

**NOTICE OF RELEASE OF 17 GERmplasm LINES OF UPLAND (*Gossypium hirsutum*)
COTTON, EACH WITH A DIFFERENT PAIR OF *G. BARBADENSE* CHROMOSOMES OR
ARMS SUBSTITUTED FOR THE RESPECTIVE *G. HIRSUTUM* CHROMOSOMES OR ARMS**

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The exceptional fiber length, strength and fineness of Pima and Sea Island cotton (*Gossypium barbadense*) give it a 30% to 50% price advantage over the more widely grown Upland cotton (*G. hirsutum*) because of its superior spinning and manufacturing performance. Attempts to incorporate genes from *G. barbadense* into Upland have generally not achieved stable introgression of the *G. barbadense* fiber properties. Associated with these attempts have been poor agronomic qualities of the progeny, distorted segregation, sterility, and limited recombination due to incompatibility between the genomes. An alternative approach to introgress *G. barbadense* fiber quality genes into Upland cotton would be to use backcrossed alien chromosome substitution lines. The Texas Agricultural Experiment Station, the Agricultural Research Service of the United States Department of Agriculture, and the Mississippi Agricultural and Forestry Experiment Station announce the release of 17 unique germplasm lines of backcrossed chromosome substitution lines of different *Gossypium barbadense* chromosomes in a *G. hirsutum* genetic background. This material forms a unique set of germplasm lines which are genetically similar except that each differs by the replacement of a specific homologous pair of chromosomes or chromosome segments from 3-79 (*G. barbadense*) into TM-1, Upland cotton (*G. hirsutum*). Using an integrated approach of cytological and conventional breeding methods by hypoaneuploid-based backcross chromosome substitution, we have replaced individual *Gossypium hirsutum* ('TM-1') chromosome pairs with the respective *G. barbadense* ('3-79') chromosome pairs. This material forms a unique set of germplasm lines which are genetically similar except that each differs by the replacement of a specific homologous pair of chromosomes or chromosome segments from 3-79 (*G. barbadense*) into TM-1, Upland cotton (*G. hirsutum*). Our preliminary results from crossing program using these lines as one of the parents with TM-1 showed that these lines are very useful in mapping important traits including QTLs and improving germplasm for fiber and agronomic properties. These germplasm lines were developed and evaluated by, D.M. Stelly and W. Raska of Texas A&M University, S. Saha, J.N. Jenkins, J.C. McCarty, and O.A. Gutierrez of the USDA/ARS, Mississippi State, MS in a collaborative research program.

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The Texas Agricultural Experiment Station, the Agricultural Research Service of the United States Department of Agriculture, and the Mississippi Agricultural and Forestry Experiment Station announce the release of 17 unique germplasm lines of backcrossed chromosome substitution lines of different *Gossypium barbadense* chromosomes in a *G. hirsutum* genetic background (Table 1). This material forms a unique set of germplasm lines which are genetically similar except that each differs by the replacement of a specific homologous pair of chromosomes or chromosome segments from 3-79 (*G. barbadense*) into TM-1, Upland cotton (*G. hirsutum*). TM-1 is an inbred line derived from the commercial variety Deltapine 14 and maintained over 40 generations by self pollination, as described by Kohel et al., 2001; in *Euphytica* 121:163-172. Line 3-79 originated as a doubled-haploid from Pima germplasm with higher fiber quality than modern Pima germplasm. The high fiber quality and genetic uniformity of 3-79 and the availability of a large number of hypoaneuploid stocks in TM-1 background influenced our choice of parental lines.

These germplasm lines are being released because attempts to incorporate genes from *G. barbadense* for exceptional fiber length, strength and fineness into Upland have generally not achieved stable introgression. Poor agronomic qualities of the progeny, distorted segregation, sterility, and limited recombination due to incompatibility between the genomes have been associated with previous attempts to incorporate genes from *G. barbadense*. An alternative approach to introgress *G. barbadense* genes into Upland cotton is to develop and use backcross-derived alien chromosome substitution lines. By hypoaneuploid-based backcross chromosome substitution, we have replaced individual 'TM-1' chromosome pairs with their respective '3-79' chromosome pairs and largely reconstituted the other *G. hirsutum* chromosomes. Collectively, this set of substitutions covers about half of the genome. For non-substituted chromosomes or arms, the amount of alien genetic material is expected to be low or nil (random expectation *ca.* 1.6%) at the BC5 generation, because the backcross process is expected to eliminate half of the alien genetic material each generation. When one of these CS-B lines is crossed with *G. hirsutum*, the entire substituted *G. barbadense* chromosome or arm is expected to pair and recombine with the same chromosome or arm from *G. hirsutum*. The strong differential representation between substituted and non-substituted chromosomes offers a number of additional analytical and genetic advantages.

The development of these lines followed principles of cytogenetic behavior, transmission, and inheritance as outlined by En-drizzi et al. 1985, *Advances in Genetics* 23:271-385. Key among these is that whereas transmission of hypoaneuploidy through the ovule parent is common (up to 50%) for most monosomic and monotelodisomic conditions, transmission through cotton pollen is rare to nil for all whole-chromosomes and most large-segment deletions (e.g., telosomes). The backcrossing process used in cotton is facilitated by this differential transmission between mega- versus micro-gametophytes, i.e., between the “ovule” (“seed” or “female” parent), versus the pollen (“male”) parent.

For each line, the following procedure was followed: The initial cross was made between a cytogenetic derivative of *G. hirsutum* TM-1 that was deficient for one copy of a specific chromosome (“monosomic” plant) or chromosome arm (“monotelodisomic” plant), as female, and a chromosomally normal (euploid) *G. barbadense* 3-79 line, as male. Due to their chromosomal constitution, monosomic, monotelodisomic and euploid plants form diagnostic metaphase I meiotic configurations (25 II + I; 25 II + Ii; and 26 II, respectively) in microsporocytes (“pollen (microspore) mother cells”). An interspecific F1 plant deficient for the chromosome or chromosome arm was selected based on metaphase I analysis of the microsporocytes. This interspecific aneuploid (BC0F1) plant was used as male parent and backcrossed with the recurrent aneuploid TM-1 plant. The aneuploid BC1F1 plant was selected based on metaphase I analysis, as in the BC0F1 generation. This procedure was continued until the fifth backcross at which point a euploid plant (BC5F1 26II) was selected based on cytological analysis of the metaphase microspores. The euploid BC5F1 plant was selfed to establish euploid BC5S1 lines. Table 1 provides additional information about the pedigrees of these lines. Petal color and leaf or stem hairiness are segregating in some of these BC5 self-pollinated plants. Segregation for these traits is due to background residual effect and is independent of the homozygous condition of the substituted chromosome or arm from *G. barbadense*. Our preliminary results from crossing program using these lines as one of the parents with TM-1 showed that these lines are very useful in mapping important traits including QTLs and improving germplasm for fiber and agronomic properties. We are currently conducting this experiment in three different locations in replicated plots for two year periods. We plan to present this data in a separate manuscript.

These germplasm lines were developed and evaluated by, D.M. Stelly and W. Raska of Texas A&M University, S. Saha, J.N. Jenkins, J.C. McCarty, and O.A. Gutierrez of the USDA/ARS, Mississippi State, MS in a collaborative research program. We label these lines as CS-B series (Table 1) where CS represents chromosome substitution lines and B represent from *Gossypium barbadense* species and the number represent the respective chromosome.

A limited amount of BC5 self-pollinated seeds are available for distribution to cotton geneticist, breeders, and other research personnel upon written request to Dr. D. Stelly, Dept. Soil & Crop Sciences, Texas A&M University, College Station, TX 77843-2474 USA or Dr. S. Saha, USDA-ARS, P.O. Box 5367, Mississippi State, MS 39762, USA. Genetic materials of this release will be deposited in the National Plant Germplasm System where these materials will be available for research purposes, including development and commercialization of new materials. It is requested that appropriate recognition of the source be given when these germplasm lines contribute to research or the development of improved line, cultivar or hybrid.

Table 1. Interspecific chromosome substitution lines of cotton in 'TM-1' *G. hirsutum* background.

Designation of Released Line	Cytological Parent in TM-1 Used as Recurrent Parent	Substituted Chromosome or Arm from <i>G. barbadense</i> 3-79¹
CS-B01	H01, monosomic for chromosome 1	1
CS-B02	H02, monosomic for chromosome 2	2
CS-B04	H04, monosomic for chromosome 4	4
CS-B06	H06, monosomic for chromosome 6	6
CS-B07	H07, monosomic for chromosome 7	7
CS-B16	H16, monosomic for chromosome 16	16
CS-B17	H17, monosomic for chromosome 17	17
CS-B18 ²	H18, monosomic for chromosome 18	18
CS-B25	H25, monosomic for chromosome 25	25
CS-B05sh	Te05Lo, monotelodisomic for long arm of chromosome 5	5 short arm
CS-B11sh	Te11Lo, monotelodisomic for long arm of chromosome 11	11 short arm
CS-B12sh	Te12Lo, monotelodisomic for long arm of chromosome 12	12 short arm
CS-B14sh	Te14Lo, monotelodisomic for long arm of chromosome 14	14 short arm
CS-B15sh	Te15Lo, monotelodisomic for long arm of chromosome 15	15 short arm
CS-B22sh	Te22Lo, monotelodisomic for long arm of chromosome 22	22 short arm
CS-B22Lo	Te22sh, monotelodisomic for short arm of chromosome 22	22 long arm
CS-B26Lo	Te26sh, monotelodisomic for short arm of chromosome 26	26 long arm

¹Caution should be exercised in when drawing conclusions about positions of the centromere, genes and molecular markers based on BC5S1 chromosome arm substitution analysis. Users should recognize that while it is likely that the centromere is close to the respective junction between *G. hirsutum* and *G. barbadense* chromatin, the exact position of the junction is unknown at this time. Users are thus encouraged to share and post data that will help define the positions of these junctions on integrated chromosome maps.

²Homozygous for Open bud mutant conditioned by a double recessive gene with one gene in each genome.