centromere, are 11.4 ± 1.2 map units apart. The additive 11.4 map units between ob Y2 obtained in 1982 with the monotelodisomics did not agree with disomic analysis of the map distance between ob Y2 determined in 1979, which was found to be only 1.25 map units.

This year a second disomic testcross analysis with linkage in the repulsion phase, Ob y2/ob Y2 was conducted to reevaluate the map distance between ob Y2. These data are given in Table 1, and they show that in this testcross, the ob Y2 loci are 7.26 ± 2.33 map units apart, which is much greater than the 1.25 map units observed between ob Y2 in the 1979 test. But the 7.26% recombination is in close agreement with the additive map distance obtained with the monotelodisomic 18S and 18L.

The 7.26 and 11.45 recombination values are significantly different at the 68% confidence limits but not at the 95% confidence limits.

Table 1. Segregation of ob and Y2 in testcross of ob y2 x Ob y2/ob 2.

	Number of plants in each class			
Ob Y2 co*	**Ob y2 nco***	**ob Y2 nco**	**ob y2 co**	**Total**
5	56	59	4	124

*co = crossovers, nco = nco or parental type

$$\text{Percent recombination} = \frac{9}{124}(100) = 7.26 \pm 2.33$$

GENETIC TESTS FOR THE ASSOCIATION OF MONOSOMES AND TELOSOMES WITH MARKER GENES

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Table 1 lists the tests that were completed for this year for the association of marker genes with specific aneuploid chromosomes. These tests show that independence was observed for mono 3 and glandless stem and boll (gl_1), mono 9 and brown lint (Lc_yLc_z) and yellow and orange pollen (P_1P_2), mono 12 and glandless stem and boll (gl_1) and virescent-4 (v_4), telo-20L and cupleaf (cu) and virescent-2 (v_2), and the telo 20S and virescent-2 (v_2).

The above results are the completion of a study started in 1981 and reported in part in 1982. The complete results for the

segregation of the mutant characters and the anueploid lines in the F_1, F_2 and testcross for 1982 and 1983 are given in Table 2.

Table 1. Genetic tests for association of marker genes with monosomes and telosomes. - = not associated.

	Genetic Marker Genes					
Mono- or Telo-some	**cu**	**gl_1**	**v_2**	**v_4**	**Lc_yLc_z**	**P_1P_2**
Mono 3		-				
Mono 9					-	-
Mono 12		-		-		
Telo 20 L	-		-			
Telo 20 S			-			

Table 2. Tests for association of mono and telos with market genes. 1982 & 1983.

		V_1	V_1	V_2	V_2	V_4	V_4	V_9	V_9	Pg	pg	Gl_1	gl_1	Cu	cu	Crp	+	P_1P_2	P_{1p2}	P_1P_2	Lc_yLc_z	lc lc	Y_1	y_1
	2n-1	1	0	0	0	2	0			2	0													
H3F_1																								
	2n	9	0	18	0	18	0			18	0													
	H3			49	9	29	9			35	15													
F_2																								
	2n			52	17	40	8			41	21	75	20											
	2n-1	3	0					2n-1-1-1--1:1			0	4	0			4	0	1	0	0	3	0		
H9F_1																								
	2n	75	0							29	0	74	0			15	0	29	0	0	27	0		
	H9															110	90	19	3	9	40	59	24	8
F_2																								
	2n															117	94	35	5	12	24	14	37	15
	H9															64	77							
Tc																								
	2n															42	50							
	2n-1			6	0	4	0			3	0													
H12F_1																								
	2n			10	0	12	0			13	0													
	H12			12	0	66	15			17	11	71	9											
F_2																								
	2n			7	3	127	35			38	17	72	0[1]											
T20S	Telo	1	8	4	0	2	0	4	0	2	0	11	0	11	0									
F_1	2n	31	0	16	0	14	0	16	0	18	0	32	0	32	0									
	Telo			15	5	51	18	68	30	23	28													
F_2																								
	2n			7	4	92	34	70	19	39	21													
T20L	Telo	16	0	3	0	7	0	7	0	6	0	16	0	16	0									
F_1	2n	23	0	16	0	12	0	13	0	13	0	23	0	23	25									
	Telo	55	24	13	9	108	31	21	6	97	37	73	11	52	30									
F_2																								
	2n	104	39	7	1	103	33	29	16	79	42	101	42	113										

[1] F_1 was not heterozygous for gl_1. telo 16L indep A_2

GENETIC ANALYSIS OF A NECROTIC-LEAF-SPOT MUTANT OF DELCOTT 277R

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In 1981, we reported on a genetic study of a necrotic-leaf-spot mutant that was found segregating in the Delcott 277R line. Delcott 277R is an Upland cotton with the cytoplasm and the restorer gene(s) of G. harknessii that was developed by the late