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FISV 2008 - 10th Annual Congress

Riva del Garda, 24-27 September 2008

<http://fisv2008.azuleon.org>

Bioinformatics, Genomics and Proteomics

26/09/2008, 08:30 - [---]

(Organisers: [G. Pavesi](#), [D. Cavalieri](#))

Abstract UAI: 2497de820625152705

Characterization and analysis of the expression pattern of microRNAs in the grapevine *Vitis vinifera*

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MicroRNAs are small (19-24 nt) noncoding RNAs that play an important role in the regulation of multiple cell events, inhibiting gene expression at the posttranscriptional level by binding target mRNAs that are subsequently degraded or sequestered from translation. The availability of the complete genome sequence of the grapevine (*Vitis vinifera*), has already permitted genome-wide predictions of microRNAs by purely computational methods. Here we integrate transcriptomic data derived from high-throughput Illumina SOLEXA and ABI SOLiD sequence tags derived from both polyA+ transcripts and isolated small RNAs with oligonucleotide array data. We are thus able to detect both mature microRNAs and to establish whether genomic loci corresponding to the pre-miRNA are expressed in various tissues. In many cases, the unambiguous alignment of sequence tags derived from polyA+ RNA to the genomic sequence allow provisional mapping of primary microRNA transcripts, a first step towards bioinformatics characterization of elements potentially regulating microRNA expression.