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PROJECT 2 ABSTRACT

(1 Page Limit)

A number of QTL contributing to FHB resistance have been mapped in cultivars from China, Korea, and Brazil, as well as some European winter wheats. As a result, these resistance sources are currently the focus of most marker-assisted selection being done for FHB resistance. There has been some genetic mapping has been done soft winter wheat cultivars Ernie, Freedom and Goldfield. The QTL detected in these sources require validation prior to deployment by marker-assisted selection (MAS) and analysis of germplasm potentially having these resistances is needed. This proposal focuses on providing information about mapped sources of FHB resistance (native and exotic) in soft winter wheat backgrounds by providing in-depth marker analysis of collaborative FHB screening nurseries. The uniform regional scab screening nurseries have been used by breeders to obtain multi-location data on reaction of soft wheat lines grown in FHB inoculated nurseries. While these data have been used to make decisions for advancement and for use as parents, little information has been available about the genetic basis of resistance. We are proposing to participate in a coordinated regional effort to better characterize FHB resistant eastern soft wheat germplasm utilizing molecular markers. By combining the abundant phenotypic data collected on the nurseries at multiple locations each year with molecular markers data, we will pursue an association mapping (AM) approach for resistance QTL identification. In this manner, new QTL or new alleles at previously identified QTL may be identified. We are also participating in coordinated mapping efforts by haplotyping parents with markers linked to previously mapped FHB resistance genes and conducting genome wide polymorphism screening. The specific objectives of this proposal are (1) to characterize entries in the Southern (SUWWSN) and Northern (NUWWSN and PNUWWSN) scab screening nurseries with markers linked to FHB QTL (VDHR goal 3); (2) to investigate association analysis as a means of identifying QTL associated with resistance (VDHR goal 4); and (3) to provide haplotype and marker polymorphism data on parents of mapping populations (VDHR goal 4).