MOLECULAR CONFIRMATION OF *GOSSYPIUM HIRSUTUM* CHROMOSOME SUBSTITUTION LINES AND INTERSPECIFIC F_1 HYPOANEUPLOIDS

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Abstract

The tetraploid *Gossypium* species *G. barbadense, G. tomentosum, and G. mustelinum* (2n=52) are useful sources of important genes for pest and disease resistance, and for improved agronomic and fiber traits in Upland cotton (*G. hirsutum*). Cytological analyses of hybrids and comparative linkage mapping indicate that structural genomic differences among the tetraploid *Gossypium* species are minimal and do not preclude introgression of their germplasm into Upland cotton. Nonetheless, previous introgression efforts using conventional breeding methods have had very limited success, indicating deep-seated genetic conflicts in the hybrids preclude facile recovery of agronomically useful types. To help overcome these barriers, we are developing alien chromosome substitution (CS) lines. The development of each CS line involves four stages: (*i*) create isogenic Upland chromosome-deficient stocks, by backcrossing various chromosome deficiencies (monosome or telosome) to a common line, namely 'Texas Marker-1' (TM-1); (*ii*) create a F_1 substitution stock that is monosomic or monotelodisomic (i.e., partially hemizygous) by recurrent backcrossing to each isogenic cytogenetic stock as a recurrent seed parent; (*iii*) inbreed the backcrossed hypoaneuploid derivative to recover a euploid disomic substitution line; (*iv*) confirm the cytogenetic and genetic constitution of the disomic lines by cytological analysis and chromosome-specific SSR markers. Seventeen CS-B lines (CS lines from *G. barbadense*) were developed using the above procedure and released for use in Upland cotton improvement. These substitution lines are nearly isogenic to the common parent TM-1 for 25 chromosome pairs, as well as to each other, for 24 chromosome pairs. At the time development was initiated for some CS lines, molecular markers did not exist, and by the time several lines were released, very few accurately mapped chromosome specific SSR markers were available in the public domain. Recently in addition to the cytological analysis, we have been using SSR markers from one or more linkage maps to assess the constitution and genetic identity of the CS lines. For genetic evaluation of chromosome-deficient F_1 and $BCnF_1$ hybrid chromosome substitution intermediates, e.g., 2n=51 monosomics, we followed the principles of deletion analysis, e.g., loss of heterozygosity. For CS euploid lines (2n=52), we compared marker profiles of CS lines, parents and other CS

germplasm. For most CS lines and most mapped markers, the observed SSR profiles were concordant with expectations. For a minority of markers and lines, however, the results were discordant; these markers, linkage groups, and CS lines are being further investigated to better define these research and breeding resources.