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miRNA DISCOVERY IN GRAPEVINE BY *IN SILICO* APPROACHES

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The key role of non-coding RNAs in many different biological areas has become clear in the last ten years. microRNAs are a group of non-coding small RNAs (20-22 nt long) which are often conserved between related organisms and which are coded by specific genes called MIR genes. All the transcripts that give rise to the same miRNA are grouped in a single family.

microRNAs are involved in post-transcriptional gene regulation, inducing transcript cleavage or translation inhibition, throughout sequence similarity. Target genes are associated with many different biological processes and possess no significant similarity to their respective miRNA genes, apart from the 21 nucleotide sequence. In plants, target genes are typically involved in stress response and plant development. They are broadly present in the plant kingdom; in recent years many new species have been investigated and many miRNAs have been discovered, mainly through *in silico* comparative genomic approaches.

Here we present a double *in silico* approach applied to the complete sequence of the grape (*Vitis vinifera* L.) genome focused on the discovery of both conserved plant miRNAs and new species-specific miRNAs. Interesting comparative and phylogenetic analyses have been performed that explicit how different miRNA gene families behave during evolution, following gene-expansion or gene-loss, showing in some cases a similar genomic organization, among different species.

Moreover, to further characterize these miRNAs and investigate their putative roles, a detailed target analysis has been performed. As expected targets of related families are highly conserved between species, belonging to the same functional categories. Nonetheless a further characterization of these targets and their corresponding miRNAs can clarify their role and possible involvement in plant growth and fruit development.