PRELIMINARY ASSESSMENT OF THE EFFICACY OF A CORE MARKER SET IN REVEALING GENETIC DIVERSITY IN THE U.S. GERMPLASM COLLECTION

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Abstract

A comprehensive knowledge of the genetic diversity within the U.S. *Gossypium* Germplasm Collection is necessary to achieve its most effective utilization and the greatest efficiency in its maintenance. To improve our knowledge of the collection's diversity, a project was initiated in 2009 to characterize between 20 and 25 percent of the collection using a candidate core marker set of 105 SSRs. Labeled primers for the SSRs were created using FAM, HEX, or NED labels, creating 35 primer sets for multiplex PCR amplification. A pilot project using a 96 accession subset of the collection representing the tetraploid species and the A and D genome diploid progenitor species was conducted to verify the efficacy of the multiplex primer sets, develop protocols for amplification, develop data collecting bins for a data file, and assess the ability of the markers to reveal genetic diversity within the collection. Good amplification occurred for 101 of the 105 markers. A total of 961 alleles were observed among the markers for an average of 9.5 alleles per SSR primer. Within *G. hirsutum*, an average of 6.3 alleles per marker was observed in race stock accessions, whereas cultivar accessions only produced an average of 2.9 alleles per marker. Lower levels of variation were observed within *G. barbadense*. Cluster analyses and dendrograms revealed good differentiation of species by the core marker set. Species specific and introgressed alleles were identified in *G. barbadense* and *G. hirsutum*. Introgressed alleles in both *G. barbadense* and *G. hirsutum* were more prevalent in wild or commensal accessions than in cultivars, and made up 9.2% and 12.3% if the alleles observed, respectively Overall, the candidate core marker set, with some further modification, appears sufficient for the task of characterizing diversity of the larger collection.