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Fusarium head blight (FHB) epidemics were widespread in Virginia in 1998 and 2013, and much of the crop was devastated in 2003 and 2009 in Virginia and the southeastern U.S. Because of the limited level of FHB resistance in currently grown barley cultivars, there is a need for new cultivars with improved FHB resistance and lower DON accumulation. There has been renewed interest in high quality feed barley in both domestic and export markets and new demands for locally grown malt barley from the craft brewing industry, which is expected to increase by 50% over the next five years. This has heightened the needs of our program to provide growers and end users with superior feed and malt barley cultivars that are adapted to the eastern U.S. and have high yields, desirable quality, and disease resistance especially to FHB. In order to supply these industries with quality raw materials, there is a pressing need for germplasm with genes that confer resistance to FHB in barley, where there are relatively few natural sources of FHB resistance.

Each year winter barley entries in Virginia's state variety trial are evaluated for resistance to FHB and DON in an inoculated and mist irrigated scab nursery. Data from these tests are reported to producers in extension publications and online. In addition to FHB resistance identified and validated in native sources in Virginia's winter barley program, resistance identified in spring barley lines is being incorporated into adapted winter barley lines. Each year, single and top crosses including superior hulled, hullless, and malting barley parents will be made to parents having FHB resistance. Molecular markers previously identified in known resistance sources will be used to haplotype parents and progeny and to enrich breeding populations. FHB breeding populations in the F₂ and higher generations are evaluated each year in a scab nursery. Heads selected from F₄ and higher generation populations having FHB resistance parents will be screened with molecular markers in our lab and evaluated in headrow nurseries to identify desirable FHB resistant pure lines. Superior lines will be evaluated and advanced sequentially in replicated preliminary, advance, state, and regional trials as well as in FHB nursery tests prior to release.

Prior testing of our winter barley genotypes in scab nurseries indicates that a number of lines possess native resistance to FHB and DON. Tests conducted at two locations in 2010 and 2011 identified three genotypes having FHB indices significantly less than the test average in both testing environments. The hullless cultivar Eve had a two year mean FHB index (0-100) of 8.6, a DON concentration of 2.9 ppm, and 6.4% *Fusarium* damaged kernels (FDK). The hullless line VA06H-48 had a mean FHB index of 6.8, a DON concentration of 3.4 ppm, and an FDK value of 6.4%. The hulled cultivar Nomini had a mean FHB index of 8.7, a DON concentration of 3.3 ppm, and an FDK value of 7.4%.

Mapping populations consisting of 300 or more RILs are in the final stages of development and include: Thoroughbred / Nomini, Eve/VA07H-35WS, and Eve/Doyce. Phenotypic data including FHB incidence, severity and index, FDK and DON will be collected in spring 2015 and 2016 in inoculated and mist-irrigated nurseries. Putative QTL governing resistance to FHB and DON accumulation will be identified using bi-parental and/or association mapping analysis of single nucleotide polymorphisms (SNP) and phenotypic data. Initial data on a small subset of winter barley lines indicates the presence of putative quantitative trait loci on chromosome 6H for DON concentration and chromosome 7H for FHB incidence, severity and DON concentration. We will collaborate with Shiaoman Chao (USDA-ARS Genotyping Center in Fargo, ND) on haplotyping and validation of current and new markers for FHB resistance.

To accelerate development of FHB resistant winter barley varieties, 300 or more doubled haploid lines will be developed from a cross between the winter barley varieties Secretariat and Nomini. While the primary goal of this research is to develop superior varieties, the DH population also will be genotyped and evaluated for reaction to Fusarium head blight to validate results obtained from the Thoroughbred/Nomini mapping population.