	5S-6L parent	Break position in chromosome 5	Break position in chromosome 6	Total plants	% fertile**	Recombination values bm-pr	Recombination values pr-ys	Recombination values total plants
1.	5-6 (5622)	S.87*	L.47*	376	0.8	24.1	9.6	270
2.	5-6 (6522)	S.87	L.7	400	19.0	36.2	7.5	213
3.	5-6 (4933)	S.23	L.89	420	26.3	16.3	11.6	190
4.	5-6 (5765)	S.19	L.32	381	0.0	5.4	3.1	353
5.	5-6 (5906)	S.28*	L.28*	408	3.6	36.4	4.1	406
Checks 5-6c/bm pr ys						24.8	13.3	1030
Checks N/bm pr ys						17.5	11.2	268

*Phillips (1966).
**The other plants were all semisterile.

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 pr-ys region are all lower than for the 5-6c check, some considerably lower. In the bm-pr 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

Since many fertile plants were observed in one of the crosses, one would expect to recover the complementary semisterile class which carries both interchanges on the same two chromosomes. The recombination values were similar to those in the check, but the data are limited, since only part of the crosses segregated for the 3 markers.

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10. A new method of using interchanges as chromosomal markers.

The single interchange stocks that have been used in the past for genetic analysis of complex characters require a large number of stocks for an adequate coverage of the chromosomes. In the test with each interchange only two of the four arms of the chromosomes involved in the interchange are marked with breakpoints. If the two chromosomes had a second interchange with breaks in the other two arms (breakpoints in each of the four arms of the two chromosomes), one should be able to detect the presence of any gene located in those two chromosomes. A method of developing such stocks is as follows: Cross two interchange stocks that involve different arms of the same two chromosomes and then cross the F_1 with a standard normal stock. Progeny that come from crossovers in the two differential segments, and which bring the two interchanges together in the same two chromosomes, would be semisterile. They could be distinguished from the semisterile noncrossover sibs by testcrosses with the parental interchange stocks, and established as a double interchange stock that is homozygous. These could be used in linkage tests in a manner similar to that used for the single interchange stocks. In backcross linkage tests, the parental classes would be semisterile or fertile. Single crossovers in either of the differential segments would not be recovered. Also even when single crossovers occur in both differential segments, both complementary crossover classes are semisterile, and hence only one is recognizable as a recombinant. This should furnish a more efficient test for linkage.

A set of five such double interchange stocks, e.g. 1-2, 3-4, 5-6, 7-8 and 9-10 should completely test the ten chromosomes and narrow the location of a major gene to two chromosomes. A set of nine such double interchange stocks in which one of the two chromosomes interchanged was the same, e. g. 1-9, 2-9, 3-9, 4-9, 5-9, 6-9, 7-9, 8-9 and 9-10, should locate a major gene to an individual chromosome. If on 9, it should show linkage with all or most of the stocks in the series.

An extension of the method to 3-chromosome interchange stocks is possible also. As an illustration, if there are three interchange stocks T1-2 (1S-2L), T1-7 (1L-7L), and T2-7 (2S-7S), the cross of T1-2 x T1-7 will have a ⊙ 6 at meiosis. Crossing over in the differential segment of chromosome 1 can give rise to a combination of chromosomes (T1-2 + T1-7) that includes both interchanges. This stock marks arms 1S, 2L and 7L, but does not mark arms 2S and 7S. If T2-7 (S-S) could be added, all arms of the three chromosomes would be marked. This can be accomplished by producing a second 2-interchange stock, e. g. 1-7 + 2-7. If