Identification of 700 New Microsatellite Loci from Cotton (*G. hirsutum* L.)

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Microsatellite markers, also known as SSRs, comprise a keystone technology for genetic linkage analysis, QTL mapping, marker-assisted breeding, and genome analysis. In order to contribute to a growing body of molecular marker resources for cotton research and improvement, 700 primer pairs were developed to amplify new microsatellite markers, designated Gh for *Gossypium hirsutum*. These primers were designed using microsatellite sequences that were isolated from genomic DNA of *G. hirsutum* cv. Tamcot Sphinx by a biotinylated-oligonucleotide capture method. A total of 4,512 clones from $(GA)_n$, $(AGA)_n$, and $(CA)_n$ microsatellite-enriched libraries were sequenced. From these, 1,059 primer pairs were developed. Of the first 700 primer-pairs to be characterized, 602 primer pairs (86%) produced one or more distinct PCR amplification products within the expected size range in at least one of the test cotton genotypes, *G. hirsutum acc*. TM-1 and *G. barbadense acc*. 3-79. Further, 201 primer pairs (28.7%) yielded size polymorphisms between TM-1 and 3-79 that were easily resolved using high-resolution agarose electrophoresis. A subset of 165 polymorphic markers was fully genotyped on a TM-1 x 3-79 interspecific recombinant inbred (RI) population of 191 individuals. In this analysis, segregation distortion was low (10.3% of loci) and functional redundancy of marker loci was low (1.2% of loci). Data from these markers are being incorporated in an integrated SSR map from the TM-1 x 3-79 recombinant inbred population. Updates regarding sequence, primer, polymorphism, and linkage information from the remainder of the Gh microsatellite collection will be uploaded directly to CottonDB and CMD databases.

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