

The Transfer of Caducous Bract Traits to Commercial Cultivars

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The transfer of caducous bract trait from hexaploid cottons to commercial cultivars is progressing on schedule. Our goal is a 52-chromosome caducous bract tetraploid cotton.

The back-crossing program started several years ago involved the hybridization between commercial cultivars with 52 chromosomes and the 78-chromosome caducous bract hexaploid cotton. The first cycle of crossing reduced the chromosome number to a 65-chromosome pentaploid. The pentaploids were allowed to self-pollinate and their progenies grown out for evaluation. From these progenies, three caducous bract aneuploids were selected - two with 58 chromosomes, and one with 60 chromosomes. These plants were dug up and transplanted into pots in the greenhouse for cross-pollination during the winter months.

To increase the number of caducous bract plants for the second cycle of back-cross breeding, cuttings were made from these plants. Many cuttings have rooted, and at the present time, there are 21 clones from the three caducous bract aneuploids.

The second cycle of back-cross breeding was initiated using the clones of the aneuploids with commercial cultivars as the recurrent parents. Seed from these crosses should contain on the average, about 55 chromosomes. They will be allowed to self-pollinate, and the seed will be planted as soon as they mature for evaluation of the progenies. This should further reduce the chromosome number in the plants close to our goal of a 52-chromosome cotton with caducous bracts.

Chromosome numbers as well as the pairing configurations of the plants are being monitored, step by step, to evaluate each phase of the breeding project including camera lucida drawings of the chromosomes of the caducous bract cottons.

A variation of chromosome number has been found in the hexaploids. Microscopic examinations of pollen mother cells show plants ranging from 74 to 81 chromosomes. The majority, however, had 78 chromosomes. Multivalents containing 3, 4, and 6 chromosomes and univalents were observed in all cells. These are formed when D_h from G. hirsutum and D_{2-1} chromosomes from G. armourianum pair with each other. This leads to exchange of D_h and D_{2-1} genes. A trait such as caducous bract could be influenced by the number of allelic genes present in the plant. This number could vary from zero to four D_{2-1} alleles. The best type would be one with four D_{2-1} alleles which would drop the bracts before anthesis similar to G. armourianum, the wild lintless diploid species from which the trait was transferred.

Pentaploids obtained from the hexaploid back-crossed with G. hirsutum varied in chromosome numbers from the expected 65 chromosomes. Numbers ranging from 62 to 66 were counted. Trivalents formed by D_{2-1} univalents pairing with its D_h homoeologous pair were observed.

The formation of trivalents leads to loss of chromosomes with each generation. In one case, a 64-chromosome plant had progenies varying from 54 to 59 chromosomes. Three other pentaploids had caducous bract progenies. Two caducous bract aneuploids had 58 chromosomes, and the other 60 chromosomes. Thus, with each generation the chromosome number is dropping. As we get closer to the tetraploid level, selection pressure for caducous bracts is maintained.

Ovule Culture in Cotton Breeding

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A wide assortment of agronomic traits are available to cotton breeders through the hybridization between commercial cultivars and the wild Gossypium species. Cytoplasmic male sterility has been brought into the cultivated cottons by crosses with the lintless wild species G. harknessii. Disease and insect resistance might similarly be introduced through crosses with wild species.

There are problems in using wild species in a hybridization program. Only a small percentage of hybrid bolls remain on the plant until maturity. The problem is G. hirsutum and G. barbadense are tetraploids and most of the wild species are diploid. The incompatibility between the cultivated cottons and the wild species is usually due to a difference in chromosome number.