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## PROJECT 1 ABSTRACT
(1 Page Limit)

Wheat head scab (*Fusarium graminearum*) significantly reduced grain yield and quality of wheat. Growing resistant cultivars is the most effective measure to control the disease. However, resistance genes used in breeding programs worldwide are mainly from Sumai 3, exploring resistance genes from other sources will enhance genetic diversity and facilitate pyramiding of resistance genes from different sources. Our objectives in this proposal are to characterize resistance quantitative trait loci (QTL) from Wangshuibai, a resistant Chinese landrace unrelated to Sumai 3 and develop high-throughout DNA markers for scab resistance QTL in Wangshuibai. The $F_{7:9}$ recombinant inbreed population derived from the cross between Wangshuibai and Alondra's (highly susceptible to scab) will be repeatedly evaluated for scab resistance in the greenhouse. Amplified fragment length polymorphism and simple sequence repeat markers coupled with bulked segregant analysis will be implemented for identification of QTL and fine mapping in the QTL regions. Some markers closely linked to these QTL will be selected for marker-assisted selection. DNA markers will be analyzed in a DNA sequencer to improve resolution and throughput of marker analyses. The results will gain new knowledge on the inheritance of scab resistance in Wangshuibai, provide new markers for marker-assisted breeding, and diversify scab resistance genes in breeding programs, which meets the research goals: *developing as quickly as possible effective control measures that minimize the threat of scab to the producers, processors, and consumers of wheat* as proposed by USWBSI.