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**Project Title: A Genome Wide Screen to identify Novel Genes for FHB**

### **PROJECT 1 ABSTRACT**

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Trichothecene mycotoxins, including deoxynivalenol (DON) target the ribosome and can cause cell death by permanently disrupting translation. However, the molecular mechanisms that control sensitivity of wheat and barley to DON are not well understood and cellular factors that influence how the toxin is taken up, processed, and transported before binding to the ribosome have not been identified. The goal of the proposed research is to develop a better understanding of the genetic basis of eukaryotic cell susceptibility to DON and Fusarium Head Blight (FHB). The availability of several complete sets of deletion and overexpression libraries in yeast provides a powerful approach to identify the genes that are critical for conferring resistance to trichothecenes. The main goal of the proposed study is to carry out a genome wide screen of the yeast deletion libraries to identify yeast genes that confer resistance and susceptibility to trichothecenes. A complementary approach to the deletion library screens will be a multicopy suppression screen for genes that will confer resistance to trichothecenes when overexpressed. A genome wide screen of an overexpression library of yeast genes will be carried out to identify genes that confer trichothecene resistance. Comparisons between the different library screens may lead to the identification of gene networks and pathways that influence trichothecene susceptibility and resistance. In preliminary Studies, we have identified the optimal growth conditions and the trichothecene concentrations to conduct the genome wide screens. The proposed studies will likely identify novel genes involved in toxin uptake, intracellular transport, translation, ribosome, RNA/DNA binding, protein turnover, membrane biogenesis, defense response signaling and programmed cell death. These studies address a key goal of the GDER section of the Scab Initiative, which is to identify novel candidate genes for resistance to FHB and reduced DON accumulation. In future studies, we will demonstrate the potential of this approach to uncover wheat and barley genes involved in DON resistance by identifying the wheat and barley orthologs of the yeast genes and demonstrating their involvement in resistance to FHB. Knowledge gained from the proposed studies may lead to the development of more effective approaches for the prevention of mycotoxin contamination of cereals.