RESISTANCE TO *PLASMOPARA VITICOLA* IS ASSOCIATED WITH A COMPLEX PATTERN OF STILBENOIDS AND WITH SPECIFIC HOST TRANSCRIPTIONAL RESPONSES

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Downy mildew, caused by the oomycete *Plasmopara viticola*, is a serious disease in *Vitis vinifera*, the most commonly cultivated grapevine species. Several wild *Vitis* species have instead been found to be resistant to this pathogen and have been used as a source to introgress resistance into a *V. vinifera* background (Gessler et al., 2011). They may benefit from a higher level of constitutive resistance to *P. viticola* and display post-infection resistant mechanisms which trigger the accumulation of reactive oxygen species, antimicrobial phenolic compounds, as well as pathogenesis-related proteins and peroxidases. These events lead to morphological changes in the cell, including cell-wall thickening, necrosis and in some cases localized hypersensitive response (HR) (Kortekamp, 2006).

Stilbenoids represent the major antimicrobial phenolic compounds in grapevine, and their toxicity is closely related to the specific compound. They may be constitutively expressed in the lignified organs and in the grapes, or they may be elicited by fungal infection, abiotic stresses or elicitors (Jeandet et al., 2002, Gatto et al., 2008, Zamboni et al., 2009).

In the present work, we report the results of a combined metabolic and transcriptional profiling of the Merzling (M) × Teroldego (T) cross segregating for resistance to *P. viticola* (Malacarne et al., 2011). The metabolic part of the study has included the validation of a novel method of analysis by HPLC-DAD-MS for quantification of different classes of stilbenoids in infected grapevine leaves (Vrhovsek et al., 2012) and their isolation and structural characterization (Mattivi et al., 2011).

A three-year analysis of the population's response to artificial inoculation showed the quantitative character of the resistance trait with the individuals distributed in nine classes ranging from total resistance to total susceptibility. In addition, quantitative profiling of stilbenoids in the population identified three distinct groups differing for concentration and profile. The high producers were characterized by the presence of *trans*-resveratrol, *trans*-piceid, *trans*-pterostilbene and up to thirteen different viniferins, nine of them new in grapevine (Fig.1). Accumulation of these compounds turned out to be often linked with a resistant phenotype suggesting they may contribute to the resistance response.

A preliminary transcriptional study using cDNA-AFLP selected a set of genes modulated by the oomycete in a resistant genotype. The expression of this set of genes in selected resistant and susceptible genotypes of the progeny population was then assessed by comparative microarray analysis. A group of 57 genes was found to be exclusively modulated in the resistant genotype suggesting that they are involved in the grapevine-*P. viticola* incompatible interaction. Functional annotation of these transcripts revealed that they belong to the categories defense response, photosynthesis, primary and secondary metabolism, signal transduction and transport (Fig. 2).

These results will be valuable to future grapevine breeding programs.

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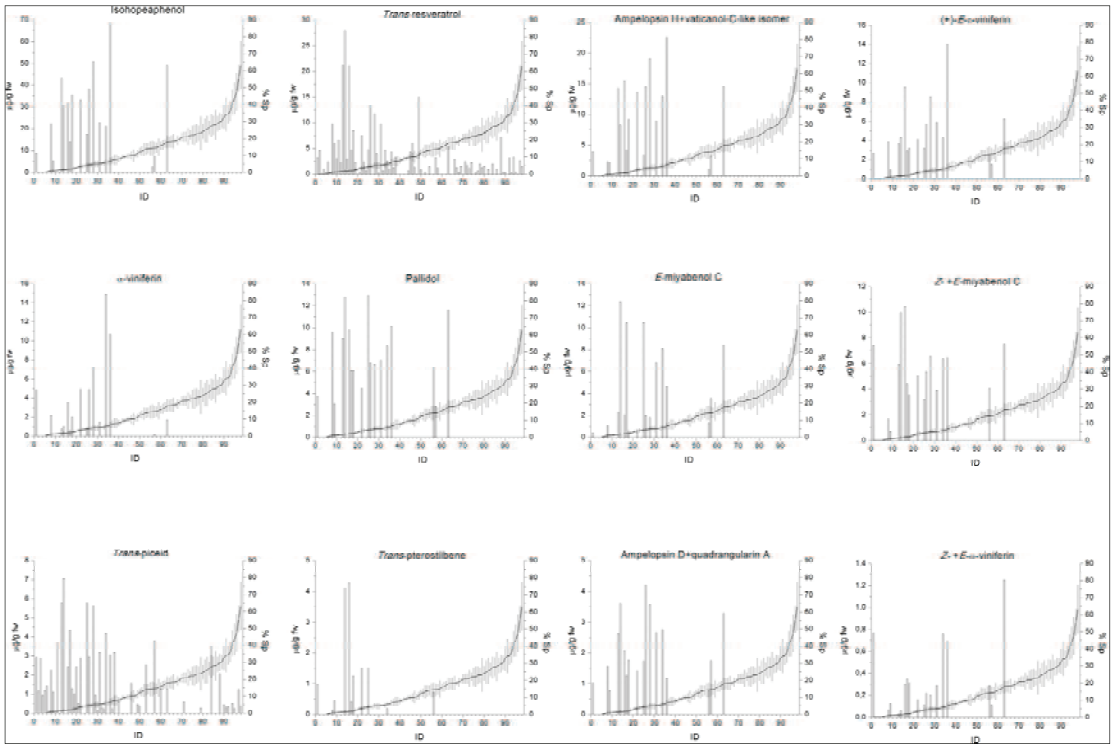

Fig. 1. Double-y plots of the concentrations (µg/g fw) of the 16 stilbenoids in infected leaves of the 106 individuals of the Merling (M) × Teroldego (T) cross (first y axis) and the percentage area of sporulation (% Sp) (second y axis). Individuals were ordered on the basis of the percentage area of sporulation (% Sp) on the lower side of leaves.

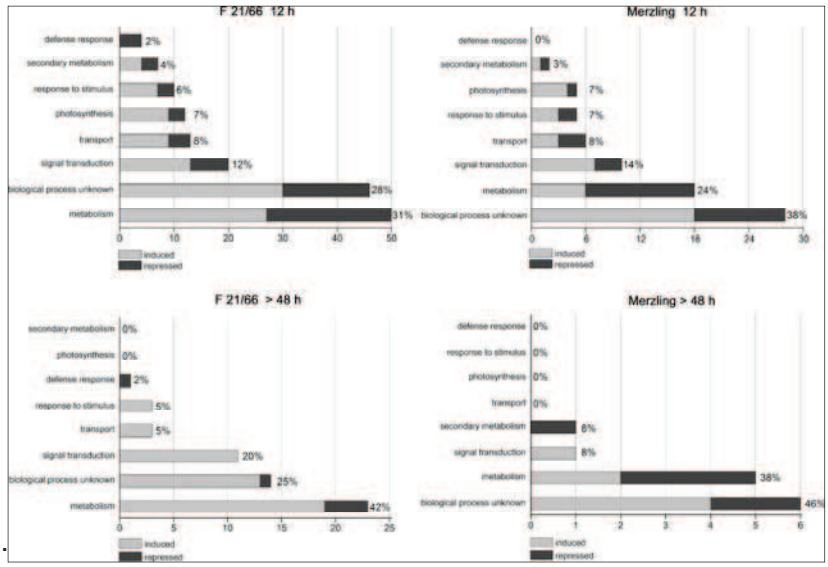

Fig. 2 Functional categories of transcripts identified as modulated in the resistant F1 21/66 and in Merzling upon infection with *P. viticola* by cDNA-AFLP analysis.