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GENE EXPRESSION PROFILING OF THE POLYPHENOLS PATHWAY OF GRAPEVINE USING ARRAY TECHNOLOGY

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The cultivated grapevine (*Vitis vinifera*) produces a range of secondary metabolites both constitutively and in response to biotic and abiotic stress. Among them, stilbenes and flavonoids are of increasing interest for many aspects: they are crucial factors that influence wine making, they are involved in plant defense and they have been strictly correlated with some pharmacological properties of red wine. Although considerable progress has been made in studying the pathway of stilbene and flavonoid biosynthesis in other plants, less is currently known in grapevine about the regulators of the pathway and the production of resveratrol derivatives The premise of this work is to dissect the regulatory basis of flavonoid and stilbene synthesis in grapevine by a functional genomic approach based on high-throughput transcript profiling methods.

Appropriate cDNA arrays were generated to compare transcript profiles in grape cultivars with high and low anthocyanin or resveratrol content for three different developmental stages (véraison, ripening and post-ripening). The gene expression analysis was carried out in order to identify candidate genes involved in the regulation of the stilbene biosynthesis and of berry development, taking advantage of berry sampling at different phenological stages. From the transcript profiling experiments, it turned out that the differentially expressed genes fall mainly into the disease and defense category transport, signal transduction and transcription factors. Validation of the cDNA array results by means of RT-PCR and Real-Time PCR are underway.

The mechanisms underlying the control of stilbene accumulation were also investigated in grape liquid cell cultures under the influence of a cyclic oligosaccharide molecule. In details, stable liquid cell cultures of a cross between *Vitis riparia* and *Vitis berlandieri* were used to induce resveratrol biosynthesis after treatment with DIMEB (heptakis (2,6-di-O-methyl)-β-cyclodextrin). A cDNA subtractive hybridization experiment (PCR Select™, Clontech) was performed to underline differences in gene expression between control and treated sample after two hours from DIMEB induction, while GeneChip® *Vitis vinifera* Genome Array (Affymetrix) will be used to characterize gene expression of these grape cell cultures after six hours from DIMEB treatment.