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The extensive economic damage caused by *Fusarium* head blight (FHB) or scab to the North Dakota durum and wheat producers is well recognized. The most cost-effective way of reducing losses from this devastating disease is through the development of genetic resistance in the host plant. Pedigree based association analysis of North Dakota hard red spring (HRS) wheat lines carrying Sumai3 derived FHB resistance, their susceptible parental and sister lines indicated the presence of a QTL region significantly associated with resistance on 3BS. Even though, this study only confirmed previous results it proved that pedigree based association mapping methodologies can be developed and adapted to plant populations for a relatively quick and statistically robust study. This type of analysis also has great benefit as the lines and markers identified are part of, and integrated into a breeding program as opposed to analysis of bi-parental mapping populations. In collaboration with **DURUM** and **HRS** breeding programs at NDSU we have identified number of advanced breeding lines (both resistant and susceptible) with known pedigrees, derived from new and novel sources of FHB resistance. These collections will be the core subject of this proposal with following objectives:

- 1. characterize collection of advanced durum breeding lines with known pedigrees and novel sources of resistance for allelic variation in markers distributed throughout the genome;**
- 2. characterize the same collection of lines in the same environment for reaction to FHB; and**
- 3. associate allelic variation with resistance loci present in FHB resistant lines.**

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 cultivars. 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. Again the beauty of this analysis is the integration of derived information **directly** into the breeding programs.