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Project Title: Validation and Fine Mapping of Three QTLs For Resistance to Scab in Common Wheat.

PROJECT 1 ABSTRACT
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The major objective of current study is to validate three FHB QTLs on chromosomes 2BS, 3BS, and 5AL previously identified in a Chinese wheat line W14. Eighteen SSR markers in the three target QTL regions were used for a marker assisted selection (MAS) backcrossing study in 2003 to incorporate type II resistance from W14 and a related source Futai 8944 into two adapted wheat varieties Roane and Ernie. W14 and Futai8944 were backcrossed four times to the recurrent parents Ernie and Roane, respectively. The BC_4F_1 and BC_4F_2 progeny were genotyped for the eighteen SSR markers. A total of 84 recombinants were selected having allele or allele combinations of two resistant parents (RP) at four SSR loci in 3BS QTL region, two SSR loci in 2BS QTL region, and two SSR loci in 5AL QTL region. These recombinants were also identified as having alleles of the two recurrent parents (RCP) for the remaining ten SSRs. The 3BS QTL spans a relatively large interval of four SSR markers (BARC75-Xgwm533a-BARC133-Xgwm533b) in the map. The intervals in this QTL region have been divided into smaller segments in a Roane backcross population in which 23 homozygous NILs having different allelic combinations in this region have been derived. The precise location and composition of the 3BS QTL will be further delineated via evaluation of these NILs for resistance to FHB compared to their marker composition in current study. A total of 330 plants including parents of these lines will be evaluated for type II resistance in greenhouse and for resistance to FHB in a replicated field test at Blacksburg, VA. Differences among these NILs for FHB resistance will be determined via analysis of disease severity of these lines in both field and greenhouse tests. NILs with good field performance will be released as unique germplasm. Thirty-three recombinants of BC_4F_2 are heterozygous at 1 to 3 marker loci in the same or different QTL regions in one or both RCP backgrounds. The $BC_4F_{2:3}$ populations derived from these recombinants and two F_2 populations derived from three NILs will be used to determine the interactions between six marker loci. A total of 790 plants including parents will be evaluated for type II resistance in greenhouse. These plants will also be characterized for the six SSR loci in the three targeted regions. Differences in direct contribution to resistance and interactions of these marker loci will be determined by segregation of these loci versus type II disease reaction in 18 $BC_4F_{2:3}$ and 2 F_2 populations. Allelic contribution will be determined by segregation of alleles at single loci versus type II reaction in 15 $BC_4F_{2:3}$.