mRNA-seq ANALYSIS OF *VITIS VINIFERA* TRANSCRIPTOME

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Illumina mRNA-Seq protocol was applied to study three stages of berry development in *Vitis vinifera* cv. Corvina, in particular post fruit set, véraison and ripening. The aim of the work is to determine if mRNA-Seq data deepen the previous knowledge about berry development and ripening process. cDNA was generated from mRNA extracted from total RNA and the standard mRNAseq Illumina protocol was followed to create cdsDNA libraries. Analysis of sequences obtained by Solexa Genome Analyzer II from cdsDNA libraries replicates showed a high correlation and it let have a suitable cover of the reference *Vitis vinifera* genome 8.4X. Bioinformatics analysis of expression difference, alternative splicing and SNPs between cv. Corvina and cv. Pinot noir, were examined with specific software implemented by in silico algorithm: ELAND and BOWTIE for sequence alignment, ERANGE for the calculation step. With regard to the alternative splicing search, it was necessary the construction of a database of possible exon junctions, both constitutive and alternative, for the sequence mapping, because until now is not available a splicing alternative database for *Vitis vinifera*. Differential expressed genes were subdivided in three categories based on the expression level: genes with low (0≤RPKM<5), medium (5≤RPKM<50) and high (RPKM≥50) transcription. Manual annotation of each category sequences was performed using the Gene Ontology (GO) Classification. Transcripts were then grouped into 11 GO functional categories, based on GO 'biological process' terms. Cluster analysis of the gene set was based on the k-means method using Pearson's correlation distance calculated on the gene expression profiles. Transcripts were divided into ten groups representing the minimum number of profiles that could be obtained with three time-points (Figure Of Merit analysis). To confirm mRNA-Seq data, the expression profile of some gene families, as MYB transcription factor genes, was validated by real time RT-PCR. It is improving a method to confirm alternative splicing observed in the three stages of berry development.