of corn, does not synapse with any of the corn chromosomes. Twenty-one chromosome plants are indistinguishable from 20 chromosome plants on the basis of gross morphology. Test crosses with multiple recessive stocks give normal disomic ratios for all markers tested with the possible exception of g_1 for which classification was difficult and recessive progeny seemed to be deficient. Tests with chromosome 10 tester stocks are currently underway.

This Tripsacum chromosome is particularly interesting, however, because of the fact that it is transmitted by 21 chromosome plants through the egg to about 84 percent of its progeny. Twenty-one chromosome plants are highly pollen and ovule sterile. In microsporogenesis the Tripsacum chromosome lags in about 89 percent of anaphase I cells. It divides in about 54 percent of pollen mother cells and is apparently included in telophase I nuclei without having divided in most of the remainder. In those cases where the Tripsacum chromosome divides in the first division it lags at anaphase II and is sometimes excluded from telophase II nuclei so that it is present in about 30 percent of microspores. Scant data available from selfing are consistent with the interpretation that the Tripsacum chromosome actually is transmitted through the pollen with about the same frequency with which it occurs there. So far no anaphase configurations have been found at megasporogenesis, but the basal megaspore has been functional in all of the 44 ovules examined which were at the appropriate stage for such a determination. Genetic tests indicate that parthenogenesis cannot explain the high transmission frequency of the Tripsacum chromosome, and it is thought unlikely that it divides twice or has extra centric activity in megasporogenesis since neither of these seems to occur in microsporogenesis. The most likely explanation for the high transmission frequency at present appears to be that eggs or embryos not carrying the Tripsacum chromosome are strongly selected against in the maternal background in which this Tripsacum chromosome is present.

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1. Teopod-2 and sr_2 in relation to preferential segregation in chromosome 10.

In crosses of Tp_2 with chromosome 10 stocks, it was found that R-Tp_2 showed about 36% recombination, while g-Tp_2 showed independence. This placed Tp_2 distally to R in the long arm of chromosome 10. In a cross with T9-10b (break in short arm of chromosome 10), Tp_2 showed independence to wx, and so, corroborated the location of Tp_2 far distally on the long arm of chromosome 10.

Later we combined Tp_2 with Rhoades's abnormal 10, and crossed it to sr_2. Abnormal 10 and sr_2 came to us from Maize Genetic Coop. stocks. The one segregating sr_2 and R:r, showed an R-sr_2 recombination of 25%.

In the experiment presented in Table 1, which includes four points, several striking results are noticeable. The following brief comments are offered as tentative suggestions.

a. - Locus sr_2 is responsible for, or closely associated with, preferential segregation, (a neocentromeric locus?), as revealed by the asymmetrical frequencies in members of complementary classes.

b. - The region distal to sr_2 concentrates an enormous amount of crossingover. More than half of the total of contributed gametes originated as crossovers in the region between sr_2 and Tp_2.

c. - We did not make cytological verifications of the distribution of the abnormal piece of chromosome 10 among the progeny. But if we assume that the favored classes and the presence of abnormal 10 are correlated (as obtained by Rhoades), then the gametes (r-Sr_2-tp_2) indicated in Table 1 as a product of single crossovers in region-2, must contain the abnormal 10 piece, being really double crossovers (2+3). Also, the complementary and less favored gametes (R-sr_2-Tp_2) must be double crossovers (2+3) deprived of abnormal 10.

d. - There is indication of incompatibility of the allele sr_2 and the piece of abnormal 10 which prevents their inclusion in the same gamete. The combination sr_2-abnormal 10 in the same chromosome (as the single crossover in region 2) is believed to be inviable.

e. - We may infer that the crossover activity in the region distal to Tp_2 is as high as that in the region sr_2-Tp_2, the majority of effective gametes being double crossovers (2+3) as a result of a balanced mechanism.

f. - Another, and altogether different interpretation of the data, would be that Tp_2 is not located in chromosome 10, but exhibits a spurious association with it.

Table 1. Linkage Data from the Cross:

$$\frac{r^r \quad + \quad Tp_2 \quad \text{abn.}}{R^g \quad sr_2 \quad + \quad N} \quad (1) \quad X \quad \frac{r^r \quad sr_2 \quad + \quad N}{r^r \quad sr_2 \quad + \quad N}$$

Constitution of chromosome 10 in maternal gametes								Total	Ratio of R:r on ear
(0)	(0)	(1)	(1)	(2) or (2+3)?	(2) or (2+3)?	(1+2)	(1+2)		
r	R	r	R	r	R	r	R		
Sr_2	sr_2	sr_2	Sr_2	Sr_2	sr_2	sr_2	Sr_2		
(+)(2)	(-)	(-)	(+)	(+)	(-)	(?)	(?)		
Tp_2	tp_2	tp_2	Tp_2	tp_2	Tp_2	Tp_2	tp_2		
53	23	2	6	67	18	0	0		49 R:146 r
76		8		85		0		169	R = 25.1%

(1) One ear obtained with 195 seeds.
(2) The signs (+) and (-) in this place indicate preferential segregation associated with the locus Sr_2 as revealed by the asymmetrical frequencies of members of complementary classes.

R - sr_2 recombination = 4.7% % R in total plants = 47/169 = 27.8%
R - Tp_2 recombination = 55.0% % sr_2 in total plants = 43/169 = 25.4%
sr_2 - Tp_2 recombination = 50.9% % tp_2 in total plants = 92/169 = 54.4%

% R in parental classes = 23/76 = 30.3%

% R in classes: non-crossover with sr_2 locus = 41/161 = 25.4%
crossover with sr_2 locus = 6/8 = 75%

% R in classes: non-crossover with tp_2 locus = 23/76 = 30.3%
crossover with tp_2 locus = 24/93 = 25.8%

% sr_2 in classes: non-crossover with tp_2 locus = 25/84 = 29.7%
crossover with tp_2 locus = 18/85 = 21.2%

% sr_2 in classes: non-crossover with R locus = 41/161 = 25.4%
crossover with R locus = 2/8 = 25%

% tp_2 in classes: non-crossover with R locus = 23/76 = 30.3%
crossover with R locus = 69/93 = 74.2%

% tp_2 in classes: non-crossover with sr_2 locus = 25/84 = 29.7%
crossover with sr_2 locus = 67/85 = 78.8%

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