4. Defective endosperm mutants from maize-teosinte derivatives.

At least twenty-eight defective endosperm mutants have been recorded in our maize-teosinte derivatives. To indicate their origin, they are designated as de^{t1}, de^{t2}, etc. Tests to determine how many different loci are involved and to identify cases of allelism have not yet been completed, but the data so far obtained suggest that the majority of the mutants are genetically different.

One of the common features of these mutants is a characteristic heterogeneity in their segregation. The number of recessives on a segregating ear may, on the average, approach the expected twenty-five percent, but individual ears vary greatly. Chi-square tests for heterogeneity are summarized in Table I.

Table I. Heterogeneity in segregation of defective endosperm mutants.

de^t factor	no. ears	no. kernels	average percent de	heterogeneity chi-square	p. value
de^{t1}	38	9682	24.3	106.7	4.001
de^{t2}	55	13243	19.8	276.9	<.001
de^{t5}	10	2960	21.1	93.6	<.01
de^{t13}	8	2342	24.5	62.0	< .01
de^{t17}	7	1650	28.1	37.1	< .01
de^{t20}	6	1468	26.3	1.0	.96
de^{t21}	5	1569	25.2	13.5	< .01
de^{t22}	7	2598	23.1	12.0	.05-.10

This marked heterogeneity may be due to one or more of the following causes. The mutant genes are themselves mutable and highly unstable. This is known to be true of de^{t5}, which Mangelsdorf is studying extensively, and on which he is reporting elsewhere in this News Letter. Genetic background may result in poor "penetrance." De^{t1}, for example, segregates poorly in the selfed strain but gives good ratios in hybrids. Differential fertilization, due either to gametophyte factors or to the de^t genes themselves, may be involved. In the case of de^{t9}, the upper part of the ear shows higher frequencies of defective than the lower.

Data have been obtained on weights and germination of the normal and defective seeds on the same ears. Weights, expressed in percent of the normal seed, range from 4.0 - 7.9 percent for de^{t12}, de^{t21}, de^{t13} to 62 - 72 percent for de^{t19}, de^{t20}. Germination varies from 0 - 1 percent for the more defective mutants to 91 - 98 percent for de^{t14} and de^{t19}. Germination does not seem to be a simple function of the weight of the defective kernels; also there is an interaction between some of the defective seed types and su.

The linkage relations for de^{t1}, de^{t2}, amd de^{t3} are shown in Table II.

Table II. Crossing over values for de^t genes on the 4th chromosome.

factors	linkage	number of individuals	recombination

couple	phase	number of individuals				
		XY	Xy	xY	xy	recombination
de^{t1}-su_1	RS	2009	942	771	89	31.0 ± 1.0
de^{t1}-su_1	CS	4203	893	813	663	32.2 ± .5
de^{t2}-su_1	RS	2384	943	484	67	35.4 ± .9
de^{t2}-su_1	CS	1924	529	296	274	33.9 ± .7
de^{t3}-su_1	RS	778	276	142	32	43.5 ± 1.6
de^{t3}-su_1	CS	349	81	68	61	32.2 ± 1.7
de^{t2}-gl_3	RS*	522	613	67	39	29.9 ± 3.2

*glossy:non-glossy segregating 9:7 for gl_1 and gl_3.

The data suggest that de^{t2} and de^{t3} may be alleles. They indicate that de^{t2} is on the short arm of chromosome 4. Crosses of de^{t1} and de^{t2} show about 33 percent of crossing over, but the figures undoubtedly high because of a deficiency in both of the defective classes.

Linkage relationships between fourteen other de^t genes and marker genes for chromosomes 2, 4, 5, 6, 7, and 9 have been tested. Omitting the cases in which significant deviations do not indicate linkage and for which gametophyte factors probably should be postulated, Table III shows the crosses in which significant deviations indicate the possibility of linkage.

Table III. Linkage between de^t genes and marker genes

factors couple	linkage phase	number of individuals				heterogeneity chi-square for linkage	probability	recombination percent - pr. error
		XY	Xy	xY	xy			
De^{t11}-Lg_1	RS	1164	500	91	26	8.77	< .01	44.3 ± 1.3
De^{t20}-Su_1	RS	1224	465	167	39	6.05	~ .01	43.1 ± 1.3
De^{t20}-Gl_3	RS	501	188	55	16	1.05	~ .30	46.5 ± 1.9
De^{t23}-Gl_1	RS	1291	515	104	35	3.58	~ .05	48.7 ± 1.2
De^{t26}-Pr	CS	143	41	41	20	2.67	~ .10	42.6 ± 2.9
De^{t28}-Y_1	CS	224	64	31	46	4.02	~ .02	29.0 ± 2.0

Cytological studies do not reveal any chromosome aberrations regularly associated with the defective mutants. If the defective seeds are a result of small deficiencies, these are too minute to be seen under the microscope.

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