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**PROJECT 2 ABSTRACT**

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Improving Fusarium Head Blight (FHB) resistance in cultivars is the most reliable and economical way to control scab. Breeding for resistance is difficult in wheat due to the complex inheritance of resistance and large environment on phenotypes. Marker-assisted selection (MAS) offers great promise to improve resistance by enabling breeders to select for resistance genes directly, identifying resistance genes from exotic sources, and minimizing the effect of environment on selection.

Some exotic resistance alleles have already been tagged with markers. Most of these come from Chinese sources that have very poor agronomic and quality traits. It is important that we continue to search for better sources of resistance. One such source is the Brazilian line Frontana. Canadian soft winter wheat breeders have successfully used Frontana to develop commercial cultivars. There are conflicting reports on the location of the major resistance genes of Frontana, perhaps due to different sources of Frontana seed used in crossing or due to evaluation methods. It is important to sort out this information so MAS can be used for Frontana allele in SRWW. In addition there is considerable resistance in SRWW yet we know very little about the genetic of this resistance. Genetic information would allow use to better exploit the inherent resistance of our adapted gene pool as well as predict which exotic alleles are likely to be useful in improving resistance in SRWW. Our objectives are:

1. Map and evaluate MAS for FHB resistance QTL alleles from Frontana
2. Evaluate segregation and selection for FHB resistance in crosses of moderately resistance SWW cultivars and tag QTLs.

We plan to create near-isogenic lines and mapping populations to further map Frontana QTLs from the source used by Canadian SRWW breeders. We will also further investigate the genetic of resistance from Freedom by creating NIL and an improved mapping population. Finally we will investigate the segregation for FHB resistance in crosses between moderately resistant SRWW lines and combine selection and marker analyses to suggest the location of the resistance genes.