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Research Category: **GDER** **Duration of Award: 1 Year**

Project Title: Rapidly Identifying Scab Resistance Genes and Developing Scab Resistant Wheat.

PROJECT 2 ABSTRACT

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Fusarium head blight (FHB, scab), a fungal disease of small grain crops caused by *Fusarium graminearum*, threatens to reduce wheat and barley to economically unviable crops in the United States. During infection the fungus produces trichothecene mycotoxins such as deoxynivalenol (DON) that have been shown to increase fungal virulence. To complement the current breeding efforts, my laboratory seeks to develop and characterize transgenic wheat exhibiting trichothecene and FHB resistance. Previously, my laboratory developed transgenic wheat carrying a barley UDP-glucosyltransferase (*HvUGT13248*) and showed that these transgenics exhibit high levels of FHB resistance via conjugation of DON to DON-3-O-glucoside (D3G). D3G is considered a "masked mycotoxin" because it is not generally assayed for in harvested grain and can go undetected and pose a health risk due to the ability of gut microbes to reactivate D3G to DON. Thus, an important question is whether reduced infection due to the conjugation of DON to D3G results in reduced DON and D3G in harvested grain.

There are three major objectives in the proposed work including: (1) develop elite wheat cultivars with FHB resistance; (2) characterize the accumulation of trichothecenes and trichothecene-glucoside conjugates in transgenic wheat carrying *HvUGT13248*; and (3) test potential trichothecene resistance genes.

We will introgress the *HvUGT13248* transgene into two elite cultivars: Linkert and Rollag. We will develop BC_2 families containing the *HvUGT13248* transgene in both genetic backgrounds and test these plants for resistance to FHB in the greenhouse and field.

We will also characterize the accumulation of trichothecenes and trichothecene-glucoside conjugates in transgenic wheat carrying *HvUGT13248*. Since D3G is characterized as a masked mycotoxin, we will examine our wheat transgenics for the accumulation of DON and D3G throughout disease development and in harvested grain.

We have conducted a wide array of RNA profiling experiments on barley and wheat during *F. graminearum* infection and identified potential trichothecene resistance genes. We will test these potential resistance genes in functional assays in yeast and *Arabidopsis*. Through these assays we will continue to identify genes that exhibit resistance to trichothecenes. All genes that exhibit resistance will be transformed into wheat and tested in the greenhouse and field.

The proposed research meets the objectives of the USWBSI and fits within the Gene Discovery and Engineering Resistance (GDER) area of research. The proposed research has specific reference to the priorities of efficiently identifying and characterizing genes that provide FHB resistance and DON reduction, and engineering transgenic wheat exhibiting FHB resistance and DON reduction.