

Abstract #2135

Searching key proteins for the pathogenesis and development of the cucurbit powdery mildew pathogen *Podosphaera xanthii*

Alejandro Perez Garcia¹, Jesus Martinez Cruz², Alvaro Polonio², Laura Ruiz-Jimenez², Monserrat Grife-Ruiz² and Dolores Fernandez-Ortuño², (1)University of Malaga, Malaga, Spain, (2)University of Malaga, Spain

Abstract Text:

Podosphaera xanthii is the causal agent of cucurbit powdery mildew and one of most important limiting factors for cucurbit production worldwide. Current management practices are based on the use of resistant cultivars and the repetitive applications of fungicides, thus favoring the development of new races of the pathogen and the selection of populations with resistance to multiple fungicides. This scenario has led to the need to develop new tools for disease control. As a preliminary step to the development of new control strategies, in our laboratory we focus on the search for key proteins for the pathogenesis and development of *P. xanthii*. Among the transcripts identified in the epiphytic and haustorial transcriptomes, we have paid attention to three different set of genes: secreted protein-coding genes, conserved non-annotated protein-coding genes, and new protein-coding genes. First, these genes were analyzed *in silico* for predicted function and ligand binding using diverse software such as I-TASSER, Phyre2 and others. Second, those genes to which a certain function could be attributed computationally were subjected to functional genomic analysis by *Agrobacterium tumefaciens*-mediated host-induced gene silencing (ATM-HIGS). *Podosphaera* genes with a strong phenotype after gene silencing in terms of reduction of fungal growth and/or activation of host defense responses were selected. An overview of the essential genes and functions identified so far will be presented.

Title:

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Submitter's E-mail Address:

aperez@uma.es

Category

Microbial Manipulation of the Host

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No

First Presenting Author

Presenting Author

Alejandro Perez Garcia

Email: aperez@uma.es -- Will not be published

University of Malaga
Prof.
Malaga 29071
Spain

Second Author

Jesus Martinez Cruz

Email: jesusmcruz@uma.es -- Will not be published

University of Malaga

Spain

Third Author

Alvaro Polonio

Email: polonio@uma.es -- Will not be published

University of Malaga

Spain

Fourth Author

Laura Ruiz-Jimenez

Email: laura110493@uma.es -- Will not be published

University of Malaga

Spain

Fifth Author

Montserrat Grife-Ruiz

Email: montsegrife@uma.es -- Will not be published

University of Malaga

Spain

Sixth Author

Dolores Fernandez-Ortuño

Email: dfernandez-ortuno@uma.es -- Will not be published

University of Malaga

Spain