Breeding Cotton for Annual Growth Habit: Remobilizing End-of-season Perennial Reserves for Increased Yield

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Abstract: Cotton (Gossypium spp.) is the primary source of natural fiber in the U.S. and a major crop in the Southeastern U.S. Despite constant efforts to increase the cotton fiber yield, the yield gain has stagnated. Therefore, we undertook a novel approach to improve the cotton fiber yield by altering its growth habit from perennial to annual. In this effort, we identified genotypes with high-expression alleles of five floral induction and meristem identity genes (FT, SOC1, FUL, LFY, and AP1) from an upland cotton mini-core collection and crossed them in various combinations to develop cotton lines with annual growth habit, optimal flowering time and enhanced productivity. To facilitate the characterization of genotypes with the desired combinations of stacked alleles, we identified markers associated with the gene expression traits via genome-wide association analysis using a 63K SNP Array (Hulse-Kemp et al. 2015 G3 5:1187). Over 14,500 SNPs showed polymorphism and were used for association analysis. A total of 396 markers showed association with expression traits. Out of these 396 markers, 159 mapped to genes, 50 to untranslated regions, and 187 to random genomic regions. Biased genomic distribution of associated markers was observed where more trait-associated markers mapped to the cotton D sub-genome. Many quantitative trait loci coincided at specific genomic regions. This observation has implications as these traits could be bred together. The analysis also allowed the identification of candidate regulators of the expression patterns of these floral induction and meristem identity genes whose functions will be validated via virus-induced gene silencing.

Keywords: cotton, GWAS, QTL, expression traits

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