid genome assembly of Tempranillo, we identified genome structural variations (SV) specific of this clone: translocation events involving chromosomes 1-3, 7-11, and 8-17. The presence of the SV breakpoints was validated using PCR and Sanger sequencing. The analysis of self-cross progeny of the mutant clone showed that low pollen viability and reduced number of seeds per berry co-segregate with the SV event between specific haplotypes of chromosomes 1 and 3, suggesting a causal effect for this rearrangement. Inspection of Nanopore read alignments identified that the SV 1-3 event corresponds to a complex reciprocal translocation with duplications at the breakpoints of the two involved chromosomes. Considering that heterozygous reciprocal translocations associate with partially incompatible chromosome pairing during meiosis, we propose that this type of SV decreases fruit set rate by lowering gamete viability, ultimately reducing bunch compactness.

Keywords: bunch compactness, clonal variation, genome structural variation, pollen viability, reciprocal translocation.