CHROMOSOME SUBSTITUTION LINES (CS-B) REVEALED THE PRESENCE OF CRYPTIC BENEFICIAL ALLELES IN G. BARBADENSE WITH POTENTIAL TO INCREASE LINT AND SEEDCOTTON YIELD IN UPLAND COTTON

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Abstract

One of the most promising opportunities to improve the genetic diversity of Upland cotton is from interspecific germplasm introgression from the other tetraploid species, including *Gossypium barbadense* L. Past efforts to utilize other species as sources for genetic improvement of cultivated types of *G. hirsutum* L. has been hampered by the paucity of information of the beneficial alleles in the other species. In addition to the many biological and genetic challenges associated with the interspecific introgression, the potential value of the wild non-adapted species is often not manifest, due to effects of differing genetic backgrounds, e.g., phenotypically antagonistic and deletorious genes. To test for epistatic interactions, which theoretically might have greater influence when breeding at interspecific levels, we have evaluated intercrosses among quasi-isogenic backcross chromosome substitution lines (CS-B), each carrying a different pair of alien chromosomes. The results revealed otherwise cryptic beneficial alleles in *G. barbadense* (3-79) with potential to increase lint and seedcotton yield in Upland cotton (TM-1). The findings underscore the value of alien germplasm as a source of new and valuable genes, including those affecting yield and other complex traits. More importantly, they greatly strengthen evidence that epistatic effects are a major contributor to complex trait variance. Thus, breeding methods that capture the value of epistatic interactions should be more efficient for genetic improvement programs using alien germplasm. The results demonstrate usefulness of interspecific chromosome substitution lines for detecting beneficial alleles in specific alien chromosomes and chromosome arms. Most significantly, the results underscore the value of interspecific chromosome substitution lines as a means to capture the largely untapped potential wild unadapted species for the genetic improvement of cotton.