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Data collected recently showed that Glenn does not show the presence of the closest markers to the main FHB resistance gene *Fhb1* from Sumai 3. These results have been confirmed by many labs including U of MN, USDA-ARS-Fargo,...etc. All these results show that haplotyping Glenn is consistent with our data that Glenn may not have *Fhb1* markers as we previously believed based on Glenn pedigree. This has raised a major question among breeders involved in this project: does Glenn carry a new combination of FHB resistant genes derived from a diverse pedigree tracing to Chinese, US, and wild type wheat origin or have breeders at NDSU who developed this cultivar broken the linkage between the *Fhb1* and the new flanking markers. To confirm either case and develop diagnostic markers, more research is needed. Similarly among the most popular cultivars developed by NDSU, Parshall exhibited consistent tolerance to FHB across many years. Parshall parentage does not trace to any exotic origin such as Chinese germplasm. We believe Parshall has an indigenous source of resistance that may be of great interest to the wheat breeders. Therefore the objective of this project is to map genes/QTLs for resistance to FHB in spring wheat Glenn and Parshall. In order to achieve our objectives, Recombinant Inbred Lines (RILs) populations involving these two parents were developed by NDSU. Glenn/MT0245, Glenn/MN00261-4, and Parshall/Reeder have 115, 110, and 120 RILs, respectively. In summer 2010, except for the Parshall/Reeder RILs which will be F_{2:10}, the other three RILs population would be at the F_{2:8} generation. Two of the three RILs populations, their parents, and appropriate susceptible and most resistant FHB checks will be included in four experiments in this project. The experiments will be planted in three to four FHB field nurseries located in the three states, ND, MN, and SD in summers of 2010 and 2011. The field FHB experiments are laid out in a RCBD with two to four replicates and inoculated with the FHB pathogen and misted according to the standard protocols used by each cooperating institution. Data will be collected on some agronomic traits including heading height and FHB diseases notes. These include incidence and severity visually estimated and recorded for each plot approximately 21 days after anthesis. Plots will be harvested to determine tombstone and DON.

In the lab, DNA will be extracted from the RILs of all populations, their parents, and checks; and will be screened with Diversity Array Technology (DArT) markers. This data will be used to generate a basic map and identify important QTL regions. We will then augment the identified QTL regions with microsatellite markers (SSR) that show polymorphism between parents. Subsequently, linkage maps will be constructed using Map Manager QTXb20 (Manly et al., 2001) with a logarithmic of odds of 3 and Kosambi function. The population data will be subjected to marker regression analysis using Map Manager QTXb20 (Manly et al., 2001) and putative markers associated with FHB will be identified. Finally, composite interval mapping (CIM) will be performed to detect QTLs for FHB on those potential genomic regions. Composite interval mapping will be performed in each environment based on the recombinant inbred lines means. The empirical LOD threshold at 5% probability level was determined by a 1,000-permutation test.