

ACCELERATED BREEDING FOR SCAB RESISTANCE IN SOFT RED WINTER WHEAT AND BARLEY

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The overall project goal is to accelerate development of adapted and commercially viable scab resistant small grain varieties by identifying, incorporating and pyramiding diverse types of resistance into elite genotypes. The specific objectives of this project are to: 1) Incorporate and combine scab resistance genes from the newly-developed and characterized scab resistant and/or scab tolerant SRW wheat lines into commercially viable SRW and specialty wheat varieties; 2) Apply molecular marker assisted selection to accelerate development of scab resistant wheat lines and cultivars and; 3) Continue breeding activities on barley scab resistance.

We have developed adapted FHB resistant SRW wheat lines by deploying a combination of top-cross, doubled haploid, and backcross methods. We also have characterized haplotypes of FHB resistant lines and have identified breeding lines possessing QTLs on 3BS and 5AS associated with type I, type II and type III resistance. Availability of adapted germplasm and adequate QTL-marker information will accelerate breeding activities in deploying newly-developed lines possessing two major resistance QTL on 3BS and 5AS and implement MAS to pyramid these two major QTL and other minor QTL for all components of FHB resistance in adapted backgrounds. The proposed objectives will be fulfilled via simultaneous evaluation of FHB resistance, marker haplotypes, and agronomic performance of breeding lines in greenhouse and field experiment at two locations.

In the 2006 crop year, 60 elite lines in the Scab Advance test, 85 advanced lines in the Scab Preliminary test, and 300 lines in Scab Observation nurseries will be evaluated in yield performance trials at two locations. All lines in these nurseries also will be evaluated for scab resistance in replicated disease assessment tests at Blacksburg, VA. Entries in Scab Advance and Preliminary Tests also will be characterized with SSR and STS markers at 8 known QTL associated with all components of FHB resistance. An additional 200 SRW wheat genotypes, including entries in the two Uniform Scab Nurseries, and entries from Virginia's State Wheat Test, will be evaluated for scab resistance in replicated disease assessment trials at Blacksburg, VA. In headrow tests, 2,000 topcross and backcross derived lines and 1,000 NILs derived from a genetic study will be evaluated and selected based on agronomic traits and resistance to other prevalent diseases at Warsaw, VA prior to being evaluated for FHB resistance in replicated disease assessment tests the following year at Blacksburg, VA. A set of 180 FHB breeding populations (87 F₂, 28 F₃, 47 F₄, 9 F₅, and 9 F₆) will be planted, evaluated and subsequently selected in 160 ft² blocks in an irrigated scab nursery at Mt. Holly, VA this fall.

MARKER ASSISTED SELECTION FOR IMPROVED FHB RESISTANCE IN ADAPTED SRW WHEAT BACKGROUNDS

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Objectives of the current proposal are to: 1) Accelerate evaluation, genetic characterization, release and efficient use of adapted germplasm recently developed at Virginia Tech via backcrossing of FHB resistance to initial infection, spread, and DON accumulation into different genetic backgrounds; 2) Validate molecular markers linked to eight known FHB resistance QTL; and 3) Identify and characterize ideal haplotypes of newly developed FHB resistant SRW wheat lines using verified SSR and STS markers to facilitate MAS in wheat breeding programs.

In the proposed study, the presence of one or more of the eight known QTL for FHB resistance will be characterized and their effects on three components of FHB resistance and phenotypic performance in newly developed FHB resistant SRW wheat lines will be determined in four experiments at two locations. The expected outcome is to provide breeders with a useful package including adapted resistant germplasm and/or varieties and ideal marker haplotypes for use in MAS.

A total of 145 newly developed FHB resistant SRW wheat lines will be used in the current study. These lines were developed via backcrossing FHB resistance from six exotic sources (W14, Futai 8944, Shaan85, Ning7840, Ning9016, and VR95B717) into seven adapted SRW wheat backgrounds (Sisson sib, Roane, Pion2684, McCormick, Renwood3260, Ernie, and OH552). Type I resistance, assessed as FHB incidence, of these lines will be evaluated using a spray-inoculation method in a mist-irrigated field experiment at one location. Type II (FHB severity) and type III (DON accumulation) resistance will be evaluated in both greenhouse and field experiments at one location using floret inoculation and spray-inoculation methods, respectively. Effects of different genetic backgrounds and genetic contributions by donor, recurrent and/or adapted parents on overall phenotype and agronomic performance versus FHB resistance also will be assessed in field experiments at two locations.

Around 100 SSR and 4 STS markers at 8 QTL regions (2B, 2D, 3A, 3BS, 3BSc, 4B, 5A, 6B) previously reported as having association with at least one component of FHB resistance will be used to characterize haplotypes of lines following linkage analysis. Desirable and ideal haplotypes will be identified for three components of FHB resistance. These haplotypes subsequently can be used in selection of FHB resistance QTLs in breeding programs. The advanced lines with desirable haplotypes will provide breeding programs with a source of unique and adapted FHB resistant parents and some of the lines may have potential for release as cultivars. In addition, new QTL may be identified via comparison of characterized haplotypes.