CYTOGENETIC STUDIES IN UPLAND COTTON

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Linkage study of Hirsute (H_1) and monosomes

The dominant Hirsute marker H_1 was crossed to the A genome monosomes in 1968. In 1969 the 2n-1 F_1 plants were testcrossed to TM1 (h_1h_1) for test of the association of H_1 and the monosomic chromosomes. The segregation observed in these testcrosses are given in Table 1.

Observing the segregation ratios in the table reveals that H_1 is on chromosome 6 (M5). Here it can be seen that when the 2n-1 F_1 is used as the female parent in the testcross all disomic plants are Hirsute and all monosomic plants are non-Hirsute. These results are verified in the reciprocal cross involving this monosome. In this case all progeny are disomic and all are Hirsute.

An important plant was recovered in the cross of M5 2n-1 F_1 * TM1 which provides the necessary information to determine the arm location of H. This single plant was non-Hirsute and it contained a large unequal or heteromorphic bivalent which was telocentric for the short arm. Since the 2n-1 M5 F_1 was used as the female it is assumed that the telocentric chromosome came from M5 monosome through misdivision. Since the long arm is missing and since the plant is non-Hirsute this shows that the H_1 locus is located in the long arm of chromosome 6.

Table 1. Segregation results for linkage of H_1 and monosomes.

Family	Hirsute (H_1)		Non-Hirsute (h_1)		Total
	2n	2n-1	2n	2n-1	
M3 H2 2n-1 F_1 x TM1	6	6	6	11	29
M5 H6 2n-1 F_1 x TM1	25	0	1 = 1 ≠ 11	4	30
TM1 x M5 H6 2n-1 F_1	33	0	0	0	33
M6 H2 2n-1 F_1 x TM1	21	12	26	2	61
M17 H1 2n-1 F_1 x TM1	4	6	10	10	30
TM1 x M17 H1 2n-1 F_1	21	9	0	0	30
Mo7 H7 2n-1 F_1 x TM1	14	3	11	1	29
Mo7 H7 2n-1 F_1 Self	20	5	6	0	31

Linkage study of male-sterile 2 (ms-2) and chromosome 1

The group at Texas had reported evidence from monosomic analysis that suggested that the ms-2 locus might be located on chromosome 1 of the A genome. Seed from the cross of M17 H1 2n-1 x Ms_2ms_2 were available for further testing for this association. In 1969, fifteen 2n-1 F_1 plants were present in the field for backcrossing as male parent to ms_2ms_2. All 2n-1 F_1 plants were pollen fertile, but the fertility varied and was usually less than in normal or MsMs plants. In dealing with recessive alleles it is generally assumed that the hemizygous recessive may not express the characteristic mutant phenotype of the homozygous recessive. Consequently, it is necessary to test the 2n-1 F_1 plants. Backcross seed representing six different 2n-1 F_1 were selected for planting.

If the ms_2 locus is on the monosomic chromosomes, the 2n-1 F_1 plants when backcrossed as males to ms_2ms_2 should produce progeny that all are either male sterile or male fertile; i.e., if linkage exist, no single 2n-1 F_1 should segregate. The backcross results for the six selected F_1 plants are given in Table 2. The results in the table seem to preclude any linkage of ms_2 and chromosome 1.

Table 2. Backcross segregation from the cross of ms_2ms_2 x M17 H1 2n-1 F_1 (2n-1 x Ms_2ms_2)

Family	Pollen Fertile (Ms_2)	Pollen Sterile (ms_2)	Total
ms_2ms_2 x E18-2-69 2n-1 F_1	9	5	14
" x E18-6-69 "	7	7	14
" x E18-7-69 "	12	6	18
" x E18-10-69 "	10	0	10
" x E18-13-69 "	15	0	15
" x E18-15-69 "	8	6	14

Cytogenetic study involving Sm_2 and heteromorphic bivalents of chromosome 6

In 1969, the smooth plant allele Sm_2 was located on chromosome 6 by monosomic analysis. Telocentric chromosomes involving both arms of this chromosome were available for determining the arm position of the Sm_2 locus. Plants with a heteromorphic bivalent, either for the long arm or the short arm of chromosome 6, were crossed to AG108 Sm_2Sm_2. The F_1's were analyzed cytologically to substantiate the phenotypic identity of the F_1's carrying the heteromorphic bivalents. Lee (Genetics 60:567-575) has reported that the allele is an incomplete dominant and that the recessive sm_2 allele is active in production of plant hairs. These observations were confirmed in the present study when the 2n F_1's were compared to normal hairy TM1 (sm_2sm_2) and homozygous Sm_2Sm_2.

All F_1's were scored phenotypically for the expression of the Sm_2 allele. These results are presented in Table 3.

The important thing to note in Table 3 is the amount of hair development in the three types of F_1's. Both the 2n F_1 plants and the F_1 plants with the hetermorphic bivalent for the long arm have the same degree of hair development. However, in the case of the F_1's involving the heteromorphic bivalent for the short arm, those F_1's carrying the telocentric chromosome for the short arm are much less hairy than their sib 2n F_1 plants. This suggests that Sm_2 is located in the long arm of chromosome 6.

Previous studies have shown that the H_2 gene which enhances hair production on plant parts is also located in the long arm of this chromosome.

To locate the distance Sm_2 is from the centromere, F_1 plants having the heteromorphic bivalent for the long arm have been backcrossed to TM1 and AG108, Sm_2Sm_2.

The plants with the heteromorphic bivalent for the long arm used in making the F_1 also carried the Lc allele from Brymer Brown lint which is located close to the centromere in the short arm. Therefore, the 2n F_1 plants are heterozygous for both the Sm_2 and Lc loci. These are now being testcrossed with Tm1 to determine the linkage relationship of Sm_2 and Lc.

Table 3. Phenotypic characteristics of the F_1's of heteromorphic bivalents of chromosome 6 crossed with Sm_2Sm_2.

Kind of F_1	Cytotype of F_1	Phenotype
Telo long arm		
——●—— sm_2 x Sm_2	2n	Intermediate hairy
——●	hetero II	Intermediate hairy
Telo short arm		
——●—— sm_2 x Sm_2	2n	Intermediate hairy
●—	hetero II	Near smooth