4. Mutations induced in preembryo stage.

In 1959 a stock of $\underline{Yg_2}/\underline{Yg_2}$ was pollinated by $\underline{yg_2}/\underline{yg_2}$. The first set of plants was placed in the radiation field where they received 33r/hr for 23.5 hours to give a total dose of 775r. Every day thereafter for 10 days a different set of plants was radiated.

No mutations were scored in the material radiated on the first day. However, the ears radiated on the second day produced several seedlings which were yellow green and several which were one-half yellow green. Ears radiated at later stages of development produced seedlings which showed streaks of yellow green. The size of the streaks decreased with the later stages.

The mutations remain to be analyzed. This seems to be a desirable stage for the induction of recoverable mutations in maize, possibly other material as well. Severely damaged cells will be eliminated, thus giving an automatic screening of most harmful changes. Other genes will be tested in 1960.

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1. Translocations.

The following list of translocations were obtained from irradiation of CC5/L317 and closely related stocks (numbers 8001 to 8864) or from irradiation of a high knob stock (8890 to 9021).

Symbol	Chromosomes	Chromosomal Designation	
8001	1-9	1S. 51	9L. 24
8041	1-5	1L. 80	5L. 15
8004	4-8	4S. 27	8L. 84
8045	2-7	2S. 12	7L. 06
8006	3-7	3L. 88	7L. 90
8048	1-3	1L. 11	3S. 18
8302	1-9	1S. 55	9L. 29
8103	4-7	4S. 81	7L. 76
8104	3-5	3L. 05	5L. 08
8069	4-5	4S. 34	5S. 71
8108	4-5	4S. 37	5S. 72
8249	1-4	1L. 26	4L. 63
8023	3-8	3L. 18	8L. 16
8027	2-4	2L. 15	4L. 43
8143	6-7	6L. 35	7L. 36
8145	3-6	3L. 17	6L. 26
8032	3-9	3S. 26	9L. 96
8219	2-10	2L. 50	10L. 35
8219	5-6	5L. 71	$6S.\ 84^{sat}$
8321	2-5	2L. 86	5L. 11
8322	2-7	2L. 76	7L. 74

Symbol	Chromosomes	Chromosomal Designation	
8339	4-6	4L. 87	6L. 79
8345	5-10	5L. 87	10S. 61
8346	7-8	7S. 49	8S. 30
8347	1-5	1S. 84	5L. 51
8349	3-10	3S variable	10 variable
8350	3-8	3L. 75	8S. 60
8351	3-5	3L. 68	5L. 76
8367	3-8	3S. 28	8S. 52
8368	1-4	1S. 14	4S. 30
8374	4-7	4L. 24	7L. 55
8375	1-10	1L. 69	10L. 64
8376	2-8	2L. 95	8L. 03
8380	4-6	4S. 47	6L. 18
8383	7-9	7 near cent.	9 near cent.
8386	5-9	5L. 87	9S. 13
8388	1-5	1S. 30	5S. 25
8389	1-9	1L. 74	9L. 13
8395	4-5	4L. 63	5L. 82
8397	3-4	3S. 74	4S. 55
8405	1-3	1L. 60	3L. 31
8412	3-10	3S. 39	10S. 36
8415	1-6	1L. 29	6S. 82$^{org.}$
8420	5-8	5S. 90	8L. 33
8428	4-6	4L. 32	6L. 28
8428	2-8	2L. 16	8L. 10
8439	6-9	6L. 06	9S. 73
8441	2-6	2L. 94	6S. 79$^{org.}$
8443	3-4	3L. 12	4L. 13
8447	3-9	3S. 44	9L. 14
8452	1-6	1S. 80	6L. 52
8456	4-8	4S. 22	8L. 78
8457	5-9	5L. 78	9S. 83
8460	1-9	1S. 13	9L. 24
8465	3-9	3S. 27	9L. 41
8483	2-3	2L. 14	3L. 12
8491	1-10	1L. 45	10L. 76
8513	5-8	5S. 34	8L. 24
8525	8-9	8L. 06	9S. 63
8536	6-9	6L. 18	9S. 81
8553	2-5	2L. 24	5L. 23
8558	7-9	7S. 22	9L. 16
8562	3-9	3L. 65	9L. 22
8563	1-4	1L. 39	4S. 21
8580	7-8	7 variable	8 variable
8590	5-6	5S. 29	6L. 56
8591	5-9	5S. 09	9L. 25
8602	1-4	1S. 41	4L. 81
8607	4-8	4S. 30	8L. 33
8622	4-5	4L. 30	5L. 52

Symbol	Chromosomes	Chromosomal Designation	
8628	2-3	2L. 54	3L. 44
8630	9-10	9S. 28	10L. 37
8630	5-7	5L. 38	7L. 24
8634	3-4	3S. 71	4L. 75
8637	1-3	1L. 37	3S. 50
8640	1-8	1L. 11	8L. 16
8645	6-10	6L. 21	10L. 28
8651	6-10	6L. 27	10L. 48
8658	1-6	1L. 81	6L. 90
8659	7-9	7S. 55	9S. 55
8662	2-3	2S. 78	3L. 83
8663	1-4	1S. 09	4S. 36
8665	5-6	5L. 58	6L. 25
8666	3-8	3S. 30	8L. 14
8671	5-7	5L. 96	7L. 67
8672	3-6	3L. 44	6L. 87
8679	5-7	5S. 09	7S. 26
8682	2-4	2S. 70	4S. 25
8683	1-8	1L. 11	8L. near cent.
8696	5-6	5L. 89	6S. 80$^{org.}$
8704	5-9	5L. 35	9L. 85
8746	5-8	5S. 84	8L. 25
8764	4-6	4L. 32	6L. 90
8768	6-9	6L. 89	9S. 61
8770	1-10	1L. 05	10L. 38
8782	1-5	1 near cent.	5 near cent.
8786	2-6	2S. 90	6S. 77
8796	5-8	5L. 76	8L. 11
8806	5-8	5L. 72	8S. 59
8818	5-6	5S. 91	6L. 93
8824	1-9	1S. 06	9L. 83
8854	5-9	5S. 33	9S. 36
8857	2-6	2S. 08	6L. 24
8864	2-10	2S. 10	10L. 76
8890	1-9	1L. 28	9L. 22
8891	4-9	4 near cent.	9 near cent.
8895	5-9	5L. 37	9L. 17
8904	6-10	6L. 51	10L. 83
8906	6-9	6L. 27	9L. 59
9028	4-10	4S. 57	10L. 89
8918	1-9	1S. 21	9L. 20
8919	1-8	1S. 53	8L. 44
8927	4-6	4L. 70	6L. 18
8936	5-9	5L. 43	9L. 80
8963	3-6	3S. 24	6L. 14
8969	3-4	3S. 75	4L. 75
8972	1-5	1S. 56	5S. 29
8987	4-8	4S. 58	8L. 76
8995	1-3	1S. 49	3L. 06

Symbol	Chromosomes	Chromosomal Designation	
8997	5-8	5L. 16	8L. 08
9002	2-6	2L. 57	6L. 58
9020	8-10	8L. 13	10S. 50
9021	1-9	1L. 26	9L. 83

E. G. Anderson
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CLYDE BLACK & SON HYBRID SEED FARMS
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1. Yield, stand and lodging of restored and of male sterile single crosses of maize compared to their regular counterpart single crosses.

Tests were conducted in the summer of 1959 to compare thirteen restorer single crosses and thirty-one male sterile single crosses on T cytoplasm with their regular counterpart single crosses on normal cytoplasm for yield, stand and lodging. All the single crosses in these tests were samples from lots produced by open pollination in isolated fields and represent material available for the production of commercial hybrid seed corn.

All the lines were regular corn belt dents and none of them originally were on T cytoplasm or carried the dominant allele of the full restoring gene designated as the "Rf" gene. However, some of the lines used, namely, M14, Oh41 and K166, carried a gene or genes for heavy partial restoring which made it impossible to follow the "Rf" gene in the conversion process and are therefore designated with the suffix "TRp" or "NRp", depending on whether the line had been converted to T cytoplasm or not. All other lines were non-restorers, unless the dominant allele of the Rf gene had been introduced in the conversion process. All converted lines were on T cytoplasm, whether they carried the full restorer gene, the partial gene or genes or were cytoplasmic male sterile. The suffixes TRf, TRp and Tms were used with the regular line designations to give the pertinent added information concerning the hereditary make-up of these converted counterpart lines.

Four donors for the Rf gene were used in the pollen restorer conversion matings. These had all been tested to determine that the restorer gene which they carried was allelic with the full restorer gene carried by the I153 inbred line. All the converted lines (TRf, TRp and Tms) had been back-crossed five generations or more after the initial outcross to introduce the T cytoplasm and the Rf gene, if also introduced. In addition, the restorer line L317TRf had been selfed twice before the production of the restorer singles in which it was used. The line K166 had not been converted onto T cytoplasm but was known to carry a gene or genes for heavy partial restoring. This line was used as the pollinator in the production of one of the restorer single crosses. All the other restorer (TRf) lines used were in the last backcross generation and the plants shedding pollen in the single-crossing field were therefore heterozygous for the Rf rf alleles. As seed parents in making up several of the restorer single crosses, some inbred lines on T cytoplasm but without restorer genes, (Tms lines), were used.