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PROJECT 2 ABSTRACT

(1 Page Limit)

In the US spring wheat (*Triticum aestivum* L.) region, Fusarium head blight (FHB), caused primarily by *Fusarium graminearum* Schwabe [teleomorph *Gibberella zeae* (Schwein.)], results in significant losses due to its impact on yield and grain quality through the production of the fungal mycotoxin, deoxynivalenol (DON). A primary overall goal of the US Wheat and Barley Scab Initiative is to develop as quickly as possible effective control measures that minimize the threat of FHB, including the reduction of mycotoxins, to the producers, processors, and consumers of wheat and barley. One successful breeding approach to reducing mycotoxin production has been to combine different sources and mechanisms of FHB resistance. Critical to the efficiency of implementing this approach is the need to identify and characterize different sources and mechanisms of FHB resistance. The Host Genetics and Genomics Research Area Program lists research priorities under Gene Discovery, Mechanisms of Resistance as identifying potential genes involved in FHB resistance and characterizing the mode of action or function of a specific candidate gene. The most widely utilized source of FHB resistance in hexaploid, bread wheat, Sumai 3, is a type II resistance to the spread of the Fusarium fungus. The Brazilian spring wheat, Frontana, represents a genetically different source of resistance, and indications are that its mechanism of action prevents or limits initial fungal infection (type I resistance) or prevents the accumulation of DON (type V resistance). We have developed unique reciprocal backcross monosomic (RBCM) lines using Frontana and the spring wheat cultivar Chris, which is susceptible to FHB. *Our main objective is to conduct a preliminary test to establish the effectiveness of the detached leaf assay using only the parents of the RBCM lines.* We will use pathological and molecular approaches to characterize and compare these parents *in vitro* detach leaf assay to measure incubation period, latent period, and lesion length in the inoculated leaf of each parent using digital imaging system, (ii) use quantitative real-time PCR assay based on TaqMan probe and primers specific to ß-tubulin gene to quantify *F. graminearum* biomass in inoculated wheat leaves, (iii) 1000-grain weight (as a measure for scabby grains), and (iv) amount of DON content (3A-DON, 15A-DON and NIV as a measure for mycotoxin contamination) will be analyzed in the greenhouse experiments.