

Chromosome Substitution Lines: Useful Genomic Resources in Cotton

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The genus *Gossypium* is a very diverse one with about 50 species. However, a very narrow germplasm base is presently being used for genetic improvement of Upland cotton. The wild tetraploid cotton species are reservoirs of important genes for pest and disease resistance, and for improved agronomic and fiber traits. Two of the most important forces impeding Upland cotton improvement are: 1) the paucity of information about genes that control important traits, and 2) the need for extensive usage of diverse germplasm. Interspecific germplasm introgression has not been exploited well in Upland cotton improvement because considerable time and effort are required to overcome biological, genetic and cytogenetic hurdles in interspecific crosses. A complementary approach to conventional method of interspecific introgression is to utilize chromosome substitution lines (CS). The utilization of CS in crossing with Upland cotton will reduce interspecific incompatibility at the whole-genome level, and it will allow introgression while targeting one or more specific traits that are associated with one or more specific alien chromosomes or chromosome arms into upland cotton. This will reduce the deleterious effects of unrelated loci that if transmitted would confer some poor agronomic qualities from the wild alien species. Also contrary to conventional breeding methods, CS entails the use of hemizygoty to preclude recombination during introgression, so that all genes within a given alien chromosome or chromosome segment are transferred into upland cotton. Thus, this method largely precludes the loss of alien germplasm during conventional backcrossing. The overall goal of this project is to develop CS from the multiple tetraploid species in *G. hirsutum*. The backcrossed chromosome substitution lines are nearly isogenic to TM-1, an upland cotton (*G. hirsutum*) genetic standard, and to each other, except that each line differs by the replacement of a specific homologous pair of chromosomes or chromosome segments from the donor alien species. We have developed backcross-substituted (BC₅) 20 different chromosomes and chromosome arms of *G. barbadense* into quasi-isogenic upland cotton (CS-B) lines. We demonstrated the great potential of the CS-B lines for improving fiber and agronomic traits in upland cotton. Currently we are in the process of developing CS lines from the other tetraploid species of *G. tomentosum* and *G. mustelinum*. The CS lines will provide the unique opportunity of dissecting the complex cotton genome based on individual chromosome and chromosome pieces. They provide a unique powerful tool to analyze and understand the complex cotton genome and in the discovery of many new genes important for agronomic and fiber traits. The CS lines open new paradigms of cotton breeding such as improving complex quantitative traits based on individual chromosome or chromosome segment.