



HAL
open science

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

Véronique Decroocq, Stephane Decroocq, David Tricon, Timothée Flutre, Thierry Pascal, Christophe Tuero, J. Salava, S. Liu, W.S. Liu, J. Rubio, et al.

► To cite this version:

Véronique Decroocq, Stephane Decroocq, David Tricon, Timothée Flutre, Thierry Pascal, et al.. Resistance to sharka in Stone Fruit trees: Genetic and genomic technologies for new breeding strategies. 9. International Rosaceae Genomics Conference, Jun 2018, Nanjing, China. hal-01819033

HAL Id: hal-01819033

<https://hal.science/hal-01819033v1>

Submitted on 5 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

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

Decroocq V.¹, Decroocq S.¹, Tricon D.¹, Flutre T.², Pascal T.³, Tuero C.³, Salava J.⁴, Liu S.^{1,5}, Liu W-S.⁵, Rubio J.⁶, Sanchez E.⁶, Prieto H.⁶

¹UMR BFP, INRA-Univ. Bordeaux, Villenave d'Ornon, France, ²INRA AGAP, Montpellier, France, ³UGAFL, UR1052 INRA, Montfavet, France, ⁴CRI, Prague, Czech Rep, ⁵Liaoning Institute of Pomology, Xiongyue, Yingkou City, China; ⁶INIA, La Platina Station, Santiago, Chile.

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