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The long-term goal of the project is to gain understanding of Fusarium head blight resistance and susceptibility gene function by identifying and characterizing genes important for host pathogen interactions. The specific objectives of this proposal are: 1) identify fast neutron induced barley mutants with disrupted FHB resistance and susceptibility genes; 2) generate a transposon tagging population to tag the genes underlying the FHB resistance QTL on chromosome 2H.

These mutant populations will be an important genetic resource for future work to identify and characterize resistance genes, pathways and factors important in host pathogen compatible and incompatible interactions. Barley seed from the FHB resistant line CIho4196 and susceptible malting cultivar (cv) Morex were mutated by fast-neutron irradiation. M2 generation single head hill plots were grown in FHB nurseries in Fargo and Langdon, ND in 2010. Putative mutant lines (58 total) were identified from CIho4196 with FHB disease scores of 3 or higher based on a 0-5 rating scale. Wild type CIho4196 had an average score of 1. Putative mutant lines of cv Morex (98 total) with FHB disease scores of 2 or lower were also identified. These CIho4196 and Morex mutant lines may contain deletion mutations that disrupt FHB resistance genes or susceptibility factors, respectively. The putative mutants will be further evaluated in field nurseries in 2011. Confirmed mutants will be backcrossed to the respective wild type parents to clean up any background mutations. The confirmed mutants will be utilized in micro array experiments to identify the mutated genes responsible for the phenotype. A transposon tagging system was developed in barley using the maize Ac/Ds elements (Cooper et al., 2004). We have obtained the Ds element insertion line (DsT-41) containing a Ds element tightly linked to the chromosome 2 FHB resistance QTL in CIho4196, one of the best sources of resistance against FHB in barley. We will produce a Dst-41 transposon mutagenesis population by introducing the Ds element linked to the chromosome 2 QTL into a CIho4196 background followed by induced transposition. The transposition population will be screened for identification of transposon insertion mutants with disrupted gene/s underlying the chromosome 2 QTL. This gene tagging method should facilitate the rapid identification of genes underlying the chromosome two resistance QTL.