0203-GR-020 Identification, Characterization, and Confirmation of Major QTLs for Scab Resistance in Common Wheat.

PI: Griffey, Carl A.; E-mail: cgriffey@vt.edu
VA Polytechnic Inst. and State Univ., Dept. of Crop & Soil Environmental Sciences, Blacksburg, VA 24061

Grant #: 59-0790-9-038; $28,000; 1 Year
Research Area: BIO

PROJECT ABSTRACT
(1 Page Limit)

The overall goal of the proposed research is to accelerate development of scab resistant wheat varieties and germplasm via identification and confirmation of linkage associations between DNA markers and quantitative loci (QTL) conferring scab resistance and use of such DNA markers to select for resistance. Identification and characterization of new QTL-marker loci will be conducted using F_2 and doubled haploid populations. Two different scab-resistant wheat lines, W14 and Ernie, identified in previous studies, are being used in the current study. The Chinese line W14 was developed via recurrent selection and has Type II resistance likely derived from several unknown sources. Ernie is a soft red winter wheat line that lacks any of the known scab resistant sources in its ancestry and possesses resistance other than Type II. W14 was crossed with the susceptible soft red winter wheat cultivar Pioneer 2684, and the F_2 population is being used in preliminary mapping studies. A total of 28 loci have been mapped to five chromosomal regions in the Pioneer 2684 x W14 population. Twelve markers significantly ($P < 0.05$) associated with scab resistance were identified, and explained 27, 30, 22, and 36% of the total variation in percentage of scabby seeds, DON toxin content, and scab severity in 82 F_2 individuals and scab severity in 82 corresponding $F_{2:3}$ families, respectively. Two new QTL in addition to the QTL located on chromosome 3BS were putatively identified on chromosomes 2B and 7B. Additional markers in these chromosomal regions will be identified and mapped in the Pioneer2684 x W14 population to confirm these QTL and to develop a saturated DNA marker map providing effective and selectable markers. QTL-marker associations identified in the F_2 mapping population will be verified using 122 genetically-pure doubled haploid (DH) lines that were developed from the same cross of Pioneer 2684 x W14. Four to five plants per DH line will be evaluated for Type II resistance via single floret inoculation procedures in two greenhouse studies this winter. DNA will be extracted from DH lines and markers identified in the F_2 mapping population will be verified in DH lines.

Differences in mode of inheritance and number of genes conferring scab resistance in W14 and Ernie were identified in our genetic studies, and DNA polymorphism was observed between these two lines for marker loci associated with postulated resistance genes in our mapping studies. Identification and comparison of scab QTL in these two sources will facilitate effective use of such genetic resources in breeding programs and provide a logical means and strategy for incorporating and pyramiding Type II and other types of resistance. W14, Ernie and 400 F_2 plants (W14 x Ernie) will be evaluated for Type II resistance in spring 2002 greenhouse tests. DNA from these materials will be extracted via mini DNA extraction method and used in mapping studies to differentiate resistance QTL in these two sources using DNA markers associated with postulated resistance genes identified in W14 mapping population.