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**P496** : Fruit Trees

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### Grapevine miRNAs: Towards A Structural And Functional Characterization

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In plants, microRNAs (miRNAs) are key post-transcriptional regulatory elements approximately 21 nt long, coded by MIRNA genes, which regulate plant architecture, nutrient homeostasis and stress response. The crucial role they play in fine tuning gene regulation clearly implies that a complete characterization of genomes structure and function cannot be attained without a deep analysis of this class of regulatory elements. Here we present the characterization of miRNA genes in grapevine, following the annotation of 140 conserved MIRNA genes (Jaillon et al., 2007). Starting from the description of their transcriptional landscape (Mica et al., 2009) we analyzed their genomic structure and interaction with putative targets. We experimentally validated primary transcript boundaries and alternative splicing events of several miRNA genes, confirming bioinformatic predictions and showing different splicing patterns and alternative transcription end points. Putative targets were identified and validated by means of 5' modified RACE experiments. We are currently focusing on target genes involved in several physiological pathways such as phenylpropanoid pathway and that, according to transcriptome analysis using oligo-chips, are up- or down-regulated in berries after light and heat stress treatments.

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