

ANALYSIS OF GRAPEVINE GENE EXPRESSION IN RESPONSE TO *PLASMOPARA VITICOLA* BY COMBIMATRIX MICROARRAY

POLESANI M.*, ZAMBONI A.**, FERRARINI A.*, LOVATO A.*, PEZZOTTI M.**,
DELLEDONNE M.*, KORTEKAMP A.***, POLVERARI A.**

*) Dipartimento Scientifico e Tecnologico, Università di Verona, Strada Le Grazie 15,
37134 Verona (Italy)

**) Dipartimento di Scienze, Tecnologie e Mercati della Vite e del Vino, Villa Ottolini–Lebrecht,
37029 San Floriano di Valpolicella (VR)

***) Institute of Special Crop Cultivation and Crop Physiology, University of Hohenheim,
70593 Stuttgart (Germany)

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A comprehensive analysis of transcriptional changes associated to the infection process of *Plasmopara viticola* in susceptible (*Vitis vinifera* cv. Pinot Noir) and resistant (*Vitis riparia* cv. Gloire de Montpellier) grapevine genotypes has been undertaken by microarray analysis, at different time points after infection. The analysis was performed on Combimatrix platform at Verona University, on a Grape chip carrying 24562 specific probes in triplicates from assembly of Tentative Consensus of the last TIGR *Vitis vinifera* Gene Index release 5.0 and from non redundant genomic sequences produced by the genome annotation in the International Grape Genome Project.

Leaves of resistant and susceptible grape plants grown *in vitro* were infected with *P. viticola* or treated with distilled water as a control, and collected at 12 and 24 hours post-inoculation (hpi). Hybridisations were carried out with samples deriving from three independent biological replicates. Differentially expressed genes were selected using the multi experiment Significance Analysis of Microarray test, and gene clustering was performed using Genesis software.

Results showed an increase in the steady state level of more than 1500 genes in the resistant genotype and of about 300 in the susceptible Pinot Noir, as early as 12 hpi. While in the resistant genotype the transcriptional up-regulation remains sustained also at 24 hpi, the response of the susceptible genotype is characterized by a massive down-regulation of gene expression, which could support the hypothesis of a pathogen-driven suppression of general defence responses. Genes have been assigned to putative functional categories according to the Gene Ontology tool. Candidate genes possibly involved in signal transduction during early phases of infection will be the object of future investigations.