Project Abstract

Project Title:	Use of Traditional and Molecular Breeding to Develop FHB Resistant SRWW for Ohio	
Principal Investigator:	Clay Sneller	The Ohio State University

Breeding for high yield and FHB resistance requires a multi-pronged approach. The overall goal of this proposal is to develop an efficient breeding pipeline to improve yield and FHB resistance in SRWW cultivars adapted to the upper mid-west. Our specific objectives are

1. Breeding
   a. Generate new populations from elite parents chosen for yield and FHB resistance. *Outcome: populations that will produce a large number of progenies that meet our yield and FHB targets*
   b. Use MAS and GS to select superior lines. *Outcome: Cost-efficient identification of lines with good FHB resistance at early generations*
   c. Screen inbred lines in an FHB resistance. *Outcome: The nursey ensures acceptable heritability of FHB scores and effective selection for resistance*

2. Coordinated Phenotyping
   a. Evaluate the FHB resistance of all entries in the P+NUWWSN. *Outcome: Accurate assessment of the FHB resistance of the best lines from all programs and distribution of results and germplasm*
   b. Coordinate the phenotyping of the PNUWWSN and NUWWSN. *Outcome: The coordination facilitates the screening of member lines in multiple environments for accurate assessment of resistance and reporting of results.*
   c. Evaluate the FHB resistance of all entries in the OSU Official Variety Trial. (OVT) *Outcome: The FHB resistance of all commercial cultivars will be assessed and distributed to Ohio growers so they can select cultivars with high yield and FHB resistance.*

3. Resistance to toxin accumulation
   a. Assess levels of resistance to toxin accumulation (RTA). *Outcome: we will identify lines with superior RTA for use as parents and release to growers*

Germplasm pertaining to all objectives will be phenotyped for FHB resistance in a misted and inoculated nursery. All germplasm (except OVT entries) will be genotyped with GBS and with FHB QTL markers. All lines in the objective 1 will be assessed for yield and other agronomic traits. The sample collected for objective 3 will be assessed for levels of fungal biomass using qPCR.