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ESTABLISHMENT OF THE STANDARDIZED COTTON MICROSATELLITE DATABASE (CMD) PANEL

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Abstract

Cotton is a genetically complex organism that makes genetic manipulations and advancements very time intensive. DNA markers linked to agronomic traits can improve the efficiency of cotton breeding tremendously by significantly reducing backcross generations and obviating costly, lengthy and subjective phenotypic assays. In order to make significant and timely advances in the genetic improvement of cotton, many thousands of portable DNA markers are needed for a tetraploid genome of the cultivated cotton. Thus, development of large numbers of PCR-based DNA markers is proposed as the first one of the short-term objectives on the structural genomics research of the International Cotton Genome Initiative (ICGI). One type of such portable markers is called microsatellite or simple sequence repeat (SSR) markers that are easily assayed and are abundant in the cotton genome. Polymorphic DNA markers arising from variation in SSR numbers have shown great utility in genetic mapping and other applications. Currently there are several cotton research groups across the Cotton Belt and worldwide working on the development of cotton SSR markers. The source material for SSR discovery includes large insert BAC clones or physical contigs, random enriched small genomic clones, and fiber ESTs or other coding sequences. Over the past couple of years, Cotton Incorporated has been funding and coordinating the effort to expedite the development and characterization of new cotton SSR markers. This effort is also reflected in the establishment of a standard cotton DNA genotype panel. After extensive consultation and discussion with many cotton researchers, a panel of 12 cotton genotypes was selected that consist of TM-1, 3-79, Acala Maxxa, DPL 458BR, PM 1218BR, FM 832, Stoneville 4892BR, Pima S-6, G. arboreum (A2-8), G. raimondii (D5-3), G. tomentosum (AD3), and G. mustelinum (AD4). This panel represents a balanced diversity of the core Gossypium germplasm that includes genetic standards, base mapping parents, BAC donors, subgenome representatives, unique breeding programs, exotic introgression sources, and four contemporary Upland cottons each with significant acreage. Three to five individual plants are maintained for each of 12 cotton genotypes in a USDA-ARS greenhouse in College Station, Texas. Only one single plant for each genotype is flagged for tissue harvest and DNA extraction, and standard protocols are followed for DNA purification and evaluation, providing the best uniformity of DNA stocks for cotton researchers with ongoing SSR marker development. With this standard genotype panel, cotton SSR markers derived from different sources or groups can be evaluated in a systematic way to minimize the potential duplications and to determine the markers' Polymorphic Information Content (PIC) values for ready applications. The information on the clones, sequences, primers, amplification conditions in addition to the PIC values will be entered in the public domain via a dedicated database, Cotton Microsatellite Database (CMD), which is being set up at Clemson University. An Advisory Committee is formed to oversee the CMD and to coordinate it with the CottonDB, a comprehensive cotton genome database.