same ear have been inspected and no dots are present. Furthermore, a second backcross of plants arising from these pale $\underline{Sh}$ kernels has produced no dotted kernels and no obvious pale $\underline{sh}$ crossovers on 6 ears.

One of the two exceptional alleles (designated $\underline{a}^{p*}$) has been studied further. The $\dfrac{T\ a^{p*}\ sh}{N\ a\ \ sh}$ plant arising from one of the two pale $\underline{sh}$ kernels was self pollinated and used as male parent in a cross with $\dfrac{T\ a^{s}\ \ Sh}{N\ a\ \ sh}$ female parents.

Both crosses gave pale kernels with infrequent small dots as well as some pale kernels without dots. Backcrosses of resulting $\dfrac{a^{p*}}{a}$ and $\dfrac{a^{p*}}{a^{s}}$ individuals revealed that the dotting was a property of the $\underline{a}^{p}$ allele and not due to an independent mutator gene. The pale kernels without dots contain the same $\underline{a}^{p*}$ allele and appear to be "escapes"; the progeny of plants from such kernels includes dotted pale kernels. There is no evidence of a new $\underline{Dt}$ factor at the $\underline{a}^{p}$ locus since the $\underline{a}$ allele on the homologous chromosomes in the endosperm is unaffected. Kernels of $\underline{a}/\underline{a}/\underline{a}^{p*}$ and $\underline{a}^{s}/\underline{a}^{s}/\underline{a}^{p*}$ constitution contain the same low number of dots (1-3).

Tests are underway to determine whether unstable $\underline{a}^{p}$ alleles will arise in F_{1}'s of $\underline{a}^{p}$-D35/$\underline{a}^{s}$ constitution as well as in $\underline{a}^{p}$-D35/$\underline{a}$ plants. If the associated double crossover is a prerequisite for instability, some mutable component of the $\underline{a}$ allele (or the allele itself) may be included in the mutable $\underline{a}^{p}$ allele. If this is the case, no unstable pales should arise from F_{1}'s involving the $\underline{a}^{s}$ allele. Another cross will test whether the stable $\underline{a}^{p}$ can be recovered from the unstable $\underline{a}^{p}$ following various crossovers.

<div align="right">Ellen Dempsey</div>

7. Cytological location of rgd on chromosome 6.

One of Roman's A-B translocations, TB-6a, was used in an attempt to determine the cytological location of ragged ($\underline{rgd}$) on chromosome 6. The breakpoint in chromosome 6 is in the nucleolar organizer region (Roman and Ullstrup, Agron. J., 1951).
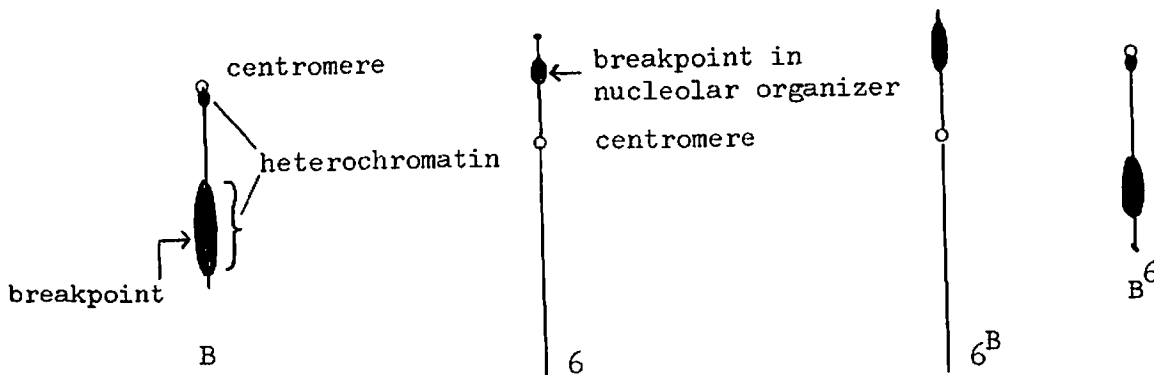
Hypoploid plants of the constitution $6^{B\underline{y}}\ 6\ ^{B\underline{y}}\ B^{6}$ (as determined by root tip examination) were transplanted to the field in May of 1967. They were crossed as male parents with plants that were phenotypically $\underline{Y\ Rgd}$. The genotype of the female parent was determined by self-pollinating the

tillers and classifying the progeny for y and rgd. Only crosses of the type Y Rgd/y rgd X 6^{By} 6^{By} B^6 were further analyzed. Roman's method of mapping genes with A-B translocations was used. Nondisjunction of the B^6 chromosome would occasionally give rise to rgd seedlings if the Rgd locus is present on the B^6 chromosome. On the other hand, if the Rgd locus is located on the 6^B chromosome, rgd seedlings would not be found. A total of 1846 seedlings were classified and no rgd seedlings were found (Table 1).

Table 1

Ear	Yellow Seed		White Seed	
	+	rgd	+	rgd
1	117	0	105	0
2	110	0	113	0
3	230	0	200	0
4	139	0	166	0
5	111	0	86	0
6	104	0	91	0
7	183	0	191	0
Total	994	0	952	0

From these results it was concluded that the Rgd locus was on the 6^B chromosome.

Several translocation heterozygotes, each with a break in the organizer region of chromosome 6, were crossed as female parents with Rgd/rgd male parents. Following adjacent-1 segregation at meiosis, some of the eggs should contain a deficiency for the terminal portion of 6S, distal to the break. Eggs of this type, when fertilized by rgd sperms, would give rise to seedlings exhibiting the recessive phenotype. The data are listed below:

Translocation heterozygote	N	rgd
T6-9$_{4778}$/N	287	0
T4-6$_{4341}$/N	732	1?
T2-6$_{5419}$/N	713	0
T6-9a/N	465	0

Only one questionable rgd seedling was observed. It was concluded from these results and those obtained with the TB-6a translocation that the rgd locus is not in the portion of 6S distal to the organizer break. However, the location of rgd in the proximal portion of the organizer was not ruled out by these tests.

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8. Somatic association of homologues induced by abnormal chromosome 10.

It has been postulated that an association of homologous chromosomes is a general phenomenon found throughout the cells of the organism (Feldman et al, PNAS 56: 1192-1199, 1966), and that the intimate synapsis of homologues in meiosis is the extreme condition. Therefore, an effort was made to determine whether or not homologous maize chromosomes associate at random in mitotic cells of the root tips. Since it is known from the investigations of Rhoades and Dempsey (1966) that abnormal chromosome 10 (K10) induces more intimate pairing of the homologous chromosomes in meiotic cells, root tips of plants with and without K10 were examined.

Plants from isogenic W22 stocks carrying 0, 1, or 2 K10 chromosomes were germinated, the root tips collected, and squashes were prepared according to the Feulgen staining technique. The cells were examined to determine the distances between the homologous chromosomes 6 in all three stocks, between each 6 and each K10 in the stocks with one or two K10's, and between the homologous K10 chromosomes in the stock with two K10's. The 6's could be distinguished from the other chromosomes by the terminal satellites and the K10's by the length, extreme arm ratio and the large terminal knob. Cells which were reasonably flat and circular with all twenty chromosomes visible were selected for counting.

The distances between the chromosomes were measured with an ocular micrometer and, to minimize the differences in cell size due to differential squashing, the distance between the two chromosomes in question was divided by the distance between the two chromosomes which were furthest apart in the cell. This gave a corrected value which will henceforth be referred to as distance between the chromosomes.

In order to determine whether the chromosomes were non-randomly associated, the results of the counts were compared with a theoretical distribution. This theoretical distribution is based on the frequencies with which two points will lie at various distances from each other when randomly