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PROJECT 1 ABSTRACT
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Different sources of resistance are being constantly sought as to expand the number of available genes to pyramid in a single variety with excellent resistance to FHB. However, current methods rely on developing mapping populations (e.g., recombinant inbred lines, double haploids, etc.) from resistant by susceptible crosses, phenotyping in multiple replicated trials, mapping and QTL analysis. This is then followed by the transfer of desirable segments with linked markers into acceptable cultivars. This scheme is tedious and slows the process of cultivar development. In this study we plan to explore an alternative strategy that will allow us to not only quickly map the region of interest from multiple sources but do this in breeding populations under development. Our strategy is intended to reduce the time required for QTL identification and marker assisted selection significantly.

The North Dakota Durum Wheat breeding program has identified five tetraploid wheat sources of resistance from Tunisia, which were selected among a large number of lines evaluated over 55 repeated FHB trials. Since their identification, these lines have been extensively used in the breeding program to derive resistant breeding lines. We plan to use this collection of backcross derived advanced resistant lines, susceptible sibs, and parental lines to identify markers that are associated with these novel sources of resistance. The elegance of this analysis is the integration of derived information directly into the breeding programs for verification and future marker assisted selection and pyramiding of resistance loci. Therefore, the objectives of this project are:

1) **Characterize a collection of advanced durum wheat breeding lines with known pedigrees for allelic variation in markers distributed throughout the genome;**
2) **Characterize the same collection of lines in the same environment for reaction to FHB;**
3) **Associate allelic variation with resistance loci present in FHB resistant lines;**
4) **Validate marker-FHB resistance loci association; and**
5) **Develop diagnostic markers for routine and effective screening of breeding populations.**

The ultimate objectives of this project are to utilize the extensive collection of advanced breeding lines for pedigree based association analysis; and to incorporate our findings directly into a breeding program w.

The advantages of using pedigree based association studies are four-fold. First, if appropriate material is available, fewer individuals need to be genotyped for marker loci as compared with mapping populations (del Blanco et al. 2003). For in this type of analysis a priori selection has been placed on the trait of interest as opposed to mapping populations where segregation is needed. Second, the power of detecting QTL regions associated with FHB resistance is much greater than that with mapping populations (del Blanco et al. 2003). For example, the probability that three resistant BC_3 (relative to resistant source) derived lines have the same marker locus coming from the donor parent by chance is 0.00024 (Kaeppler et al. 1993). Third, the materials used in this project are breeding populations with replicated field evaluations, precluding the need for additional screening for resistance. However, as the most advanced lines have fewest phenotypic data, we propose to evaluate the FHB reaction of this material (see objective 2). Fourth, as these are advanced breeding lines, the results of marker association analysis can directly be applied to cultivar development and pyramiding of resistance in "good by good" crosses