A compared genetic analysis of resistance to *Plasmopara viticola* from different Vitis species

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Abstract

Grapevine requires numerous fungicide treatments, in particular to control downy mildew caused by the oomycete *Plasmopara viticola*. One way to reduce the use of fungicides in viticulture, is the creation of grapevine cultivars resistant to downy mildew. Several sources of resistance to downy mildew have been identified in the genus *Vitis*. Knowledge of the genetic determinism of these sources of resistance is a prerequisite to design optimal selection strategies aiming at creating varieties with durable resistance. We considered two sources of resistance: *V. amurensis* 'Ruprecht', a wild asian species whose resistance is total and *V. vinifera* cv 'Bronner', a variety of cultivated grapevine whose resistance is partial, but high level. Used segragating populations we have established a genetic map for each of these sources of resistance and we have mapped the main resistant factors. For 'Bronner' a major and a minor resistant QTLs have been found on the LG9 and LG19 respectively. For *V. amurensis* a major QTL named *Rpv8* has been found to be responsible for the resistance. and a fine map of the region containing *Rpv8* was initiated. The interval of the QTL was reduced to a region with 7 candidate genes. Finaly, we tested the stability of the QTLs identified in the laboratory during this work and in previous studies, by confronting them with 6 strains of *P. viticola*. These knowledge will then be used to optimize the management of different resistances in breeding programs.

Keywords: *Plasmopara viticola*, *Vitis vinifera*, *Vitis amurensis*, genetic mapping, QTL, quantitative resistance, *Rpv8*, stability, durability, breeding programme, marker-assisted selection, SSR.