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**Duration of Award: 1 Year**

**Project Title: Harnessing the Basal Defense Pathway to Improve Fusarium Head Blight Resistance.**

### **PROJECT 1 ABSTRACT**

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The primary objective for the USWBSI is to develop effect strategies to control Fusarium head blight (FHB). To accomplish this the researchers of the USWBSI Gene Discovery and Engineering Resistance (GDER) Research Area are working to understand the mechanistic events that determine whether interactions lead to disease or resistance. The contemporary model for plant defense holds that plants utilize two major pathways to provide resistance to biotic threats: basal or PAMP-triggered immunity (PTI) and effector-triggered immunity (ETI). Basal defense is believed to have evolved first and utilizes leucine-rich repeat receptor kinases (LRR-RKs), called pattern recognition receptors (PRRs) that recognize highly conserved molecular features shared among broad groups of pathogens. Although PTI and ETI activate many of the same responses, their activation has lower amplitude in PTI, so that cell death does not occur. Recognition of these conserved pathogen patterns by PRRs results in the activation of a wide range of host defense responses, including changes in ion flux, production of reactive oxygen (ROS), callose deposition, MAPK activation and large-scale reprogramming of transcription. Our recent work has established three very significant findings: 1) the plant hormone ethylene (ET) has a central role in the activating the basal defense pathway, 2) ET-induced basal defense makes a significant contribution to FHB resistance in wheat, and 3) stimulation of the ET-signaling in wheat can increase FHB resistance measured by type I and II disease assays.

The research proposed here builds upon our recent findings in several ways, our objective are:

1. We propose to conduct an RNA-Seq study to thoroughly define the transcriptional changes triggered in wheat, which are able to provide effective resistance to FHB when susceptible genotypes are pretreated with ACC.
2. Genes identified in the RNA-Seq analysis as having significantly differential expression will be tested for function in wheat by FHB-VIGS assays.
3. Transgenic plants that overexpress genes in the lignin biosynthetic pathway will be generated and tested to assess if they confer improved FHB resistance.
4. Complete the evaluation of the transgenic wheat plants that were generated during the previous funding period. These transgenics overexpress wheat ethylene-responsive transcription factors as well as the wheat PRR, BAK1, which were all shown to contribute to FHB resistance in VIGS assays. The transgenics will be tested in both type I and II FHB assays in the greenhouse, as well as in the USWBSI transgenic FHB nursery.
5. Test whether or not ethylene signaling is essential for FHB resistance in barley.