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THE GENETIC BASES OF DOWNY MILDEW RESISTANCE AND STILBENOIDS PRODUCTION IN A GRAPEVINE INTERSPECIFIC CROSSING POPULATION

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Grapevine downy mildew (DM), caused by the oomycete *Plasmopara viticola* (Berk. & Curt.) Berl. & de Toni, is one of the major plagues affecting viticulture, particularly in temperate-humid climate. All traditional grapevine cultivars (*Vitis vinifera* L.) are susceptible to DM, which can attack any grapevine green tissue. Its control mainly relies on the use of synthetic fungicides which are costly and have environmental impact as well. Therefore, the characterization of non-*vinifera* genetic resources leading to the development of new varieties resistant to DM is a promising alternative.

Among phenolics, stilbenoids represent the major antimicrobial compounds in grapevine and there are compelling evidences that they contribute to both constitutive and induced resistance mechanisms. We have been investigating for several years the roles of the *Vitis* stilbenoids as determinants of DM resistance, taking advantage of an interspecific population derived from Merzling (a complex hybrid descending from *V. vinifera*, *V. rupestris* and *V. lincecumii*) _ *V. vinifera* cv Teroldego. However, the genetic bases of DM resistance as well as stilbenoids biosynthesis upon DM infection in this crossing population has not yet been elucidated.

With this aim, 136 F1 individuals of the segregating population were characterized at genotypic level by means of 190 microsatellite (SSR) markers, chosen as well-scattered and uniquely positioned across the grapevine reference genome. Moreover, these F1 individuals have been screened at phenotypic level for their disease resistance degree as well as phenolics production. Firstly, the DM resistance assessment was performed on both leaf disk bioassays and plants infected under controlled conditions. Secondly, a comprehensive analysis of 41 phenolics (of which 16 different stilbenoids) was carried out. Our results indicated an approximately normal distribution of several disease resistance parameters and a significant induction of different polymeric stilbenoids upon DM infection; the latter occurred in a subset of F1 individuals which are characterized by a high degree of resistance. The Merzling _ Teroldego linkage map has been built, whereas QTL analysis for DM resistance and stilbenoids induction, which will lead to the identification of common as well as specific genomic regions associated to both traits, is ongoing.