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PROJECT 2 ABSTRACT

(1 Page Limit)

We have identified numerous bacterial artificial chromosome (BAC) contigs that cover significant parts of the chromosome region believed to carry the FHB resistance gene or genes. In order to facilitate identification of these genes and completion of the physical map, we will sequence the BAC clones relevant to this region. Once the sequences are acquired they will be analyzed for genes and candidate genes for FHB resistance identified. This knowledge will facilitate development of FHB resistant cultivars. For example if a gene is identified whose loss of function results in FHB resistance then that gene could be specifically mutated via a tilling process. Conversely if a gain of function gene is identified it could be genetically engineered to acquire that function.