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**Abstract
Book**



strains and *A. solani* strains adapted to selection pressures from commonly used fungicides from various modes of action were reported. To monitor the spread of such phenotypes, samples were collected in important potato growing regions in Europe in 2023 as well as previous years. Additionally, molecular tools were applied to identify the mutations responsible for detected phenotypes. In both pathogens isolates were detected showing accumulation of mutations leading to resistance to multiple modes of action, which have implications for resistance management strategies. Cross-resistance studies were conducted to demonstrate the impact of detected mutations and mutation-combinations on selected compounds from the group of QoIs and SDHIs as well as OSBPIs and CAAs. Full sensitivity was confirmed for DMIs and the newly elucidated mode of action of Vacuolar-type Proton ATPase of Fluopicolide. Lastly, greenhouse experiments were conducted to elucidate the impact of the detected mutations and mutation-combinations on commercially available solutions. It's implications on fungicide resistance management strategies are discussed.

SE18 C09

UNRAVELING THE MOLECULAR BASIS OF DMI RESISTANCE IN *CERCOSPORA BETICOLA*

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Cercospora leaf spot (CLS), caused by the fungal pathogen *Cercospora beticola*, is the most destructive disease of sugar beet worldwide. Resistance to the sterol demethylation inhibitor (DMI) fungicide tetraconazole has been previously correlated to synonymous and non-synonymous mutations in *CbCyp51*. We have extended these analyses to the DMI fungicides prothioconazole, difenoconazole, and mefentrifluconazole in addition to tetraconazole to confirm whether the synonymous and non-synonymous mutations at amino acid positions 144 and 170 are associated with resistance to these fungicides. Nearly half of the 593 isolates collected in this study were resistant to all four DMIs. Another 20% were resistant to tetraconazole and prothioconazole but retained sensitivity to difenoconazole and mefentrifluconazole. We found five *CbCyp51* haplotypes and associated them with phenotypes to the four DMIs. One mutation, L144F, is found in two codon variants TTC and TTT, where TTC is associated with resistance and TTT is associated with sensitivity even though both codons encode phenylalanine. Additionally, resistance is also strongly associated with the synonymous mutation E170. Quantitative PCR did not identify obvious trends in *CbCyp51* expression between haplotypes. However, mutant strains where the native *CbCyp51* gene is swapped with a different haplotype has confirmed the role of these mutations with DMI resistance. These results will be presented.

SE18 C10

RNA INTERFERENCE, A NOVEL STRATEGY TO BE INCORPORATED INTO INTEGRATED PEST MANAGEMENT PROGRAMS FOR THE CUCURBIT POWDERY MILDEW CONTROL

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Powdery mildew fungi are plant-pathogenic ascomycetes that are among the most common and important plant fungal pathogens causing diseases in a broad range of angiosperms, including both dicots and monocots. Major crops, such as various vegetable crops are susceptible to powdery mildews, but cucurbits are arguably the group mostly affected. In Spain, the disease is caused by the biotrophic fungus *Podosphaera xanthii*. At present, the management of this disease is based on the use of resistant varieties and the application of fungicides; however, the rapid development of new races of the pathogen, the resistance generated to the most frequently employed mildewcides and the European Green Deal ("farm to fork" strategy) make necessary the development of alternative control tools and molecules with novel fungicide activity to be integrated into the IPM programs. In this study, the potential of the RNA interference (RNAi) technology to design "dsRNAs fungicides" to be used as "bio-fungicides" in crop protection was tested. For that, essential genes involved in *P. xanthii* fungal development and disease symptoms such as key proteins necessities for fungal respiration (FRAC group 7), cytoskeleton (FRAC group 1) and methionine biosynthetic pathway (FRAC group 9) were targeted. These oligonucleotides were tested alone and in combination with commercial fungicides at low doses such as boscalid, cyprodinil, fluopyram and thiophanate-methyl. In addition, the use of nanotechnology to improve the efficacy of RNAi for the control of cucurbit powdery mildew was also explored. For that, the encapsulation of the dsRNAs molecules in carbon dots (CDs) nanoparticles was carried out in greenhouse experiments to test their efficacy. The results obtained could make a major contribution towards integrated pest management and sustainable agriculture of this important disease worldwide.

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