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Project Title: Genetics of FHB Resistance in Soft Red Winter Wheat.

PROJECT 1 ABSTRACT

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We are fortunate there is significant FHB resistance in soft red winter wheat (SRWW) though we know very little of the source and effect of these native resistance genes. Our SRWW resistance has inherent agronomic advantages over exotic resources could be better utilized if we understood the underlying genetics. The information could be used to design effective recurrent selection programs, identify exotic alleles that could complement to native resistance, and design marker-assisted backcrossing that effectively enhances resistance. Given the great need for information on SRWW resistance and the multiple sources of resistance in these complex SRWW populations, research that couples QTL discovery, validation, and cultivar development is needed to elucidate the nature of FHB resistance in SRWW.

Objectives:

1. Discover and validate SRWW FHB resistance QTL using RIL populations derived from 'Ernie', 'Hopewell', and OH599.
2. Discover and validate SRWW FHB resistance QTL from 10 SRWW lines in a complex variety development breeding population by using sib-pair mapping techniques.

We are proposing to use a combination of marker analytical techniques to discover and validate FHB QTL in multiple genetic backgrounds. The approach is an effective combination of biparental cross (use of full-sibs), selective genotyping (use of lines with extreme phenotypes are analyzed), and haplotype (use of half-sibs, cousins, etc) analytical techniques in a fashion that overcomes the inherent limitations of each. The advantage of the approach is that it investigates the genetics of multiple sources of FHB resistance at one time, allelic relationships among sources can be inferred though the simultaneous analysis of multiple populations, the value of QTLs can be assessed in multiple genetic backgrounds, QTLs can be validated, the study produces phenotypic data on selected lines from cultivar development program, and it leads to a synergy of plant breeding and molecular analysis. Just like QTL discovered in analysis of biparental crosses, all the QTL discovered by analysis of sib-pairs must be validated.

QTL will be investigated in biparental crosses involving Hopewell, OH599, and Ernie. The effects of the Hopewell QTL will also be estimated in a complex SRWW breeding populations and compared to those estimated in the biparental crosses. In addition, we will search from QTL from 9 other SRWW in the sib-pair analysis of the complex SRWW population.