FY16 USWBSI PROJECT ABSTRACT

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Research Category: **HWW-CP** **Duration of Award: 1 Year**

Project Title: Improving FHB Resistance in Hard Winter Wheat by Molecular Breeding/Manipulation.

PROJECT 1 ABSTRACT

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Qfhb1, a major FHB-resistant QTL found in Spring wheat, has been introgressed into several HWW lines. How effectively *Qfhb1* works under the new genetic background has been questioned. Our previous research has identified gene *WFhb1-1 as* the functional genic component of this QTL. Currently we have the whole gene sequence of *WFhb1-1* from Sumai 3 and known that this gene exists and normally functions in every wheat line. It is the difference in regulatory elements of this gene that decide resistance or susceptibility. Our hypothesis is, therefore, that the regulatory elements of this gene are polymorphic among wheat lines and can be explored for developing allele-specific markers. Following the recommendation by HWW PC and EC, this proposed research will focus at developing PCR-based perfect marker for use in marker-aided selection of this gene in this grant period. To achieve this goal we plan to clone the regulatory sequences of *WFhb1-1* from FHB-susceptible Y1191-6 and winter wheat pairs of *Qfhb1* introgression lines and their recurrent parents: Wesley and Wesley FHB-095-103, Harding and Harding-095-107, Ning7840 and Ning/Clark NIL23, and Trego and Trego FHB-095-98. The sequences will be compared to identify SNPs that are associated with all of the resistance or susceptible lines, respectively. We plan to choose two SNPs that are closely located to each other for developing three-primer, co-dominant marker for the resistant and the susceptible alleles. This proposed research aims at improving FHB resistance in HWW by molecular breeding/manipulation. Therefore it fits both objectives of the HWW-CP for FY16-17 by developing new breading technology and germplasm to further enhance short-term and long-term improvement of FHB resistance and to efficiently introgress effective resistance genes into breeding germplasm, and by developing a greater understanding of specific biological factors influencing FHB infection/toxin accumulation.