of pairs became progressively lower for intercrosses with breaks farther out on one or more of the arms.

At pachytene in intercrosses showing 15-30% of "pairs" at diakinesis, most of the cells had an association of 4 chromosomes with 2 +-shaped pairing configurations, one in each arm of the two chromosomes. When the breaks were at .4 or closer to the centromeres (100% "pairs" at diakinesis), "pairs" were also frequent at pachytene. In an occasional figure an association between the two in regions near the centromeres could be recognized. When certain of the interchange points were close to the ends, only one "cross" was observed in many of the figures. Although no intercross combination has been studied in which the 4 breaks were close to the ends, one can predict that in the resulting "pairs," homologous ends would not be paired.

The evidence from the intercrosses in which the interstitial segments are relatively short, with breaks at .4 or less, indicates that pairing is not initiated at the centromeres. If it were, the "pairs" observed in these intercrosses would then be associated homologously in the middles. This is not the case. However, when the interchanged segments are short, pairing may be initiated on either side of the break points. There may be several sites at which pairing may be initiated. In the type la intercrosses, the centromere is not one of these sites.

Hence, in maize the "intercross method" of locating break points proposed for barley by Kasha and Burnham, 1965 (Canad, J. Genetics and Cytol.) fails for the Type la intercrosses when one or more of the interchange points is at .5 or greater. Interchanges with breaks known to be at distal positions in the chromosomes are needed in barley to test the method.

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8. Crossing over in intercrosses involving T5-6c.

The T5-6c (5L 0.89-6s 0.0) stock homozygous for bm pr, ys, v2, y was crossed with five T5-6 stocks with breaks in 5S and 6L, i.e. the opposite arms, or Type la intercross. The F_1 's were backcrossed to bm pr ys y, in some cases \underline{v}_2 , in others $\underline{V}_2\underline{v}_2$. Crossovers in both of the between breaks segments in chromosome 5 and in 6 will result in two kinds of combinations, one with normal chromosomes 5 and 6 and one in which chromosomes 5 and 6 carry both interchanges. These will appear among the backcross progeny as fertile and semisterile plants, respectively. The latter is the type desired for the new marker method described below, but cannot be distinguished from the non-crossovers which are also semisterile. The frequencies of the fertiles from 5-6c crossed with five 5-6 (S-L) interchanges are shown in the following tabulation:

	58-6L parent	Break p	osition mosome 6	Total plants	% fertile**	Recombi bm-pr	pr-ys	
7	5-6 (5622)	s.87*	L.47*	376	0.8	24.1	9.6	270
	5-6 (6522)		L.7	400	19.0	36.2	7•5	213
	5-6 (4933)		L.89	420	26.3	16.3	11.6	190
-	5-6 (5765)		L.32	381	0.0	5.4	3.1	353
	5-6 (5906)		L.28*	408	3.6	36.4	4.1	406
_						24.8	13.3	1030
Checks 5-6c/bm pr ys						17.5	11.2	268
Che	ecks N/ <u>bm</u>	<u>pr ys</u>						

^{*}Phillips (1966).

The two intercrosses that had 19 and 26% of fertile plants are the only crosses in which a long differential segment (in this case, also interstitial) in 6L was available for the crossing over needed for the recovery of the crossovers in the differential segment in 5. In the other three intercrosses, the interstitial segment in 6L is a region in which crossing over frequency is low.

Recombination values in the <u>pr-ys</u> region are all lower than for the 5-6c check, some considerably lower. In the <u>bm-pr</u> region, two are high, two low and one about the same as the T5-6c check. Since single crossovers within only one of the differential segments are not recovered, one might expect reduced recombination within those segments, and this in turn to be related to the recovery of fertile progeny. No explanation of the data can be offered at present.

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9. Crossing over in intercrosses involving T1-5 interchanges.

Intercrosses in which the parents had genetic markers for chromosome 5, mostly pr ys_1 yg_1 , were backcrossed to the multiple recessive. The frequencies of fertile progeny for three of the crosses are as follows.

	total plants	% fertile
1-5 (4597) x 1-5 (5525)	446	18.6
1-5 (5045) x 1-5 (4597)	151	0.7
1-5 (4597) x 1-5b	542	0.0

^{**}The other plants were all semisterile.