

Genome-Wide Association and Selective Sweep Studies Reveal the Complex Genetic Architecture of DMI Fungicide Resistance in *Cercospora beticola*

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ABSTRACT

The rapid and widespread evolution of fungicide resistance remains a challenge for crop disease management. The demethylation inhibitor (DMI) class of fungicides is a widely used chemistry for managing disease, but there has been a gradual decline in efficacy in many crop pathosystems. Reliance on DMI fungicides has increased resistance in populations of the plant pathogenic fungus *Cercospora beticola* worldwide. To better understand the genetic and evolutionary basis for DMI resistance in *C. beticola*, a genome-wide association study (GWAS) and selective sweep analysis were conducted for the first time in this species. We performed whole-genome resequencing of 190 *C. beticola* isolates infecting sugar beet (*Beta vulgaris* ssp. *vulgaris*). All isolates were phenotyped for sensitivity to the DMI tetraconazole. Intragenic markers on chromosomes 1, 4, and 9 were significantly associated with DMI fungicide resistance, including a polyketide synthase gene and the gene encoding the DMI target *CbCYP51*. Haplotype analysis of *CbCYP51* identified a synonymous mutation (E170) and nonsynonymous mutations (L144F, I387M, and Y464S) associated with DMI resistance. Genome-wide scans of selection showed that several of the GWAS mutations for fungicide resistance resided in regions that have recently undergone a selective sweep. Using radial plate growth on selected media as a fitness proxy, we did not find a trade-off associated with DMI fungicide resistance. Taken together, we show that population genomic data from a crop pathogen can allow the identification of mutations conferring fungicide resistance and inform about their origins in the pathogen population.

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