Oral presentations

Breeding for grapevine downy mildew resistance *via* gene editing

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Abstract

Downy mildew (DM) caused by the oomycete *Plasmopara viticola* ranks in the top diseases affecting grapevine (*Vitis vinifera* L.) cultivation and its control requires every year a large use of fungicides. The Farm to Fork strategy newly promoted by the EU aims to accelerate the transition to a sustainable food system and has set very ambitious targets including the reduction by 50% of the use and risk of pesticides by 2030. The introduction of disease-tolerant grapevine varieties or clones clearly represents a step forward to reach this goal.

The recent advent of new breeding tools such as genome editing and *cis*-genesis offers a great opportunity to obtain resistant plants with higher precision and speed than by conventional breeding, either by knocking down susceptibility genes or by introducing known resistance-genes in commercial cultivars. Based on reports in other crops, the family of *Downy Mildew Resistant 6* (DMR6) and DMR6-like oxygenases (DLOs) are candidate susceptibility genes for the control of DM resistance in *V. vinifera*.

Deep-sequencing the putative susceptibility genes in 190 genetically diverse grapevine genotypes identified several Single Nucleotide Polymorphisms then screened for their impact on protein structure/function and association with DM resistant genotypes. Gene expression and gene network analysis suggested that grapevine *DMR6* and *DLO* genes have distinct functions, and that *VviDMR6-1* is co-regulated with several Pathogenesis-related genes. Based on this evidence, we generated a large collection of *DMR6-1* and *DMR6-2* single and double knock-out mutants in multiple grapevine cultivars and evaluated their resistance to DM. Phenotypic resistance data upon artificial infection are being collected and will be presented here. In parallel, we also developed a new DNA-free gene editing methodology and obtained non-transgenic and non-chimeric edited grapevine plants regenerated from a single cell.

Keywords: *Vitis*, *Plasmopara viticola* resistance, new breeding technologies, susceptibility genes, DMR6, gene network analysis