

## A NOVEL INTEGRATED GENE MAP BASED ON 280 SSR AND 500 SNP MARKERS AMONG FIVE ELITE CULTIVARS OF *VITIS VINIFERA* L.

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In the last ten years several genetic maps of *Vitis vinifera* or *Vitis* genus have been developed creating a productive background stimulating a new deal of grape assisted breeding. These maps, mainly based on SSRs, share a framework of markers which supply a backbone for next improvement. A new source of markers, based on single nucleotide polymorphisms (SNPs), identified in coding sequences and unique BACend sequences, has been added to the reference set of SSRs. SNPs and insertion/deletion mutations (indels) represent the most frequent genetic differences within a species. They are genetically co-dominant and useful for integration into high resolution genetic maps. Minisequencing has recently been described as an affordable moderately high-throughput method for SNP assay and has efficiently been applied in this mapping work.

The main objective of this work was to develop an integrated gene map among five elite cultivars of *Vitis vinifera* L: 'Syrah' (S), 'Pinot noir' (P), 'Grenache' (G), 'Riesling' (R), and 'Cabernet Sauvignon' (CS). A number of SSR and SNP markers has been selected 'ad hoc' to build a common framework between all maps, while cross specific markers have been added to increase the total number of markers in the integrated map. The total number of markers shared at least between two cultivars is about 400, while the total number of markers, including 380 AFLPs, in the integrated map is about 1160. Among them, 652 markers, anchoring hundreds of BACs, were used for the integration between the S x P genetic map and the Pinot noir genome sequence ([www.research.iasma.it/genomics](http://www.research.iasma.it/genomics)). Additional 58 BACend-based markers mapped in S x G and R x CS provide the possibility to anchor new clones. Moreover, through BAC pooling 157 SSRs segregating in S x G and/or R x CS represent a great potential to improve the coverage of the genome. Finally, the integration among crosses segregating for different traits of interest, along with the anchor to the Pinot noir BAC clones, allows to identify the genome regions responsible for these characters.