

THE COTTON CYTOGENETICS COLLECTION

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Abstract

The Cotton Cytogenetics Collection is critical to our national cotton improvement effort, particularly as related to genetic analysis and genetic manipulation. The Collection has been particularly important to genetics for the identification and nomenclature of genomes, chromosomes and their subregions. For genetics and breeding, the stocks allow for selective manipulations of specific chromosomes or segments – e.g., for mapping or interspecific introgression. Their utility is now being extended into the realms of high-throughput structural and functional genomics, e.g., for refined dissection, analysis and mapping of agronomically important traits, genes and markers. Moreover, as the only means of guaranteeing introgression from one end of the chromosome to the other, they are an integral part of efforts aimed expanding the germplasm base of Upland cotton. Introgression of new alleles and genes should help alleviate insufficient genetic variation within elite *G. hirsutum*, which is thought to be partially responsible for the “yield plateau” recently observed for US cotton production. The Collection primarily includes translocations, and hypoaneuploids. The translocations collectively provide a simple system by which all chromosomes can be identified. The hypoaneuploids enable facile “deletion mapping”, polymorphism-dependent mapping, and selective manipulation of specific chromosome regions for introgression and genetic analysis. Whereas monosomic and monotelodisomic types were essentially the only hypoaneuploid components in earlier times, the Collection now embraces two additional types of hypoaneuploids -- “duplication-deficients” (segmental monosomic-trisomics) and “tertiary monosomics”. Hypoaneuploids in the Collection now cover part or all of all but two chromosomes. All are useful means of rendering specific chromosome regions amenable to manipulation. Most of the aneuploids have been used to create hypoaneuploid interspecific F1 stocks with *G. barbadense* to facilitate mapping. Many were also used as a recurrent parent for backcrossing to develop BC5S1 disomic chromosome substitution lines (to be jointly released 2003). We recently initiated efforts to develop analogous disomic chromosome substitution lines for *G. tomentosum* and *G. mustelinum*. We gratefully acknowledge continued support from TAES, occasional support from USDA NRICGP for the cytogenetics, recent support for interspecific applications through cooperative agreements with the USDA-ARS in Mississippi, and grants from the Texas Food & Fiber Commission (TFFC), cotton growers in Texas (Texas State Support Committee), and national germplasm effort through Cotton, Inc.