

## IRAP, REMAP AND S-SAP MOLECULAR MARKERS IN GRAPEVINE GENOTYPE IDENTIFICATION AND PHYLOGENETIC STUDIES

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Long-terminal-repeat (LTR) retrotransposons represent a large proportion of repetitive DNA in plant genome. The ubiquitous nature of retrotransposons and their activity in creating genomic diversity by stably integration of large DNA segments into dispersed chromosomal loci make these elements ideal for development as molecular markers. In grapevine genome the complete sequence of one *gypsy*-like retrotransposon (*Gret1*) and the partial sequences of two *copia*-like retrotransposons (*Vine-1* and *Tvv1*) have been isolated, and some molecular markers based on the insertion polymorphisms of the above mentioned retrotransposons have been recently tested for identification of grapevine species and varieties.

In this study we analysed the capacity of Inter-Retrotransposon Amplified Polymorphism (IRAP), Retrotransposon-Microsatellite Amplified Polymorphism (REMAP) and The Sequence-Specific Amplified Polymorphism (S-SAP) molecular markers in the discrimination of 18 *Vitis* genotypes: 6 *Vitis* species (*Vitis arizonica*, *Vitis cinerea*, *Vitis labrusca*, *Vitis rupestris*, *Vitis rotundifolia* and *Vitis vinifera* subsp. *sylvestris*) and 12 *Vitis vinifera* subsp. *sativa* varieties (“Cabernet Franc”, “Cabernet Sauvignon”, “Chasselas”, “Fiano”, “Malvasia Bianca Cenaia 2”, “Moscato bianco di Canelli”, “Pinot Nero”, “Rkatzitely”, “Sauvignon Blanc”, “Sangiovese”, “Sultanina”, “Vermentino”). The insertion polymorphisms of *Gret1*, *Vine-1* and *Tvv1* retrotransposons and the allocation of the *Vitis* genotypes in IRAP, REMAP and S-SAP phylogenetic trees are discussed.