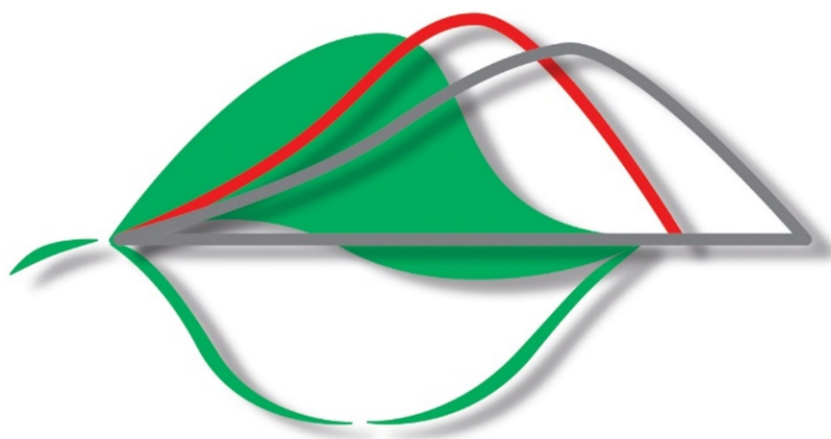


20th International Reinhardtsbrunn Symposium

Modern Fungicides and Antifungal Compounds



Friedrichroda, Germany
23th –27th April 2023

Program and Abstracts
Update April 18, 2023



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P20 ID 20 Gene Mining for Conserved, Non-Annotated Proteins of *Podospaera xanthii* Identifies Novel Target Candidates for Controlling Powdery Mildews by Spray-Induced Gene Silencing

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The powdery mildew fungus *Podospaera xanthii* is one of the most important limiting factors for cucurbit production worldwide. Despite the significant efforts made by breeding and chemical companies, effective control of this pathogen remains elusive to growers. In this work, we examined the suitability of RNAi technology called spray-induced gene silencing (SIGS) for controlling cucurbit powdery mildew. Using leaf disc and cotyledon infiltration assays, we tested the efficacy of dsRNA applications to induce gene silencing in *P. xanthii*. Furthermore, to identify new target candidate genes, we analyzed sixty conserved and non-annotated proteins (CNAPs) deduced from the *P. xanthii* transcriptome in silico. Six proteins presumably involved in essential functions, specifically respiration (*CNAP8878*, *CNAP9066*, *CNAP10905* and *CNAP30520*), glycosylation (*CNAP1048*) and efflux transport (*CNAP948*), were identified. Functional analysis of these CNAP coding genes by dsRNA-induced gene silencing resulted in strong silencing phenotypes with large reductions in fungal growth and disease symptoms. Due to their important contributions to fungal development, the *CNAP1048*, *CNAP10905* and *CNAP30520* genes were selected as targets to conduct SIGS assays under plant growth chamber conditions. The spray application of these dsRNAs induced high levels of disease control, supporting that SIGS could be a sustainable approach to combat powdery mildew diseases.

Funding: Agencia Estatal de Investigación (AEI), grant numbers AGL2016-76216-C2-1-R and PID2019-107464RB-C21, funded this research. L.R.-J. was supported by a PhD fellowship also from AEI, grant number BES-2017-080414.