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**Project ID: FY08-AN-104**

**FY07 ARS Agreement #: 59-0790-4-091**

**Research Category: GDER**

**Duration of Award: 1 Year**

**Project Title: Construction and Utilization of a BAC Library of Sumai 3.**

### **PROJECT 1 ABSTRACT**

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Funded by USWBSI and NRI, we are using a map-based cloning approach to clone the major FHB resistance QTL for wheat on chromosome 3BS (*Fhb1*). Based on FHB phenotypes of recombinants and new DNA markers derived from 'Chinese Spring' BAC sequences, *Fhb1* was narrowed down to a 260 Kb region and seven candidate genes were identified. Five of the seven candidate genes have been tested via transformation and none of them encode *Fhb1* based on the FHB phenotypes of the transgenic plants. The two remaining candidate genes will be tested in fall 2007 and spring 2008.

It is possible that Chinese Spring has a null *Fhb1* allele. In this case, it would be very difficult if not impossible to clone *Fhb1* based on the BAC sequence of Chinese Spring. Therefore, the availability of a BAC library of Sumai 3 is an essential resource in cloning *Fhb1* as well as other FHB QTLs. The specific objectives of this proposal are to:

- 1) Construct a BAC library of Sumai 3 for the wheat community.
- 2) Construct a Sumai 3 BAC contig spanning *Fhb1*.
- 3) Compare the sequences between Sumai 3 and Chinese Spring for the *Fhb1* region to identify additional candidate genes, if any.

Considering the large genome size of common wheat (16,000 Mb) and the amount of funding required to construct a BAC library of Sumai 3, we propose to construct a five genome-equivalent BAC library. Our experiences with the construction and screening of a pooled cosmid library of Sumai 3 will be helpful for the proposed BAC library. We will use the Sumai 3-specific markers developed to screen our pooled cosmid library of Sumai 3 to screen 420 pools of BAC plate clones. After PCR-based identification of positive plate pools, single positive clones will be identified by DNA hybridization. We will sequence the genic regions of a BAC clone(s) of Sumai 3, and compare the sequences with the corresponding region of Chinese Spring to identify Sumai 3-specific nucleotides or sequences. We will compare the gene content and organization in the *Fhb1* region between Sumai 3 and Chinese Spring. We are especially interested in knowing if there are any gene insertions/deletions between these two genotypes. Any additional genes identified in Sumai 3 will be validated as a candidate for *Fhb1* by transformation and virus induced gene silencing.