

Gene Expression Profiling of Defense Responses to Greenbug Feeding in Wheat

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BACKGROUND



Greenbug is one of the most important aphid pests in small grain crops including wheat in the Southern Great Plains of the U.S where the economic damage often exceeds \$100 million annually. The Texas AgriLife Research wheat breeding program within the Texas A&M University System has introduced several greenbug-resistance genes into released cultivars, including TAM 110 and TAM 112; however, the molecular mechanisms of the resistance remain unknown. A microarray study was conducted to evaluate the differences in gene expression profiling in the near-isogenic resistant (TXGBE273) and susceptible (TXGBE281) wheat lines using Affymetrix GeneChip wheat genome array with 55,000 genes. Leaf samples from resistant and susceptible wheat lines at 0, 24 and 48 hours after infestation were used for gene expression analysis.

OBJECTIVES

- Investigate the greenbug resistant gene, *Gb3*, mediated defense responses in TXGBE273.
- Assess and compare the differences in gene expression profiles of resistant and susceptible lines to identify the key genetic regulators of greenbug resistance.



RESULTS

The microarray data analysis suggested that within 24 hours after greenbug feeding, the genes-related hormone and amino acid biosynthesis, metabolism, cell wall modification, defense signaling and secondary metabolites were differentially regulated between the resistant and susceptible line (Fig. 1). These results offer numerous opportunities to understand the molecular basis of resistance to greenbug feeding and help in developing wheat cultivars with better resistance.

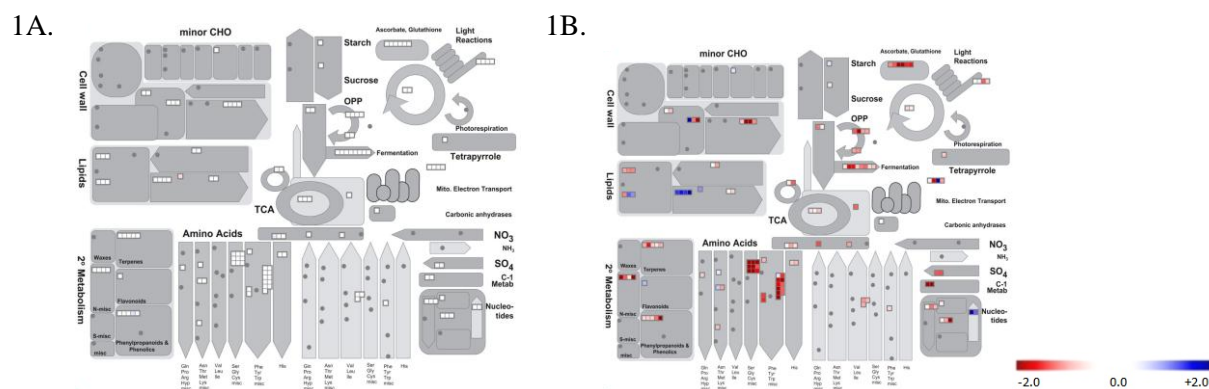


Fig. 1: MapMan metabolism overview maps showing differences in gene expression between resistant and susceptible lines at 0 hour (1A) and 24 hours (1B) after greenbug feeding.