DEVELOPMENT AND CHARACTERIZATION OF CHROMOSOME SEGMENT SUBSTITUTION LINES

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Abstract

Genetic improvements of Upland cotton (*Gossypium hirsutum* L.) must be continuous if the crop is to remain biologically and economically viable, e.g., competitive to synthetic fibers, resistant to most diseases and pests, profitable to produce, and be environmentally sustainable. The notoriously low genetic diversity found among Upland cottons constrains opportunities for improvements by breeding based on conventional elite-by-elite crosses. Fortunately, each related wild AD-genome species harbor about 80,000 genes and so introgression of a wild species germplasm can significantly increase the breadth of variation available among Upland cottons. However, for most genes, it is virtually impossible to predict whether a variant would be helpful, neutral or deleterious in Upland cotton genetic background. The history of wide-cross introgression into cotton has shown us we need more scientific and methodical approaches to effectively harness the genomes of wild species. One such method involves the breeding of Chromosome Segment Substitution Lines (CSSLs) by modified backcross-inbreeding. Each CSSL cotton would be marker-selected to contain one to several small subchromosomal introgressed alien segments but otherwise isogenic for *G. hirsutum*. Panels of CSSLs would be chosen by marker-based selection such that they collectively "capture" all or most of an alien genome. We report here progress toward a *Gossypium hirsutum* (TM-1) panel of CSSLs containing germplasm from *Gossypium mustelinum,* a wild Brazilian cotton species. These CSSLs will provide a powerful tool for introgression and characterization of *G. mustelinum* germplasm; it will significantly expand the isogenic platform, which also includes Chromosome Substitution Lines. Fiber data (HVI) were obtained from late backcross hybrid generations to look for any exceptionally strong dominant or codominant effects. The CSSLs (BC5Sn lines) will be high-density genotyped and tested for fiber (HVI, APHIS) and other traits.