R^{st} r^{r} was not quite statistically significant.

The frequency of R^{sc} mutations was significantly greater in male than in female gametes in R^{st} R^{st} plants (line 4 vs. 12), approached significance in R^{st} r^{r} plants (line 8 vs. 14), and was clearly not significant in R^{r} R^{st} plants (line 5 vs. 13).

The frequency of R^{sc} mutations was the same in male gametes from R^{st} R^{st} r^{g} (trisomic) as from R^{st} R^{st} plants (line 12 vs. 15), which indicates that the greater mutability of R^{st} when homozygous than when heterozygous with r^{g} is due to interaction between R^{st} alleles in the homozygote rather than to a mutation inhibiting action of r^{g} in the heterozygote.

R. B. Ashman

2. Gene linkages in translocation T9-10a heterozygotes.

Translocation T9-10a (9L.14--10L.92) has been used as a distal marker for R in several of our genetic studies, and a test was made to determine the linkage between the translocation and R and M^{st} on chromosome 10 and Wx on chromosome 9.

Kernels from the following cross were classified for stippled and waxy:

$$\frac{r \quad + \quad N \quad wx}{r \quad + \quad N \quad wx} \quad \text{X} \quad \frac{R^{st} \quad M^{st} \quad \text{T9-10a} \quad wx}{r \quad + \quad N \quad Wx}$$

The number of kernels in the two parental classes was 1067 R^{st} wx and 989 r Wx, and in the two crossover classes 291 R^{st} Wx and 204 r wx. An excess of R^{st} kernels was noted in both the parental and crossover classes. The uniformity of the data was tested in a 2 X 2 contingency table, and the chi-square value was highly significant, indicating inconsistencies within the class frequencies. The excess of R^{st} Wx kernels is very likely due to the functioning of some R^{st} Wx duplicate-deficient gametes, since these gametes are deficient for only about 8% of 10L. The r wx duplicate-deficient gametes would be much less likely to function, since they are deficient for about 86% of 9L. If it is assumed that r wx duplicate-deficient gametes do not function, the r wx kernels result only from crossing over, and the percentage of R^{st} Wx kernels resulting from the functioning of duplicate-deficient gametes can be estimated as 291-204/291=30%. Also, if alternate and adjacent-1 disjunction are assumed to occur with equal frequency, it can be estimated that about 7% of the R^{st} Wx duplicate-deficient gametes produced function through the pollen, even though in competition with normal gametes.

Kernels in the two crossover classes were grown out and the ears classified for the translocation (semi-sterility). Ears from the R^{st} Wx kernels were also classified for M^{st}, which is scorable only in the presence of R^{st}. Kernels in the two parental classes (R^{st} wx and r Wx) were not grown out so no data were obtained on the frequency of double crossovers.

Two adjustments were made in the data before crossover per cents were calculated: (1) the total population was adjusted for the proportion of crossover kernels verified in the classifications for the translocation and M^{st}, and (2) the frequency of kernels in the R^{st} Wx crossover class was reduced to the same proportion as the r wx crossover class to correct for the presumed transmission of duplicate-deficient gametes. The data from the R^{st} and r kernel classes are presented separately in the tabulation below, and where data for a particular chromosome segment were obtained from both classes a pooled value is shown.

The R - M^{st} distance has been measured in nontranslocation stocks (Ashman, Gen. 45:19-34) and was found to be 797/13,881 or 5.7 crossover units. The difference between this value and the one shown in the table, 0.4, represents the crossover suppression effect of the translocation. The R - T distance has been estimated by others to be about 5 crossover units; our data estimate this distance to be, at most, 2.9 units, and the pooled data gave a value of 2.3 units.

Chromosome region	R^{st} kernels Frequency	%	r kernels Frequency	%	Pooled %
R - Wx	-	-	204/1193	17.1	-
R - M^{st}	5/1136	0.4	-	-	-
R - T	19/1136	1.7	31/1070	2.9	2.3
M^{st} - T	14/1136	1.2	-	-	-
T - Wx	161/1136	14.8	144/1070	13.5	13.8

R. B. Ashman

3. The location of miniature seed (mn).

The location of the miniature seed (mn) character has been shown to be on chromosome 2 (MGCNL 39: 158, 1965). Evidence of the position of miniature seed (mn) on chromosome 2 comes from the following testcross data.

W22 was crossed by a chromosome 2 tester carrying lg_1, gl_2, v_4 and mn and backcrossed to the chromosome 2 tester. A total of 452 normal kernels from this cross was planted and scored for lg_1, gl_2, and v_4 with the following results:

+ + +	184
+ + lg_1	46
+ gl_2 +	8
+ gl_2 lg_1	142
v_4 + +	40
v_4 + lg_1	10
v_4 gl_2 +	1
v_4 gl_2 lg_1	21
	452

Marker	Total	% Recombination
lg_1	219	48.5
gl_2	172	38.0
v_4	72	15.9