

P81 – A high-density integrated map for grapevine based on three mapping populations genotyped by the *Vitis*18K SNP chip

Vervalle, Jessica A^{1,2}; Costantini, Laura³; Lorenzi, Silvia³; Pindo, Massimo³; Mora, Riccardo⁴; Bolognesi, Giada⁴; Marini, Martina⁴; Lashbrooke, Justin G⁵; Tobutt, Ken R²; Vivier, Melané A⁵; Roodt-Wilding, Rouvay¹; Grando, Maria Stella^{3,6}; Bellin, Diana^{4*}

¹Stellenbosch University, Department of Genetics, Stellenbosch, South Africa

²ARC Infruitec-Nietvoorbij, Stellenbosch, South Africa

³Fondazione Edmund Mach, Research and Innovation Centre, San Michele all'Adige, Italy

⁴University of Verona, Department of Biotechnology, Verona, Italy

⁵Stellenbosch University, South African Grape and Wine Research Institute, Stellenbosch, South Africa

⁶University of Trento, Center Agriculture Food and Environment (C3A), San Michele all'Adige, Italy

*diana.bellin@univr.it

Abstract

The improvement of grapevine through biotechnology requires identification of the molecular bases of target traits by studying marker-trait associations. The *Vitis*18K SNP chip provides a useful genotyping tool for genome-wide marker analysis. The majority of linkage maps are based on single mapping populations, but integrated maps can support QTL studies increasing marker density and providing a reference for marker genetic order. Here we present the integration of three different maps genotyped using the *Vitis*18K SNP chip. The parents consist of the well-known wine cultivars 'Cabernet Sauvignon', 'Corvina' and 'Rhine Riesling', the lesser-known wine variety 'Deckrot', and a table grape selection, G1-7720.

Three high-density population maps with an average inter-locus gap ranging from 0.74 to 0.99 cM were developed. These maps show high correlations (0.9965 – 0.9971) with the reference assembly and validate, by genetic mapping, chromosomal location of 9340 of the SNPs from the *Vitis*18K. Only 93 markers with large order discrepancies compared to expected physical positions were found, of which a third consistent across multiple populations. More recently an additional mapping study, based on a similar approach, further increased the number of the SNPs belonging to *Vitis*18K chip with a validated genetic position. Moreover, these genetic data aid the further refinement of the grapevine genome assembly, by anchoring 104 yet unanchored scaffolds.

From the three population maps, an integrated map was constructed which includes 6 697 molecular markers and reduces the inter-locus gap distance to 0.60 cM, resulting in the densest integrated map for grapevine thus far. A small number of discrepancies, mainly of short distance, involve 88 markers that remain conflictual across maps. The integrated map shows similar collinearity to the reference assembly (0.9974) as the single maps. This high-density map increases our understanding of the grapevine genome and provides useful tools for its further characterization and the dissection of complex traits.

Keywords: *Vitis vinifera*, genetic linkage maps, single nucleotide polymorphism, Consensus map building