VIRULENCE OF *MAYETIOLA DESTRUCTOR* (SAY) FIELD POPULATIONS IN THE GREAT PLAINS AND LEVANASE/INULASE-LIKE GENES IN THE HESSIAN FLY GENOME

by

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Abstract

The Hessian fly, *Mayetiola destructor* (Say), is a major pest of wheat, and is controlled mainly through deploying fly-resistant wheat cultivars. This study investigated five *M. destructor* populations collected from Texas, Louisiana, and Oklahoma, where infestation by Hessian fly has been high in recent years. Eight resistance genes including *H12, H13, H17, H18, H22, H25, H26*, and *Hdic*, were found to be highly effective against all tested *M. destructor* populations in this region, conferring resistance to 80% or more of plants containing one of these resistant genes. The frequency of biotypes virulent to resistant genes ranged from 0 to 45%. A logistic regression model was established to predict biotype frequencies based on the correlation between the percentages of susceptible plants obtained in a virulence test. In addition to the virulence test, the log-odds of virulent biotype frequencies were determined by a traditional approach to predict the logistic regression model.

Characterization of a bacterial artificial chromosome (BAC) clone identified a gene encoding a protein with sequence similarity to bacterial levanases. Blast searching with the levanase-like protein identified 14 levanase/inulase-like genes or gene fragments. In this study, we determined the expression levels of these genes in different developmental stages and different tissues of 3-d old larvae of *M. destructor*. Sequence analysis revealed that six genes encode full length proteins, three were truncated at the 5' end, and five truncated at the 3' end. Sequences of putative proteins showed approximately 42% similarities to bacterial levanases or inulases, and 36% similarity to fungal levanases or inulases. No sequence similarities were found with any known animal or plant proteins. Comparative analysis of sequences among 14 levanase/inulase-like genes revealed that positions for intron/exon boundaries are conserved

among different genes even though the length of each intron and exon varied among different genes. The expression patterns of the levanase/inulase-like genes were different among developmental stages and larval tissues of *M. destructor*. Interestingly, three genes presented alternative splicing bands in different developmental stages, and two genes exhibited splicing bands in different tissues of 3 d old *M. destructor*. This study would be useful for future studies of the characterization and function of levanase/inulase-like genes of these enzymes in plant-insect interactions.