

Characterization of downy mildew resistance in a grapevine segregating population by integration of metabolite and disease symptoms analysis

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Downy mildew, caused by the oomycete *Plasmopara viticola* (Berk. & Curt.) Berl. & de Toni, is one of the major threats of grapevine cultivation particularly in warm and humid climate. All traditional grapevine cultivars (*Vitis vinifera* L.) are susceptible to downy mildew, and its control mainly relies on the use of synthetic fungicides which are costly and have environmental impact as well. Therefore, developing new varieties that are resistant to downy mildew through breeding is a promising alternative.

Stilbenoids represent the major antimicrobial phenolic compounds in grapevine and there are compelling evidences that they contribute to both constitutive and induced resistance mechanisms. For several years, we have been investigating the roles of the *Vitis* stilbenoids as determinants of downy mildew resistance, taking advantage of an interspecific population derived from Merzling (a complex hybrid of *V. vinifera* descending from *V. rupestris* and *V. lincecumii*) × *V. vinifera* cv Teroldego.

With this aim, 130 F1 individuals of the segregating population have been characterized at both genotypic and phenotypic level. Regarding the latter, a comprehensive analysis of leaf phenolics (including 16 different stilbenoids) and resistance screening upon *P. viticola* infection has been carried out.

Preliminary results indicated a significant induction of several stilbenoids following downy mildew infection in a subset of individuals which are characterized by a high degree of resistance. QTL analysis for disease resistance and stilbenoids production is in progress and will lead to the identification of genomic regions associated to these traits.

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