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## PROJECT 1 ABSTRACT (1 Page Limit)

The overall project goal is to identify Fusarium head blight (FHB) resistance in wheat lines with increased levels of phenolic compounds, some of which can inhibit the fungus, *Fusarium graminearum*. Phenolic compounds are recognized as part of plant generalized defense responses. The easiest way to increase levels of phenolic compounds is to increase expression of genes in a pathway for their production. We have generated wheat lines with increased levels of proteins that are involved in phenolic compound production. Previous research showed that two proteins, that when increased in wheat, led to better resistance to initial infection by *F. graminearum*. We have combined the genes with increased expression for these proteins using genetic breeding. We also have incorporated each of the genes in wheat lines Sumai 3 and Alsen, with moderate resistance to FHB. We will utilize lines with increased protein expression to identify other genes and pathways whose activities have been altered that can contribute to the observed increased resistance. The project objectives are:

- 1) Investigate response of wheat lines with stacked high expression genes and each gene in resistant backgrounds, Sumai 3 and Alsen, for Type I (to infection) resistance and Type 2 (to spread) resistance following inoculations under greenhouse conditions in Lincoln, NE, and Minneapolis, MN.
- 2) Conduct gene expression analysis on increased expression lines as compared to the normal cultivar.

The expected outcomes are confirmation of greenhouse observations of increased expression lines at two locations and identification of genes and pathways contributing to increased resistance in response to *F. graminearum* infection. We have all the tools for successfully completing the proposed research in two years. We will utilize collaboration with Dr. Ruth Dill-Macky at University of Minnesota to provide a second location for greenhouse screens. Our group in Lincoln is highly adept at gene expression and pathway analyses with a total of six publications since 2016, two involving plant responses to biotic stress.

This research has mutual interests with stakeholders. Differences in gene expression when comparing our increased expression lines with the normal cultivar during response to *F. graminearum* infection will almost certainly be identified, providing a source of markers for increasing resistance to FHB. These markers can be used in future studies to screen wheat or barley lines with altered responses to *F. graminearum* that can be used for future breeding of lines with increased resistance.