

REGULATORY NETWORKS UNDERLYING THE GRAPE BERRY RIPENING

PILATI S.*, COLLER E.*, DAL RI A.*, MALOSSINI A.**, MORETTO M.*, VELASCO R.*,
MOSER C.*

*) Department of Genetics and Molecular Biology, IASMA Research Centre, Via Mach 1,
I-38010 San Michele a/Adige (TN) (Italy)

**) Engineering and computer science department, University of Trento, Via Sommarive 14,
Povo (TN) (Italy)

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Genome-wide gene expression data obtained by microarray studies strongly suggest that the process of grape (*Vitis vinifera*) berry ripening is tightly regulated at the transcriptional level.

We recently identified a core-set of 1861 genes significantly and specifically modulated during this process. About 8% of these genes were annotated as transcription factors, further supporting the hypothesis of a strict control at the RNA level. We also observed the strong accumulation of hydrogen peroxide around véraison, suggesting a possible signalling role for the reactive oxygen species (ROS) in this developmental process.

To shed light onto the regulatory networks underlying grape berry ripening, the signalling pathways mediated by the hormone ethylene and by ROS have been investigated.

Concerning the hormonal control of ripening, an *in silico* analysis of gene network inference and promoter analysis has been applied, in order to identify putative target genes of the ethylene responsive transcription factors family. In order to confirm the *in silico* analysis, an experimental assay for measuring the transcription factor/DNA interaction has been set up. First results will be presented.

ROS accumulation and ROS metabolism during ripening have been studied at the biochemical level by measuring enzymatic activities (e.g. enzymes of the ascorbic acid/glutathione cycle, catalase) and oxidative stress markers (e.g. lipid peroxidation and hydrogen peroxide intracellular levels). These biochemical data have been integrated with the available transcriptional data in order to provide a systematic overview of the pathway.