PI: **Shahryar Kianian**	**PI's E-mail:** **S.Kianian@ndsu.nodak.edu**
Project ID: **0405-KI-014**	**FY03 ARS Agreement #:** **59-0790-9-048**
Research Area: **BIO**	**Duration of Award:** **1 Year**
Project Title: **Development of Markers Linked to FHB Resistance in Durum Wheat.**	

PROJECT 2 ABSTRACT
(1 Page Limit)

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. Once resistance genes are identified, transfer into adapted wheat germplasm remains a lengthy and difficult task because undesirable traits generally accompany the transfer. Markers linked to resistance genes can accelerate selection, germplasm development and time to variety release. We will use existing markers in addition to markers currently being developed by a number of groups as a result of the ever increasing EST and sequence database to identify and develop "breeder friendly" markers to improve germplasm development and reduce time to variety release. The specific objectives of this project are to:

1) **identify markers closely linked to FHB resistance loci in durum wheat;**
2) **develop a PCR-based marker system for screening large durum breeding populations segregating for FHB; and**
3) **demonstrate the utility of these markers in populations developed by various breeding programs.**

The knowledge of 3BS location was applied to a set of 2134 Sumai3 derived durum lines to determine the efficacy of selecting based on molecular markers relative to FHB score. Results clearly indicate that we can remove the susceptible lines (as determined by FHB score) from a given population at efficiency of greater than 84% based on the absence of *Xgwm533* allele. Additionally, among the lines carrying the Sumai3 allele, resistant lines (based on single FHB score) are identified at an efficiency of 83%. Thus, marker assisted selection for this locus is now possible and being applied to various durum backcross populations and 2128 new lines developed from selections of above material. We have also identified a major QTL in durum lines derived from *Triticum dicoccoides* chromosome 3A substitution line. The markers linked to this locus explain 55% of the genetic variation relating to FHB resistance. These markers are being applied to a durum backcross selection project. We have developed 274 Wangshuibai derived (from crosses to durum line D87130) recombinant inbred lines and are in the process of screening this population for disease resistance and molecular markers. Early disease screening data indicate a great potential for use of these lines in developing resistant durum cultivars. The QTL analysis using a hexaploid population with Wangshuibai as the source of resistance is to almost complete. The information from that project will be used to develop markers linked to resistance QTL from Wangshuibai to aid speed the process of selection. Markers may represent the only mean by which the resistance QTL from *T. dicoccoides*, Sumai3, Wangshuibai and other possible sources of resistance can eventually be combined in a single variety, the ultimate objective of this project.