

Resistance to sharka in Stone Fruit trees : Genetic and genomic technologies for new breeding strategies

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Abstract: Sharka is the most detrimental disease for stone fruit trees. It is due to the infection, through aphids or grafting, by the *Plum Pox Virus* (PPV). Few sources of resistance have been described in *Prunus* sp. and it is seriously lacking in crop species, threatening fruit production.

Depending on the *Prunus* species, different approaches have been set up. In *Armeniaca*, we searched for the geographical origin and genetic diversity of resistance (Decroocq et al., 2016). We identified PPV resistant apricot natural populations among the Central Asian mountain forests. They are currently being used for mapping the resistance determinants through GWAS which will be compared to the ones identified in the cultivated germplasm (Mariette et al., 2016).

In *Amygdalus*, resistance to sharka was documented in two peach related species, i.e. *P. davidiana* and *P. dulcis* –almond- (Pascal et al. 1998, 2002). While in *P. davidiana* the number of resistance sources is limited to one clone, previous studies described almond as non-host, resistant or susceptible to PPV. Such discrepancies reflect a wide variability of responses depending on the almond genotype or on the viral isolate. In the frame of the FP7 STONE project, *P. dulcis* and related species sampled in their area of origin were assessed experimentally. The most promising are being used to map the genetic determinants for resistance and to implement genomic selection to speed up the introgression of resistance in peach.

In plum species, which are more amenable to genetic transformation, PPV susceptibility factors have been targeted through gene silencing. PPV resistant lines of diploid plums (*P. salicina*) in which one susceptibility host factor has been impaired are by now being used for introgression in other diploid *Prunus* sp. as well as for genome editing in the frame of the H2020 TESS project (2018-2021).

Keywords: sharka, *Prunus*, GWAS, genomic selection, genome editing