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Project ID: FY06-SH-118	FY05 ARS Agreement #: New
Research Area: HGG	Duration of Award: 1 Year
Project Title: Signaling Mechanism Associated with Host Defense against Fusarium	
graminearum.	

PROJECT 2 ABSTRACT

(1 Page Limit)

In the US, annual losses of wheat to scab averaged between \$ 200-400 million. However, our understanding of the signaling mechanism(s) involved in the activation of plant defense against *Fusarium graminearum* and other agents of scab, is very limited. Identification of plant signaling mechanism(s) involved in defense against *F. graminearum* and the genes associated with these signaling mechanisms will assist in breeding scab resistant plants. In addition, some of these genes could provide excellent targets for engineering scab resistance in wheat and barley. For example, the *Arabidopsis thaliana* AtNPR1 gene that regulates salicylic acid (SA) signaling in plant defense, when constitutively expressed in transgenic wheat provides enhanced resistance to scab. Scab resistance in AtNPR1 expressing wheat plants correlated with their enhanced responsiveness to chemical activators of plant defense, suggesting that a NPR1 regulated defense-signaling mechanism(s) is primed to respond faster in the AtNPR1 expressing wheat. *Arabidopsis thaliana-F. graminearum* interaction provides an excellent host-fungus system to rapidly identify the signaling mechanism(s) and genes involved in defense against *F. graminearum*. Knowledge gained from studies with this system could then be applied to wheat and barley.

In this submission, we propose to study the involvement of SA, ethylene and jasmonic (JA) signaling in plant defense against *F. graminearum*. The specific objectives that will be pursued are: (1) Characterize the involvement of SA signaling in host defense against *F. graminearum*. Multiple approaches will be taken: (a) The response of plant defense to SA and its functional analog, BTH, will be compared between scab resistant and susceptible wheat cultivars to determine if there is a correlation between sensitivity to SA/BTH and the extent of scab resistance; (b) Arabidopsis SA synthesis mutants will be utilized to characterize the involvement of Ethylene and JA signaling in plant interaction with *F. graminearum*. (a) The impact of ethylene and JA treatment on controlling growth of *F. graminearum* in wheat will be tested; (b) Arabidopsis mutants with alterations in ethylene and JA synthesis/signaling pathway will be utilized to characterize the involvement of these signal molecules in plant defense against *F. graminearum*.

Our proposed project is relevant to the HOST GENETICS AND GENOMICS initiative of the USWBSI, by promoting the characterization of molecular mechanisms of host-pathogen interaction and the identification of signaling mechanisms that can be used to enhance host resistance to Fusarium graminearum.