GENETIC EVALUATION OF COTTON BREEDING RESOURCES FROM THE PEE DEE GERMPLASM ENHANCEMENT PROGRAM

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Abstract

The Pee Dee Germplasm Enhancement Program encompasses seventy years of breeding for the improvement of cotton fiber quality and yield. Program material has not yet been characterized with high-throughput genotyping. The goals of the present study are to characterize the relationships between genotypes and patterns of inheritance within the breeding program. We genotyped 96 diverse genotypes developed from the program across eight breeding groups between 1935 and 2002 using the CottonSNP63K Array. SNPs were quality filtered by removing loci with minor allele frequency <0.25 and call rate <90%, totaling 18,637 unthinned markers. Results were cross-validated with a 1,001 marker thinned set, culled to a density of one marker/cM. The generalized numerator relationship matrix (GNRM) was used to calculate an expanded pedigree-based measure of relatedness between genotypes. Genetic distance calculated from the thinned marker set was more strongly correlated (R^2=0.19) with the GNRM results than the unthinned set (R^2=0.09), likely due to variable density of unthinned markers across linkage groups. Principal component analysis (PCA) supported modest separation between groups, with groups five and six showing the most separation. PCA with the thinned marker set revealed additional separation in PC2 that was not present with the unthinned set. STRUCTURE analysis indicated high admixture, with the unthinned (k=8) and thinned sets (k=7) supporting the existence of ~eight subgroups. Allele tracking across generations was also explored, demonstrating how this data set enables tracking marker alleles across generations. The results of this study will help us explore marker-trait associations in the Pee Dee germplasm.