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(1 Page Limit)

The objectives of this research are 1) increased acreage planted to varieties with improved FHB resistance and low DON, 2) increased efficiency of Coordinated Project breeding programs to develop FHB resistant varieties, and 3) develop new breeding technologies to further enhance short term and long term improvement of FHB resistance and to efficiently introgress effective resistance genes into breeding germplasm. The Southern Uniform Winter Wheat Scab Nursery provides public and private sector breeders with multi-environment evaluations of FHB resistance in advanced generation breeding lines compared with the resistant check varieties Ernie, Bess and Jamestown. Phenotypic data from the last five years of the Southern Uniform Winter Wheat Scab Nursery will be combined with sequence data of the nursery entries to develop genome wide marker effects for FHB incidence, severity, index, Fusarium Damaged Kernels, ISK, and DON. Statistical analysis of phenotypic information will use mixed model analysis in ASReml 3.0. The BLUE (best linear unbiased estimate) for each entry will be used in the genomic selection model. SNP calls will be obtained using a GBS approach and Genome Selection model utilized will be G-BLUP through the R-package Synbreed. The accuracy of the model will be tested with cross validation and entries in the 2016 and 2017 SUWWN and entries in the 2016 and 2017 SUNWHEAT cooperative wheat nursery will be phenotyped and sequenced. GEBV will be obtained for these entries based on the training population model. These values will be published in the uniform nursery annual report and allow for comparisons of the accuracy of the model against phenotypic data obtained for components of FHB resistance. The training population will be updated annually based on data from the SUWWN. We plan to produce 2-3,000 DH annually in-house. The primary goal will be the production of DH cultivars with moderate resistance to FHB. Each of the crosses will have one, or both, parents expressing moderate resistance to FHB. Several will segregate for known FHB resistance QTL (e.g. *Fhb1*, *Wuhan-1_2DL*, *Ning_5A*). We will conduct MAS among DH lines based on major effect QTL in-house, also paying special attention to Hessian fly, powdery mildew and leaf rust genes where appropriate. We will continue our policy of free distribution of DH lines from our program begun in fall 2010. Research concluded during the past year at NC State and Virginia Tech has added significantly to the understanding of QTL for FHB resistance in cultivars Bess (*Qfhb.nc-2B.1*, *Qfhb.nc-3B.2*), NC-Neuse (*QTL_1A*; *QTL_6A*) (Petersen et al., accepted) and Jamestown (*QTL_1B*; *QTL_6A*). A large number (>200) of breeding populations in the NCSU program were developed using one or more of these parents. Thus an expansion of MAS efforts to include these QTL in appropriate populations is being initiated. This began in summer 2015 with the genotyping of lines entering the Observation Yield trials for fall 2015, and parents entering the 2015-16 crossing block. Further confirmation of the efficacy of these QTL will be evaluated in DH populations involving parents from the NC-Neuse x Bess DH population, known to contain the four major QTLs, crossed with FHB susceptible parents.