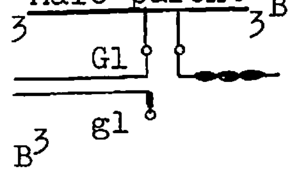
on gl_6 females. The observation of gl individuals in the progeny was taken to indicate that gl is located distal to the breakpoint of TB-3a in the long arm of chromosome 3 (3L.1). These tests have not been considered entirely critical because hypoploid offspring often have an abnormal phenotype which might have been confused with gl even though the plants carried the Gl allele.

Recently this objection was eliminated by the following crosses:

Female parent	Male parent	Gl	gl	Σ	%gl
a_1 gl_6		354	84	438	19.2
a_1 sh_2 Gl_6	"	331	0	331	0

The same male parents were used in crosses on the gl and Gl testers. In both tests a kernels were found on the ears and in the second cross these were also sh. Although hypoploids must be present in both progenies, gl plants were observed only in the backcross to gl females. Therefore, it is believed that the test is a legitimate one and that the Gl locus falls distal to .1 in the long arm of chromosome 3.

M. M. Rhoades
Ellen Dempsey

11. Recombination values in homozygous duplication and homozygous deficient plants.

In the Maize News Letter for 1960 I reported that crossing over in the Sh-Wx region was no greater in plants homozygous for a piece of 3L inserted into chromosome 9 than it was in plants homozygous for structurally normal chromosomes 9. The inserted piece of 3L was located between the Bz and Wx loci so, in the physically larger segment of chromatin between the Sh and Wx genes, one might expect to find higher recombination values. The crossover value of 17% found in Dp Dp plants is certainly no greater than the standard distance for this region and appears to be similar to the frequency found in control plants. Following publication of the preliminary report a considerable body of testcross data have been accumulated on crossing over in Dp Dp plants. They are listed below:

Female parent		Recombination percentages			Coincidence value			Population
		C-Sh	Sh-Wx					
C Sh Dp Wx / c sh Dp wx	N3 N3	7.5	16.2		1.1			2175
C Sh Dp Wx / c sh Dp wx	Df3 Df3	8.1	15.9		0.8			2233
		Yg-C	C-Wx					
Yg C Dp wx / yg c Dp Wx	N3 N3	28.0	16.7		0.7			3728
		(1) Yg-C	(2) C-Sh	(3) Sh-Wx	(1-2)	(1-3)	(2-3)	
Yg c sh Dp wx / yg C Sh Dp Wx	N3 N3	25.9	7.5	15.2	0.1	0.8	0.9	1333

Coincidence values are low for double exchanges in the studied regions of chromosome 9 in plants with structurally normal chromosomes 9. A remarkable feature of the Dp Dp data is the increase in number of double exchanges. This is particularly striking in those doubles where one exchange is in the Sh-Wx region. Although no increase in crossing over occurred in this extended segment, its physically longer length reduced the interference distance so that the probability of a second exchange taking place in either the Yg-C or C-Sh region was not markedly reduced. A second feature of the Dp Dp data is the enhanced crossover values for the Yg-C and C-Sh regions. In the latter region the recombination values are twice that normally found. The data on chromosome 9 indicate that no recombination occurs in the segment of 3L inserted into chromosome 9. The question as to whether or not recombination took place in this segment when part of a normal chromosome 3 was answered by the following data.

Female parent		Recombination percentages Gl-Lg	Lg-A	Coincidence
Gl Lg Df a / gl lg Df A	Dp9 Dp9	25.1	31.3	0.7

The deleted segment of 3L was originally located between the Lg and A loci so in homozygous Df3 Df3 plants these two genes are separated by a smaller segment of chromatin than they are in N3 N3 plants. A lower percentage of crossing over might be anticipated but the observed amount is not less than that occurring in closely related plants with normal 3's.

It may be concluded that recombination does not take place in the segment of 3L involved in the transposition either in N3 N3 chromosomes or in Dp9 Dp9 bivalents. That it is not genetically inert is evidenced by the abortion of both N9 Df3 megaspores and microspores.

M. M. Rhoades

INSTITUTO FITOTECNICO DE SANTA CATALINA
Llavallol, Argentina

1. Paramutagenic action of the C locus.

A paramutagenic gene c^{IP} (provisional designation), has been found in a strain which was the product of a cross between Euchlaena mexicana x Zea. This cross was backcrossed 10 times with the recurrent homozygous strain of genotype: a a, C C, r r, gl gl, ij ij. The action of the c^{IP} gene produces mutations of the alleles C and c and the mutational sequence is C→c and c→c^{IP} (induced inhibitor). The paramutation shows extensive areas in the ear of somatic mosaicism. The mutated genes are more unstable than the standard.

Experimental data:
(1) In the cross: c^{IP}/C(→c) x C/C the following data were obtained:

1389 Colored Kernels Pr
1414 Colorless Kernels

Data from the reciprocal cross were as follows:

808 Colored Kernels Pr
688 Colorless Kernels

In the preceding data the mutation of C→c was not detectable due to the dominant effect of the C/C parent.
(2) In the cross c^{IP}/C(→c) x c/c (tester) the following data were obtained:

426 Colored Kernels Pr
896 Colorless Kernels

The mutation C→c was detected by an excess of colorless kernels.
(3) Allelomorphism.

In the crosses c^{IP}/c x c/c (tester) 18 ears with all colorless kernels were obtained. By selfing the genotype, c^{IP}/c, 8 ears with all colorless kernels were obtained.