

Introgression of *Gossypium klotzschianum* Genome into Cultivated Cotton, *G. hirsutum*

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Exotic *Gossypium* germplasm is a rich source of useful agronomic traits for improvement programs of cultivated cotton. Efficient use of genetic variation available in the wild relatives depends on the ability to identify and introgress desirable DNA segments from wild species into cultivated cotton. To introgress genes from *G. klotzschianum* to *G. hirsutum*, a BC₁F₂ population from (*G. hirsutum* × *G. klotzschianum*) *G. hirsutum* was constructed. A total of 320 SSR primers covering the cotton genome were selected to monitor alien germplasm transmission. Only 38 markers showed segregation in the BC₁F₂ population, which were distributed in 14 different chromosomes and constituted 18 introgressed segments. The total length of the 18 introgressed segments was 595 cM based on a cotton consensus map. Two morphological traits yellow petal and open bud were mapped on chromosome 13. Our molecular and morphological identification confirmed the presence of *G. klotzschianum* chromatin in the BC₁F₂ interspecific progenies. The use of species-specific molecular markers will greatly facilitate introgression of desirable alien genes into cultivated cotton.