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AFFYMETRIX CHIPS TRANSCRIPTIONAL ANALYSIS REVEALS DRAMATIC CHANGES IN GENE EXPRESSION DURING GRAPE (*VITIS VINIFERA*) BERRY RIPENING

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Vitis vinifera, with more than 140000 ESTs corresponding to about 14000 putative transcripts deposited in the public database, is currently the fruit species with the most characterized transcriptome. This makes grape berry a suitable model to study the ripening process of non-climateric fruits.

In grapevine, such as in many other fleshy fruits, the transition from the green, hard and acidic berry to the sweet, soft, colored and sugar rich ripe fruit, involves biochemical and biophysical processes finely tuned at the transcriptional level. The berry development follows a double-sigmoid curve described by two successive growth phases. The first phase, called the green or herbaceous stage, is characterized by rapid growth and cell division with increase in both weight and volume of berries, and by high levels of chlorophyll, acid accumulation and respiration. The second growth phase, called ripening, is characterized by cells expansion, softening, accumulation of sugars, amino acids, pigment and flavors and organic acids fall. During the onset of ripening, the so called veraison, little increase in berries weight and volume occur, but these dramatic changes in the fruit metabolism are triggered.

The recently exploited microarray technology, offers the advantage to analyze the expression level of thousands of genes simultaneously, allowing a study which approaches the whole genome. Such a broad picture of the berry transcriptome has proven to be very effective in describing the extensive changes occurring during berry development.

The molecular events associated with the pre-veraison, veraison and post-veraison stages of Pinot noir berries, have been studied using the *Vitis vinifera* Affymetrix chips which contain in situ synthesized oligonucleotide probe sets for the analysis of more than 16000 *Vitis* putative transcripts.

Grape samples representative of the whole vineyard were collected weekly after anthesis, in the study site of the Istituto Agrario S. Michele a/A during the 2003 growing season and the three crucial physiological points of berry development were identified based on the sugar and acids accumulation curves. For each selected point, RNA extraction was carried out on three biological replicates. Statistical analysis of the microarray hybridization data reveals that 3100 genes are significantly modulated during the considered developmental stages when compared to the pre-veraison stage. Further analysis will select those genes with common expression patterns and those belonging to the same metabolic pathways. Moreover, based also on functional annotation, a correlation will be searched between the gene expression profiles and the biochemical and physiological profiles in order to discover new genes potentially involved in the ripening process and also to identify possible markers of grape quality.