

GENOME-WIDE EXPRESSION PROFILING OF THE BERRY TRANSCRIPTOME

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The availability of several molecular tools such as genetic and physical maps, a huge inventory of expressed tag sequences (ESTs) and last but not least the recent announce of the whole genome sequence, makes grape a promising model plant to study very important physiological processes such as, for instance, fruit ripening in non-climateric fruits.

Here we describe the results of the characterization of the transcriptome of Pinot noir berries in three key ripening stages and in two different seasons as determined by *Vitis vinifera* Affymetrix chips and of the dissection of the stilbenes pathway as observed by comparison of high and low resveratrol producers, by home made cDNA arrays.

Main results of these studies are:

- berry ripening and stilbenes production are highly regulated at the transcriptional level
- a core of about 2000 genes appear to be strongly modulated from pre-veraison to post-veraison stages in two different growing seasons
- annotation of these genes by GO terms reveals they belong to specific functional classes such as response to stress, cell wall modification and secondary metabolism as expected, but also to not yet characterized transcription factors.