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PROJECT 1 ABSTRACT
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Fusarium head blight (FHB) of wheat 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 of resistance genes and facilitate pyramiding of resistance genes from different sources. Our objectives in this proposal are to (i) characterize quantitative trait loci (QTL) for Type II FHB resistance from Wangshuibai (WSB), a new source of FHB resistance unrelated to Sumai 3 and determine the chromosome locations of QTL; (ii) develop high-throughput DNA markers tightly linked to FHB resistance QTL in WSB, (iii) investigate the relationship of the QTL between Ning 7840 and WSB and (iv) elucidate the relationships among visual FHB rating and DON content. The recombinant inbred populations derived from the crosses between WSB and Wheaton (highly susceptible to FHB) and between Ning7840 and WSB will be repeatedly evaluated for FHB resistance in the greenhouse. Amplified fragment length polymorphism (AFLP) and simple sequence repeat (SSR) 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 or converted into breeder-friendly markers. DNA markers will be analyzed in an automated DNA sequencer to improve resolution and throughput of marker analyses. The results will gain new knowledge on the inheritance of FHB resistance and low DON content in WSB, provide new markers for marker-assisted breeding, and diversify FHB resistance genes in breeding programs, which meets one of the FY04 research priorities: of mapping new sources of resistance gene in wheat as proposed by USWBSI.