

Deciphering protein interactors of the ParPMC proteins involved in Sharka resistance in apricot

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TIPO DE PRESENTATION: Poster

ABSTRACT

Sharka disease, caused by the potyvirus Plum pox virus (PPV), is one of the most limiting factors for the production of stone fruits. The development of resistant varieties is the best solution to control this disease. Recently, combining genetic, genomic and transcriptomic data, we pointed *ParPMC1* and *ParPMC2* as host susceptibility genes which silencing confers resistance to PPV in apricot. Both *ParPMC* genes are highly similar and belong to a cluster of meprin and TRAF-C homology domain (MATHd)-containing genes of unknown function. In order to deepen the study of their possible function, in this work we address the identification of putative interactors of the proteins encoded by them. For this purpose, a triple approach has been carried out: *in vitro*, *in vivo* and *in silico*. First, a yeast two-hybrid assay (Y2H) was carried out using tissue from susceptible varieties inoculated with PPV for the construction of the library. Second, these results were verified by a bimolecular fluorescence complementation (BiFC) assay. Finally, these results were combined with previous genomic and transcriptomic data to perform an *in silico* protein-protein interaction networks (PPIN) analysis. The results obtained allowed the identification of some genes putatively involved in the control of this trait. This represents an advance in the knowledge about the mechanism of PPV resistance in apricot that could also be of great interest for the stone fruit breeding programs.

Keywords: interaction, stone fruits, PPV, Y2H, BiFC, PPIN.

Acknowledgments: This research was funded by the ‘Ministerio de Ciencia e Innovación/ Agencia Estatal de Investigación de España’ (projects RTA2017-00011-C03-01 and PID2020-113276RR-I00/AEI/10.13039/501100011033). A.P.O. acknowledges the support granted with the PhD fellowship co-financed by the European Social Fund and the Generalitat Valenciana ACIF/2021/343 (DOCV 8959/24.11.2020).

