Genetic analysis of the resistance to downy and powdery mildews derived from cultivar Bronner

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A wide range of pathogens threatens viticulture. Among them, downy and powdery mildews are the most important in Europe. The current strategy to control these diseases relies totally on the use of fungicides. This practice is not only expensive but also causes a slow and progressive damage to the environment. A cost-effective and environment friendly alternative to the use of chemicals is the development of varieties resistant to pathogens. All traditional European grapevine varieties are susceptible to the main pathogens. However *Vitis* species closely related to cultivated grapevine were shown to be potential sources of resistance to a wide spectrum of grapevine diseases (Boubals 1959, Staudt and Kassemeyer 1995).

The absence of private grapevine breeders in France led the INRA to design a breeding program dedicated to create new resistant varieties. The main goal of this programme is to create varieties durably resistant to downy and powdery mildews with a berry quality suitable to produce high quality wines (Merdinoglu *et al.* 2009). In order to successfully reach the double objective of high resistance efficiency and durability, the use of multiple sources of resistance was planned as soon as the project was designed. The project was developped in close interconnection with upstream research programmes which aim at understanding the genetic bases of the resistance to downy mildew derived from grapevine-related wild species by addressing four key questions: (i) exploring the diversity available in genetic resources to chose original genitors (ii) identifying and characterizing the relevant genes/QTLs to genetically improve the targeted traits, (iii) using the data acquired on genes/QTLs (position, effects) to assist the selection with markers, and (iv) assessing the durability of the identified resistance genes/QTLs.

In the presented study, we analysed the genetic determinism of the resistance to grapevine downy and powdery mildews derived from cultivar Bronner. We used two BC6 mapping populations, respectively consisting of 96 and 143 individuals from a cross between the resistant parent Bronner and an other resistant parent derived from *Muscadinia rotundifolia* var. Dearing. The two populations were screened with two SSR markers flanking Rpv1, a downy mildew resistance QTL from *Muscadinia*, in order to discard the individuals with this resistance factor and only keep the plants segregating for the resistance derived from Bronner. Resistance to downy mildew was assessed after artificial inoculation on both populations. Plants were genotyped at 65 SSR loci which allowed us to build a genetic map covering 648 cM. The interval mapping analysis revealed the presence of a major downy mildew resistance QTL that was located on linkage group 9. This resistance factor accounted for 52% of the total phenotypic variation. Thus, we considered this QTL as a major gene.

Resistance to powdery mildew was assessed after artificial inoculation as well. The interval mapping analysis revealed the presence of two minor QTLs involved in powdery mildew resistance. The two QTLs were located on linkage group 3 and linkage group 19 and explained 8% and 16% of the total phenotypic variation, respectively.

Literature cited

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