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1. Further data on the cp_2 (collapsed-2) location.

According to Dr. Nuffer's suggestion the collapsed endosperm trait previously indicated as "cl" (M.G.N.L. 40: 77-78, 1966) will be hereafter designated as "cp_2". Additional data on the recombination between o_2, gl_1 and cp_2 are now available:

Gene pair	Phase	AB	Ab	aB	ab	Recombination ± standard error
o_2-cp_2	R*	3567	2369	1760	22	9.6 ± 0.7
gl_1-cp_2	R*	1181	614	546	5	9.2 ± 1.3
	C*	3277	164	178	768	8.6 ± 0.1
	R**	101	978	956	77	8.4 ± 0.4
o_2-gl_1	R*	2316	931	1125	15	13.2 ± 1.0
	C*	634	54	72	104	16.6 ± 0.9

*Self-fertilization data.

**Backcross data.

The cp_2 location appears now to be intermediate between o_2 and gl_1 and not distal to gl_1 as previously reported (M.G.C.N.L. 40: 77-78). The order of these markers on the chromosome 7 map should be as follows:

o_2 (9.6%) cp_2 (8.7%) gl_1

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2. A rt (rootless) mutant detectable at an early seedling stage.

In 1968 a progeny segregating for a defective root seedling was detected among breeding material. At the four leaf stage the root development of the mutant is poor (about 1/5 of normal). The mutant seedlings are also smaller than the normal and do not reach the reproductive stage. In 1969, heterozygous material was selfed and 22 progenies

obtained: 13 were segregating for the rt phenotype while 9 did not segregate. Among the segregating progenies 802 seedlings were normal while 255 (24.1% possessed the mutant phenotype. On the basis of these results the rt phenotype seems to be inherited as a monomendelian character.

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3. Induced E.M.S. mutations for kernel characters: absence of specificity for selected loci.

From ethyl methane sulphonate (E.M.S.) treatment (1.5%, 14 h, 22°C) of maize kernels, one hundred self fertilized ears were collected. A subsequent self-fertilization permitted isolation of 95 kernel mutants classified as:

1. defective endosperm (normal plant)
2. defective endosperm (lethal plant)
3. germless

Within each class of mutation, allelism tests were performed. The results are as follows:

Mutant class	Number of isolated mutants	Number of mutants considered	Number of crosses performed	Cases of allelism	Number of independent loci
1	17	12	22	3	large
2	59	35	507	3 (+ 1?)	large
3	18	8	85	6	3

The 8 germless mutations can be recognized as allelic to three independent loci. As to the endosperm defective mutations, it has not been possible to recognize them as alleles of a reduced number of loci. The conclusion follows that E.M.S. mutagenic action is not specific for selected loci.

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