These selfed plants were either Cl cl Clm-3 Clm-14 pas or cl cl-7716 Clm-3 Clm-14 pas. All of the pale yellow seeds from these selfs were seedling tested. If Clm-3 and Clm-M14 pas are allelic, no white seedlings should be observed in the F_2 seedlings from the pale yellow seeds. This turned out to be the situation. No albino seedlings were observed out of 10,588 seedlings scored. Thus the linkage tests in 1972 involved the Clm locus and placed it on chromosome 8.

Observations of seedlings with Clm-M14 grown under controlled temperature conditions revealed that the inbred M14 did not have two different modifiers (i.e., Clm-M14 gr and Clm-M14 pas). The tests demonstrated that the Clm-M14 allele is actually temperature sensitive. At high temperature (95 F) the seedlings with Clm-M14 are pale green or pastel while at low temperatures they are green.

In the 1973 report the same indication of linkage was obtained with T8-9(6673) in crosses involving the Clm-3 modifier.

Last summer testcross progeny were grown of a cross between + clm T8-9(6673)/ cl Clm-3 + plants and plants of the inbred OH43 (lacks any dominant modifiers). The testcross progeny were scored for sterility and the plants self-pollinated. All the pale yellow seeds from the selfed ears that segregated for cl were grown and scored for the presence or absence of green seedlings:

Parental		Crossovers			
clm T	Clm-3 +	Clm-3 T	clm +	Total	% C.O.
97	93	40	33	263	27.8

The Clm modifier undergoes 27.8% recombination with the T8-9(6673) breakpoint in chromosome 8. Since the breakpoint is at 8L.35 it is impossible to determine the chromosome arm in which this locus is located.

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Additional studies of a mutator locus on chromosome 10

Previous reports (M.G.C.N.L. 45:81-87, 1971 and 49:73-79, 1975) have indicated that a factor at or near the y9 locus is responsible for an increased spontaneous mutation rate. In these reports, it was noted that a given outcross family would frequently have several plants that segregated for mutants which were quite similar in phenotype. Such mutants were assumed to have arisen by individual somatic events resulting in tassel sectors. Results of a series of allele tests (Table 1) on mutants of similar phenotype within families indicate that most mutants arise by a very late somatic or a meiotic mutation, since in most cases the mutants are not allelic. In only 2 out of 11 families were positive tests observed. In family 72-3120, 2 phenotypes were noted, luteus (l) and albino (w). All allele tests for the luteus mutants were positive except that of 18(l) x 20(l). Since both 18(l) and 20(l) were allelic to 6(l), the negative results observed in the 18(l) x 20(l) cross are unexpected. These crosses will be repeated next summer. Until further data are obtained all luteus mutants of family 72-3120 are assumed to be allelic. The two albino mutants from this family also proved to be allelic. It is conceivable, since these mutants are in a heterogeneous background, that the luteus and albino mutants of family 72-3120 may be allelic. Further tests of allelism within this family are required but until such tests are performed the albino will be assumed to be different from the luteus mutants. In family 72-3125 both allelic and nonallelic mutants were observed. Thus in 2 out of 11 families, allelic mutants were observed while in 10 out of 11 families nonallelic mutants with similar phenotype were recovered. It is assumed that allelic mutants are of somatic origin while nonallelic mutants may be meiotic or the result of two independent somatic mutations which occurred late in development, resulting in very small tassel sectors.

These results indicate that in about 90% of the families tested, with two or more mutants of similar phenotype, there is evidence that mutation takes place very

Table 1. Allele tests of mutants with similar phenotypes within individual mutator outcross families.

Family No.	Plant numbers and (phenotypes)*	Number of crosses involving one heterozygous parent	Number of positive tests	Probability of allelism
72-3108	18(l) x 23(py)	11	0	< .01
72-3112	13(l) x 23(l)	13	0	< .01
72-3113	27(pg) x 33(pg)	13	0	< .01
72-3114	3(l) x 48(py)	22	0	< .01
72-3120	6(l) x 18(l)	20	10	1
	6(l) x 20(l)	16	4	1
	6(l) x 46(l)	10	6	1
	18(l) x 20(l)	30	0	0**
	18(l) x 46(l)	21	12	1
72-3120	22(w) x 35(w)	16	6	1
72-3124	5(l) x 14(l)	15	0	< .01
	5(l) x 19(l)	14	0	< .01
	14(l) x 19(l)	11	0	< .01
72-3125	18(l) x 20(l)	9	1	1
	18(l) x 23(l)	8	0	< .01
	18(l) x 24(l)	6	0	< .01
	20(l) x 23(l)	10	0	< .01
	20(l) x 24(l)	17	0	< .01
	20(l) x 29(l)	9	3	1
	24(l) x 29(l)	9	0	< .01
72-3126	11(l) x 27(l)	9	0	< .01
	11(l) x 40(l)	14	0	< .01
	27(l) x 40(l)	13	0	< .01
72-3132	13(l) x 30(l)	9	0	< .01
72-3225	43(l) x 31(l)	13	0	< .01
72-3232	12(l) x 20(l)	8	0	< .01

*phenotypes: l-luteus, py-pale yellow, pg-pale green, w-albino.

**4 female parents known to be heterozygous. These results are inconsistent with other crosses from this family. Further tests will be made.

late in development or during meiosis. Two other lines of evidence support such a conclusion. In 1974 and again in 1975 the mutator lines heterozygous for the genes for purple aleurone were crossed to a homozygous c sh bz wx stock. If somatic mutations involving these loci were occurring throughout development, seeds showing sectoring for these genes should be observed. So far in 20 such outcross ears (most of which were segregating in a 1:1 ratio for purple and nonpurple seeds) only two seeds with purple and colorless sectors were observed. No sectoring was observed for sh, bz or wx. Also, the mutator line was crossed to homozygous yg2 plants. Out of 1071 seedlings tested three had yellow-green sectors and two were entirely yellow-green. Similar crosses to yg2 plants with standard lines gave 796 seedlings of which one had a yellow-green sector and one was entirely yellow-green. These crosses do not indicate that the mutator line is consistently inducing early somatic mutations at the yg2 locus. To test for later mutations at this locus, plants of these crosses were grown to maturity. No yg2 sectors were observed at any stage in development for 302 plants of the mutator progeny or 251 plants of the standard progeny. The presence of two yg2 seedlings in the mutator cross may indicate that meiotic mutations had occurred. However, the occurrence of a yg2 seedling in the control cross would indicate that these yg2 seedlings are probably the result of contamination. The stocks involved in these crosses did not carry contamination markers.

In summary, the allele tests indicate that in the mutator line most mutations occur very late in development or during meiosis. Early mutations that give rise to sizable mutant tassel sectors can occur, however, at low frequency. Tests involving the c sh bz wx stock and yg2 gave no evidence for somatic mutants for any of the loci involved.

If most mutations are very late somatic or meiotic in origin the estimated mutation rates reported in 1975 are much too low. Instead of an average 31.5-fold increase in mutation rate it would be closer to a 50-60 fold increase.

Donald S. Robertson and Peter Mascia

Chromosome segregation in hyperploid female plants carrying compound A-B translocations

In 1967 Robertson (Genetics 55:433-449, 1967) tested the transmission of chromosomes from hyperploid TB-9b plants of the genotype $9(c\ sh\ wx)\ 9^{B}(Wx)\ B^{9}(C\ Sh)$ $B^{9}(C\ Sh)$. The evidence suggested that approximately 96% of the time the two B^{9} chromosomes separated from each other and went to daughter poles. Occasional nondisjunction of the B^{9} element would result in recessive c sh wx seeds. In one test 3.44% of the progeny were c. Included in this 3.44% are those seed that are c due to nondisjunction (2.34%) and those that are c as a result of crossing over (1.10%).

In 1974 hyperploid female plants of compound A-B translocations involving the long arm of chromosome 4 of the genotype $4(c2)\ B^{4}(C2)\ B4(C2)$ were pollinated by c2 c2 plants. Table 1 lists the translocations studied and the pertinent cytological information. The results of the hyperploid tests are given in Table 2.

Table 1. Compound A-B translocations studied in the hyperploid tests.

Compound A-B Translocation	Old A-B Transl.	Reciprocal A Transl.	A segments in new compound B^{A}	Length of A segments of new B^{A}
TB-1La-4L4692	TB-1a	T1-4(4692)	1L.20-.46, 4L.15 to end	125.0
TB-7Lb-4L4698	TB-7b	T4-9(4698)	7L.30-.74, 4L.08 to end	144.3
TB-9Sb-4L6222	TB-9b	T4-9(6222)	9S.40-.68, 4L.03 to end	116.6
TB-9Sb-4L6504	TB-9b	T4-9(6504)	9S.40-.83, 4L.09 to end	116.2

Table 2. Results of crossing hyperploid female plants of the constitution $4(c2)\ B^{4}(C2)\ B^{4}(C2)$ with c2 c2 male plants.

Translocation	No. of C2 seeds	No. of c2 seeds	Total	% C2	% c2
TB-1La-4L4692	1185	167	1352	87.6	12.4
TB-7Lb-4L4698	2239	317	2556	87.6	12.4
TB-9Sb-4L6222	2288	261	2549	89.8	10.2
TB-9Sb-4L6504	3027	319	3346	90.5	9.5

The low percentage of c2 seeds indicates that the hyperploid compound B^{A} elements regularly separate from each other, ending up in daughter cells. The small percentage of c2 seeds is due to either nondisjunction of the B^{A} elements or crossing over, as were the small percentage of c seeds in the TB-9b crosses. In the latter crosses, only 3.44% c seeds were observed while in the crosses in Table 2 c2 seeds occur in a considerably higher frequency (9.5 - 12.4%). The higher percentage of recessive seeds in the TB-4 crosses could be due to a higher rate of nondisjunction in the TB-4L translocations than in TB-9b. However, in the TB-4L translocation the segments attached to the B centromere are considerably longer (unit lengths 116.2 - 144.3) compared to that of the B^{9} element (unit