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**Project ID: FY12-SP-007**

**ARS Agreement #: 59-0206-9-070**

**Research Category: VDHR-SPR**

**Duration of Award: 1 Year**

**Project Title: Fine Mapping and Validation of QTLs for FHB Resistance from PI 81791.**

### **PROJECT 1 ABSTRACT**

(1 Page Limit)

PI 81791 (Sapporo Haru Komugi Jugo) was identified as a line with very high FHB resistance, including low visually scabby kernels and does not contain *Fhb1* according to our results with marker umn10 and our mapping results. Therefore, this genotype is a good target for a new QTL mapping effort and the QTLs are likely to be complementary to those already deployed.

Phenotypic data on FHB traits was collected from three field and two greenhouse inoculated nurseries. A genetic map was produced with SSR markers, but large gaps were present in the map and most markers were genotyped on only 94 RILs from the population. QTLs were discovered, but due to limitations in the genetic mapping, we believe that the number and locations of QTLs could be refined with a more complete genetic map.

Given the advances in genotyping technology now available, complete genotyping of the entire population is warranted. The objectives of this project are to:

- 1) Develop an SNP map of the 150 RIL population of Wheaton/PI 81791
- 2) Map QTLs for FHB-related traits
- 3) Validate QTLs in additional genetic backgrounds

We will screen the parents and 150 RIL of the Wheaton/PI 81791 population with at least 9,000 SNPs. The USDA-ARS Genotyping Center in Fargo has the technical expertise and equipment to obtain the SNP genotypes. We expect to map 1,500 – 2,000 SNPs using the 9,000 SNP chip, thus greatly increasing the QTL mapping resolution in the population. A new linkage map will be produced, integrating the SSR and SNP data. QTL Cartographer will be used to identify QTL regions associated with the FHB-resistance traits. QTL-NIL validation populations were developed based on the QTLs discovered in the initial analysis. A total of 55 such populations are at various stages in our breeding program from F<sub>4</sub>'s to preliminary yield trial lines. Included in these materials are 1,740 F<sub>5</sub> lines that are ideal for NIL development. Near isogenic lines will be developed using the methods of Pumphrey et al. (2007).