Monosomics of Cotton¹

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ABSTRACT

From 1946 to 1975, 166 monosomic plants of Gossypium hirsutum L. were placed in the monosome testing program at Beasley Laboratory. The 85 that have been identified have been deficient in one of the following chromosomes: 1, 2, 4, and 6 from the A subgenome; 16, 17, and 18 from the D subgenome. These monosomes came from irradiation treatments, translocations, tertiary monosomes, duplication-deficiencies, cytological combinations, trisomics, other aneuploids desynaptics, other Gossypium species, cultivars, and breeding stocks.

Additional index words: Gossypium hirsutum L., Allotetraploid, Subgenome, Irradiation, Translocation, Duplication-deficiency, Cytological combination, Trisomic, Aneuploid, Desynaptic, Cultivars, Breeding stocks.

UPLAND cotton, Gossypium hirsutum L., is an allotetraploid (2n=4x=52). The 13 large A subgenome chromosomes are numbered from 1 to 13 and the 13 small D subgenome chromosomes are numbered from 14 to 26. To date, 15 of the 26 possible monosomes have been found, nine from the A subgenome and six from the D subgenome (Endrizzi

and Brown, 1964; Dabral and Singh, 1975; Endrizzi and Ramsey, 1979). The first monosomic plant to be studied at Beasley Laboratory in College Station was found sometime prior to 1942 by J. O. Beasley. It was not recovered in any subsequent progeny and was therefore not identified (Brown and Endrizzi, 1964). Since that time, 166 monosomics have been found and assigned M (monosome) numbers at Beasley Laboratory.

MATERIALS AND METHODS

New monosomic plants found in the field are brought into the greenhouse and crossed to TM-1 (Texas Marker-1, an inbred tester line) and selfed for seed increase. Since most newly found monosomics are duplicates of known monosomics they are evaluated for phenotypic characters against the set of known monosomic plants (Endrizzi and Ramsey, 1979). They may either be eliminated on the basis of phenotype or crossed to a set of known translocations to establish the chromosome in question. A positive association of the monosome with the translocation results in 24 bivalents and a trivalent (24II + III); a negative association results in 23 bivalents, a quadrivalent, and a univalent (23II + IV + I).

RESULTS AND DISCUSSION

From 1946 to 1975, 166 monosomic plants were brought into the program, and 93 have been identified. Eighty-five of the identified monosomes are of independent origin and are of chromosomes 1, 2, 4,

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Origin	Monosomics for chromosome							
	A subgenome				D subgenome			-
	1	2	4	6	16	17	18	Totals
				no.				-
X-ray		1	1					2
Neutron			1					1
Gamma						1		1
Translocation		3	3	2	2		1	11
Tertiary monosomic		5	5					10
Duplication-deficiency		1	1	1				3
Cytological combination		2	4	2		1	2	11
Trisomic		1				1		2
Other aneuploids	2	2	1	4			1	10
Desynapsis			2					3
Other Gossypium species				1				1
Cultivars/breeding stocks	1	5	9	10	1	3	1	30
Totals	3	20	27	20	3	6	6	85

and 6 from the A subgenome and 16, 17, and 18 from the D subgenome (Table 1). Chromosomes 2, 4, and 6 represent 67 of the 85 identified monosomes.

The ratio of A to D subgenome monosomes is almost 5:1, a significant deviation from the 1:1 ratio expected on a random basis. It is not clear why G. hirsutum tolerates the loss of an A subgenome chromosome more readily than a D subgenome chromosome. A difference in chromosome constitution is not responsible because the two genomes are highly homeologous (Edwards et al., 1974).

Irradiation treatments (X-rays, neutrons, and gamma rays) have been used at Beasley Laboratory to produce a number of translocations and monosomes, as well as other chromosomal aberrations. The four monosomes produced directly from irradiation were for chromosomes 2, 4, and 17. A number of monosomes were also recovered from translocations, tertiary monosomes, and duplication-deficiencies which had been produced through irradiation.

Fifty monosomes came from plants used for cytological studies. The cytological material includes translocations, tertiary monosomes, duplication-deficiencies, cytological combinations, trisomics, other

aneuploids, and desynaptics. Translocations and cytological combinations have produced monosomes of three A and two D subgenome chromosomes. None of the other cytologically aberrant classes produced monosomes associated with more than one D subgenome chromosome.

Ten monosomes have come from other aneuploids. Five came from 2n-1-1 plants and were of chromosomes 1, 2, 4, and 6. Six of the monosomes derived from other aneuploids represent univalent shifts, as follows: D17 (M2) to A6 (M61); D16 (M25) to D18 (M74) (M74 came from J. E. Endrizzi (1); A1 (M17) to A2 (M83); and from D16 to A6 (M25 to M115, and M39 to M116).

Of the 166 monosomes from all sources 80 came from cultivars and breeding stocks found in nurseries and field plantings throughout the cotton belt. Thirty of these have been identified as to the missing chromosome, and they represent all seven chromosomes reported here.

Locating the 11 remaining monosomes of cotton may take innovative approaches. One such approach is to utilize a known monosome and a known translocation and through appropriate crosses produce a tertiary monosome which will in turn produce a new monosome (Edwards, 1978).

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