

Project Abstract

Project Title:	Genotyping Lines for FHB Resistance - Northern	
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This proposal supports collaborative genomics-assisted selection efforts by the Northern soft winter wheat programs. This project addresses the need to provide breeders with information about the genetic basis of resistance to FHB and other traits in locally adapted and newly introduced germplasm and to improve their ability to select for FHB resistance in cultivars using new breeding approaches.

Specific objectives of this continuing research are: (1) to characterize entries in the Northern scab screening nurseries with markers linked to FHB QTL; (2) to characterize entries with diagnostic markers for genes having major effects on plant development and genes conferring resistance to other pests; (3) to implement genome-wide markers analyses to identify QTL associated with FHB resistance and perform genomic selection (GS); (4) to investigate new methodology for collecting genome-wide marker data; and (5) collaborate with complimentary projects to implement genomic selection in eastern soft winter wheat breeding programs.

This region-wide project results in extensive use of genomic data for coordinated development of high-yielding cultivars having FHB resistance. The genotypic data provided to breeders will be used in selecting lines for advancement via marker-assisted and for identification of FHB resistant parents for crossing. Genome-wide marker data produced in the project will also be used for predicting FHB resistance traits and mapping genomic regions involved in disease resistance.

We will (1) characterize entries in the Northern scab screening nursery and lines submitted by breeders with markers linked to FHB QTL; (2) characterize wheat lines and populations with diagnostic markers for genes having major effects on plant growth and development, as well as genes conferring resistance to other pests and for quality traits; (3) collaborate breeders to develop and apply GS models that include genome-wide markers and/or markers associate with major genes and FHB QTL; (4) investigate new, amplicon sequencing approaches for cost-effective genotyping for GS.

The proposed research is part of a coordinated regional effort to develop improved eastern soft wheat germplasm utilizing molecular markers and sequencing information. Breeders will benefit from this research through improved knowledge of genomic regions associated with FHB resistance. In addition, this research will benefit breeders and growers by facilitating the use of genomic selection to increase efficiency of pipelines for developing FHB resistant cultivars.