



Book of Abstracts

Final Conference

Challenges and prospects in PNP
metabolic engineering and production

Sorrento, Italy
April 15th-17th, 2015



P-11

The genetic bases of stilbenoids biosynthesis upon downy mildew infection in grapevine

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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. As a consequence, a deep comprehension of the genetic bases of stilbenoids biosynthesis is desirable. 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 the *Vitis* hybrid Merzling × *V. vinifera* cv Teroldego.

With this aim, 130 F1 individuals of this segregating population have been characterized at both genotypic and phenotypic level. Regarding the latter, a comprehensive analysis of leaf phenolics (including 16 different stilbenoids) upon *P. viticola* infection has been carried out. Our results indicated a significant induction of several stilbenoids following downy mildew infection in a subset of individuals characterized by a high degree of resistance. Then, QTL analysis lead to the identification of genomic regions associated to stilbenoids production. Moreover, a kinetic analysis of the accumulation of the different stilbenoids and of the expression of some genes associated to their biosynthesis has been carried out upon pathogen infection. This kinetics has revealed a

significant correlation between the type of stilbenoid and specific members of the stilbene synthase gene family.

Finally, the ongoing comparison between the stilbenoids biosynthesis results and the findings derived from a QTL analysis for downy mildew resistance conducted in parallel will putatively provide common as well as specific regions associated to both traits.