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Relationship of Seed Weight to the Cytotype of Monosomic Progeny in Cotton[1]

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ABSTRACT

Seed weight was used as an indicator of cytotype for the progeny of monosomic plants of *Gossypium hirsutum* L. Data were presented from plants monosomic for chromosomes 2, 4, 6, 16, 17, and 18. On a within-boll basis lighter-weight seeds tended to produce monosomic plants in comparison with heavier seeds, which tended to produce disomics.

Additional index words: **Aneuploids, Haplo, Chromosomes, *Gossypium hirsutum* L.**

UPLAND cotton, *Gossypium hirsutum* L., is an allotetraploid species with a normal complement of 26 pairs of chromosomes. It tolerates some levels of chromosomal duplications and deficiencies in that monosomics, trisomics, tetrasomics, and certain other aneuploids are viable. Monosomic (2n-1) plants have been used in cytological and genetical studies (2, 4) and in the development of chromosome substitution lines. Since monosomics produce disomic, monosomic, and telosomic progeny, monosomics must be identified in each generation. Positive identification through cytological analysis is a tedious, time-consuming procedure; therefore, a more rapid method would be desirable. This paper reports a method for speeding the identification and isolation of monosomes.

MATERIALS AND METHODS

Research on cotton monosomes has been underway at the Beasley Laboratory at Texas A&M University for a number of years (1). Currently monosomics for chromosomes 2, 4, 6, 16, 17, and 18 have been identified. Stocks monosomic for each of these identified chromosomes have been maintained through recurrent backcrossing with Texas Marker-1 (TM-1), an inbred line that is used as the standard or "wild-type" stock in cytogenetic investigation at this station (3). Since these monosomes are now essentially in a common genetic background, they are referred to as haplo 1, haplo 2 . . . haplo 18.

To supply materials for the study reported here, monosomic plants of haplo 2, 4, 6, 16, 17, and 18 were either self-pollinated or pollinated by TM-1. Seeds were harvested from mature, individual bolls identified according to plant and progeny numbers. Each seed was weighed to the nearest 0.1 mg and planted in the greenhouse. The chromosome number per cell for each plant was determined by cytological examination at meiotic metaphase I in pollen mother cells.

RESULTS AND DISCUSSION

The distribution of seeds, in terms of 2n and 2n-1 cytotypes, from individual bolls of each of the six haplo stocks investigated is given in Table 1. Comparison of seed weights of cytologically tested cytotypes was made on an individual boll basis because variation among bolls on the same plant or among different plants is too great for meaningful comparisons of bulked seeds. As the data show, seed weight distributions overlap for 2n and 2n-1 cytotypes within three bolls derived from three different monosomic

Table 1. Weight frequency distributions of 2n and 2n-1 cotton seeds harvested from individual bools of monosomic plants.

Monosomic	Cytotype	Boll no.	Midpoints of weight class, mg									
			70	80	90	100	110	120	130	140	150	160
Haplo 2	2n	1							3	1	2	
	2n-1	1		1			4	3				
	2n	2					1		3		1	
	2n-1	2				1						
	2n	3					5	2				
	2n-1	3		1								
Haplo 4	2n	1				2	3	1				
	2n-1	1			5	3						
Haplo 6	2n	1					5					
	2n-1	1	1	1			1					
Haplo 16	2n	1			1	2	6	1				
	2n-1	1		1								
Haplo 17	2n	1					1	3	4			
	2n-1	1		1								
	2n	2									1	3
	2n-1	2								1		
	2n	3						2	8	2		
	2n-1	3			1	1						
	2n	4							5	4		
	2n-1	4					1					
Haplo 18	2n	1			2	4	1					
	2n-1	1		2	1							
	2n	2			1*			3	2			
	2n-1	2				2	1	1				

* Cells contained one telosomic chromosome.

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plants. In several other bolls the lower and upper ranges of the 2n and 2n-1 distributions, respectively, were in contiguous weight classes. Nevertheless, the distributions clearly show that the lighter weight seeds in each cytotype comparison tended to be of the 2n-1 type. Three plants in the line of haplo 18 were telosomic for one chromosome. The seeds that produced these three plants were lighter in weight than the seeds that produced disomic plants.

While precise identification, and subsequent isolation, of the monosomic condition in cotton still requires cytological examination of microsporocytes from plants grown from seeds in question, it is evident from the data presented in this paper that a preliminary screening of the seeds from individual bolls in terms of seed weight and the planting of only those seeds which fall in the lower seed-weight classes will significantly increase the recovery rate of cotton monosomes. It follows, therefore, that when identification or isolation of the monosomic condition is the main objective, the preliminary screening procedure should effect a considerable saving in time and labor spent in cytological examination.

In fact, I have used the seed-weight technique presented in this paper to isolate aneuploids from dozens of seed lots for the past 2 years. However, since only selected light-weight seed from these lots were planted, the relative degree of success could not be assessed.

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