CHROMOSOME SUBSTITUTION LINE ANALYSIS USING SNP KASP ASSAYS

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Abstract

Cotton brings significant humanitarian and economic benefits but its production and marketing are challenged due to its narrow genetic basis. Chromosome substitution (CS) is a powerful means of interspecific wild germplasm introgression, and such introgression is one of the most powerful strategies to broaden the genetic basis of Upland cotton and other domesticated forms of *G. hirsutum* (L.). One way of developing chromosome substitution (CS) lines is to use modified backcrossing, where the recurrent parent is chromosomally deficient, i.e., a monosomic or monotelodisomic individual lacking a whole chromosome or most of a chromosome "arm". Whole-chromosome or chromosome-segment substitutions collectively constitute an isogenic platform for both quantitative genetic analysis and breeding purposes, as has been demonstrated for both agronomic and fiber traits through collaborative research with collaborators at the USDA-ARS in Starkville, MS. Most cotton chromosome substitution lines have been developed on the basis of cytogenetic analyses and phenotyping but without the benefit of molecular marker analyses. We and other collaborators have recently developed large numbers of interspecific single-nucleotide polymorphism (SNP) markers for cotton. The main aim in this study has been to use the new SNP markers to firmly associate SNPs with specific chromosomes and to determine if previously synthesized chromosome substitution lines contain the intended alien chromosomes or chromosome segments. Thus, we aimed to use the SNPs to verify their desired constitution, or if incorrect, to more accurately define their genetic content. We note that any line departing from its expected alien chromosome content could be useful a germplasm resource, especially if accurately characterized. The power of this SNP-based analysis was greatly amplified by combined use of high-throughput SNP genotyping. Analyses to date have confirmed the constitution of 12 CS-B, 12 CS-T and 12 CS-M lines, which respectively contain chromosomal or segmental substitutions from *G. barbadense, G. tomentosum* and *G. mustelinum*.