PI: Shaobin Zhong **PI's E-mail: Shaobin.Zhong@ndsu.edu**

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PROJECT 3 ABSTRACT

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Cloning and characterization of FHB resistance genes is essential to understand the mechanism of FHB resistance and will greatly facilitate the use of FHB resistance in wheat improvement. Although over 100 QTL for FHB resistance have been identified in various sources of wheat germplasm, only a few large effect QTL for FHB resistance are consistently expressed across different environments and genetic backgrounds. Among them, Fhb1 in Sumai 3 is the only one that has been cloned. In previous studies, we identified and mapped two QTL for FHB resistance on chromosome 5A of PI 277012, a wheat line with a high level of resistance comparable to Sumai 3 but coming from a different source. The SNP markers closely linked to the two QTL have been identified. Further fine mapping of the major QTL on 5AL has delimited it in a genomic interval of 1.2 Mb flanked by two SNP markers based on the reference genome of Chinese Spring. To clone this resistance QTL, it is essential to have the genomic sequence of the targeted region in PI 277012, the donor of the resistance QTL. Therefore, our overall goal is to sequence the 1.2 Mb 5AL region containing the QTL for map-based cloning of the FHB resistance gene. The specific objectives of this project are 1) Construct a non-gridded BAC library with genomic DNA of PI 277012, 2) Screen the BAC library with DNA markers flanking and within the FHB resistance QTL on 5AL, and 3) Sequence the BACs and build a contig to cover the QTL. We plan to construct a non-gridded BAC library, which consists of 772 pools containing a total of 617,600 clones. Based on a mean insert size of 120 kb in the clones, the total coverage will be approximately 4.3 genome equivalents. We will use PCR-based markers to screen the BAC library pools and identify individual BACs to cover the genomic region carrying the major FHB resistance QTL in PI 277012. The identified BACs will be sequenced by the PacBio or Nanopore sequencing method. Eventually, we anticipate to build up a BAC contig for the QTL region and identify candidate genes for the FHB resistance. Having the BAC library for PI 277012 will not only speed up the map-based cloning process for this major FHB resistance QTL, but also facilitate the development of more DNA markers for this novel FHB resistance, and accelerate the development of wheat varieties with improved FHB resistance by marker assisted selection and gene pyramiding. The BAC library and the generated genomic sequences will be provided to wheat geneticists and breeders for gene mapping and cloning purposes.