

IDENTIFICATION AND CHARACTERIZATION OF A BATTERY OF WHEAT GENES REGULATED BY HESSIAN FLY LARVAL FEEDING

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Establishment of a feeding site beneath the leaf sheath near the crown of developing seedlings in compatible interactions of Hessian fly (*Mayetiola destructor*) and wheat (*Triticum aestivum* L. em Thell.) result in larval growth and development. Physiological changes induced by virulent Hessian fly larvae reduce yields dramatically. Resistance is the most efficient means of protecting wheat plants against this pest. To date, 32 genes conferring Hessian fly resistance have been identified, yet none have been cloned. Although the gene-for-gene model has been demonstrated genetically to fit the wheat/Hessian fly interaction, the molecular basis of this interaction has not been described. We identified, through GeneCalling, 73 genes regulated by virulent and avirulent Hessian fly feeding. Validation of differential expression by quantitative real time PCR of these 73 genes revealed seven genes consistently responding to Hessian fly feeding across experiments involving the wheat line Iris, which carries the *H9* resistance gene, infested with *vH9* (compatible) and biotype L (incompatible) flies. The expression profile of the seven genes in response to Hessian fly larval feeding was gathered from experiments from the whole crown tissue, from individual leaf sheaths and also from crown tissue of seedlings having 1 or 21-30 larvae feeding at the base of the plant. Blast analysis of the seven sequences to the NCBI translated data base showed the following putative functions: Lipid transfer protein, Agglutinin isolectin 2 precursor, DNA repair RAD 23, Glutathione-S-transferase, Connective tissue growth factor, Flavanone 3-hydroxylase and a Sorbitol transporter. Expression profiles were also generated following: non- and viruliferous aphids carrying compatible viruses (barley yellow dwarf virus, PAV strain and cereal dwarf virus, wounding, armyworm infestation, chemical treatment (ABA, MeJA and SA) and water stress. Near full length cDNAs were cloned for all seven genes by RACE PCR for bioinformatics analysis. Virus induced gene silencing (VIGS) experiments are in progress to confirm the contribution of this battery of genes, which will yield a better understanding of the molecular responses of wheat to the Hessian fly.