

From Table 1 it can be seen that mutants occur in ears that are not segregating for y_9 and those that segregate for this gene. Thus, the mutations are probably not confined to the chromosome 10 carrying y_9 or the homologous ten. None of the mutants in Table 1 have been located to chromosome although a mutant found in a y_9 line in 1963 turned out to be allelic to w_3 on chromosome 2. This would suggest that the mutants are not necessarily confined to chromosome 10. If the mutator locus on chromosome ten affects any locus and if it functioned in the sporocyte before microsporogenesis, it would explain the presences of possibly more than one outcross ear segregating for the same mutation in an outcross family and the occurrence of the mutations on ears with and without y_9 .

Whether the mutator locus is the same as y_9 or just closely linked to it cannot be determined from the present information. Most of the data considered in this report were obtained incidentally in experiments designed to give information on the location of y_9 . Experiments designed to clarify the apparent mutagenic nature of this stock are planned.

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2. Linkage studies involving o_5 .

In 1967 (MGNL 41:94-95) I reported on a new opaque mutant o_5 . This mutant has opaque shrunken seeds that produce pale green seedlings which grow into mature plants a little less vigorous than normals. In our previous report, preliminary linkage tests with only 70 plants had indicated this mutant was on chromosome 7, 12.9 units from the breakpoint of 7-9a (7L.63). Additional linkage information involving 7-9a are given in Table 1 which are in close agreement with the previously reported data. The results of linkage tests with gl_1 are given in Table 2.

Table 1
Linkage data from the testcross of 7-9a/o₅

Family No.	Genotype of F ₁ Gametes				Total	%CO
	T +	+ o ₅	T o ₅	+ +		
67-5094	19	14	2	5	40	17.5
67-5095	7	17	2	7	33	27.3
67-5096	16	15	2	1	34	8.8
67-5097	17	17	3	3	40	15.0
67-5098	17	18	0	3	38	7.9
67-5099	17	18	0	3	38	7.9
67-5100	8	13	1	2	24	12.5
67-5101	17	15	0	1	33	3.0
Total	118	127	10	25	280	12.5

Table 2
Linkage data from the testcross of g₁/o₅ plants

Family No.	Genotype of F ₁ Gametes				Total	%CO
	<u>g</u> ₁ +	+ o ₅	<u>g</u> ₁ o ₅	+ +		
69-5141	27	14	0	1	42	2.4
69-5142	30	17	0	0	47	0
69-5143	25	19	0	0	44	0
69-5144	17	22	0	0	39	0
69-5145	17	24	0	0	41	0
69-5146	27	20	0	0	47	0
Total	143	116	0	1	260	0.4

These data indicate that o₅ is very close to g₁. Crosses with TB-7b (7L.3) confirm this location, since this translocation which uncovers g₁ also uncovers o₅.

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