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PROJECT 1 ABSTRACT
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Traditional breeding to improve resistance to Fusarium Head Blight (FHB) remains the most reliable method of control to date. While newer technologies such as MAS and perhaps gene transformation hold great promise, both will supplement the germplasm developed through traditional methods. We are fortunate to have some very useful resistance within the soft red winter wheat (SRWW) gene pool. It may be possible to further increase this resistance by introgressing exotic alleles for resistance. This will require the use of molecular markers to assure that the exotic alleles are moved into SRWW varieties. Our objectives are

1. Screen SWW lines that are candidates for release for resistance to FHB
2. Evaluate the effect of exotic QTL alleles for FHB resistance in SWW genetic backgrounds.
3. Coordinate a uniform nursery for evaluating FHB reaction in SWW adapted to the northern US.

The project plans to field evaluate over 2000 breeding lines for FHB resistance. These lines are all derived from primarily SRWW germplasm and may be candidates for release if they are found to be acceptable for other traits. Some of these lines are derived from populations that can also be used to discover QTLs and to assess the impact of MAS in SRWW.

We plan to backcross major QTL alleles for FHB resistance from Sumai3, Wuhan-1, Frontana, and Freedom into both susceptible and moderately resistant SRWW lines to assess the impact of these alleles on FHB resistance as well as agronomic and quality traits. The proposal covers the first stages of creating the backcross near iso-genic lines (NIL). In addition we will complete the phenotyping of NIL that we created previously for the 2AS region from Freedom, and the 3BS region from Ning 7840.

Thorough phenotyping remains crucial in the development of FHB resistance. This requires multi-location data to assure the incidence of disease. We propose to coordinate the uniform testing of SRWW lines adapted to the northern US for FHB resistance.