



16,17,18 y 19 Sept. 2024

XXI CONGRESO DE LA SEF

Palacio
de Congresos
de Córdoba

www.sefcordoba2024.com





Ejemplos de mutagénesis dirigida basada en CRISPR ya en ensayo de campo en la Unión Europea son ensayos de mutantes de patata (resistencia a *Phytophthora*) o arroz (resistencia a *Pyricularia*). Hay proyectos ya avanzados con ensayos en invernadero para obtener mutantes de trigo con multi-resistencia a enfermedades fúngicas.

Se discutirán brevemente al final las condiciones para que el potencial de estas técnicas sea realizable (técnicas, sociales, económicas, regulatorias).

Financiado por: Joint Research Centre (JRC)

O.80. Management Of Cucurbit Powdery Mildew Using An Rnai Technology Strategy Targeting Virulence Genes

Nisrine Bakhat¹, Alejandro Jiménez Sánchez¹, Leonardo Velasco³, Alejandro Pérez García¹, Dolores Fernández Ortuño¹

1 Departamento de Microbiología, Facultad de Ciencias, Universidad de Málaga

2 Instituto de Hortofruticultura Subtropical y Mediterránea “La Mayora”, Universidad de Málaga, Consejo Superior de Investigaciones Científicas (IHSM-UMA-CSIC)

3 Departamento de Protección Vegetal, Centro IFAPA de Málaga

Tipo Comunicación: ORAL

Palabras Clave: Powdery mildew, *Podosphaera xanthii*, Chitin-triggered immunity, RNAi, SIGS

Resumen:

Cucurbit powdery mildew, caused by *Podosphaera xanthii*, is one of the most destructive plant diseases worldwide. Currently, chemical control and the use of resistant varieties are the main approaches for disease control. However, fungicide-resistant isolates and new strains of the pathogen make its control more difficult and require the development of innovative strategies. Chitin is an important component of fungal cell walls and an effective trigger of plant immunity. Therefore, plant-pathogenic fungi have evolved virulence factors to suppress this defense response. In this study, the molecular mechanism of chitin-induced suppression through effectors implicated in the modification of chitin immunogenic oligomers (CDA) and their degradation (EWCA), were investigated for the development of novel “biofungicides”. For this, RNA interference (RNAi) technology was used, which employs double-stranded RNA (dsRNA) to inhibit the expression of the corresponding target genes. For such purpose, different studies were undertaken. Disease suppression effect was first carried out in leaf disc assays. The processing of *PxCDA*-dsRNA by the plant RNAi machinery, was examined by small RNA sequencing (sRNA-seq) of melon dsRNA sprayed but uninfected plants, showing that the dsRNA was processed into siRNAs 24 hours after spraying. The uptake of *PxCDA*-dsRNA and *PxEWCAs*-dsRNA by *P.*



xanthii was examined by confocal microscopy, showing the presence of fluorescent-dsRNAs inside the fungal spores. Gene silencing of target genes was analyzed in infiltrated cotyledons and sprayed leaves, resulting in reductions of gene expression of about 50% that correlated with similar reductions of disease symptoms. Finally, in greenhouse experiments, the use of dsRNA protected by nanoparticles showed similar values of disease reduction that were extended up to 21 dpi. These results highlight the potential of this RNAi approach as innovative and specific control tools to be incorporated into de integrated management program for cucurbit powdery mildew.

Financiado por: This work has been funded by the projects PDC2021-121373-C21 and PID2022-136240OB-C21/MCIN/AEI/10.13039/501100011033/FEDER, UE.

O.81. Pangenome-Wide Association Study Analysis Reveals Novel QTLs and Candidate Genes Controlling Wheat Powdery Mildew in Tetraploid Wheat Landraces

Javier Sánchez Martín¹, David Encalada Bustamante¹, Gonzalo Costas Fernández¹, Victoria Widrig¹

¹ Department of Microbiology and Genetics, Spanish-Portuguese Agricultural Research Center (CIALE), University of Salamanca, 37185, Salamanca, Spain

Tipo Comunicación: ORAL

Palabras Clave: genetic diversity, wheat, landraces, wheat powdery mildew pathosystem, GWAS, resistance, plant-microbe interactions

Resumen:

Man-made wheat domestication and breeding led to genetic bottlenecks minimizing genetic diversity with which commercial varieties cannot cope with biotic and abiotic stresses imposed by climate change. Bread wheat landraces, a crop status between wild relative and elite cultivars display, compared to modern breeding material, higher genetic diversity likely to be important for adaptation. To exploit this untapped genetic diversity potential, we assembled a diverse collection of 750 Spanish tetraploid wheat landraces to identify sources of resistance against the wheat yield-reducing fungal disease powdery mildew caused by *Blumeria graminis* f. sp. *tritici*.

To identify novel sources of resistance, a *Kmer*-based genome-wide association study (GWAS) was conducted on the landrace panel genotyped with DArTseq technology for seedling resistance using four powdery mildew isolates with contrasting virulence spectra. We developed a pan-genome-wide association pipeline based on multiple wheat reference genomes, maximizing the chances of tagging responsible loci for mildew resistance, likely absent in a single reference genome. The association mapping detected some known *Pm* genes (e.g., *Pm1*, *Pm3b*, or *Pm4b*) but also novel regions associated with powdery mildew resistance in chromosomes 4A, 5B, and 6B.