<u>Trisomics</u>: A number of the supposedly dilute dotted non-shrunken seeds turned out on test to be trisomics. The number was not extremely high but they were easily obtained because the experimental design was ideally suited for picking up such cases since they resemble two of the crossover types ($\underline{\alpha}$ \underline{a}^{m} \underline{Sh} and $\underline{\alpha}$ \underline{a} \underline{Sh}) that we were looking for.

 $\underline{a^m}$ -a-sh segment: This unique combination of two \underline{Dt} responding alleles on the same segment is recognized only when the \underline{Dt} gene induces the more mutable of the two $(\underline{a^m})$ to mutate to $\underline{a^s}$ leaving a sector of $\underline{a^s}$ a tissue that permits the expression of the less mutable of the two original alleles (\underline{a}) . There are perhaps several others among the $\underline{a^m}$ sh class which will not be recognized until further tests are made.

10. Grouped crossovers.

In examining the ears for the above described experiment it was noted that a number of examples of a sector that included two or more crossovers were found. In one case for example, three α a Sh crossovers were found in a single row within the distance of six seeds. Their order on the ear was a sh, am Sh, a sh, am Sh, am Sh, am Sh, and a sh. The crossovers have double underlining. This same ear had two a a Sh cases on the other side of the ear which were separated by one noncrossover seed. The possibility of contamination has been excluded for these cases and since there were no mutator factors such as Dt or Ac present it is very unlikely that they arose by mutation. Several cases, as yet unconfirmed, of complementary crossover types in pairs have been observed, for example $\underline{\alpha}$ and \underline{a}^{m} sh. There also was found in the progeny from the α a sh/a^S Sh material, one case of three a^S sh seeds in a single sector. Their order on the ear was a a sh, as sh, a a sh, as sh, as sh, and a a sh. A total of 341,421 seeds have been examined and at most 450 crossover cases have been found (later confirmation tests will give an accurate figure). Thirty-six of these were found in 17 sectors of two or more essentially adjacent seeds. This suggests something more than coincidence. Among the possibilities being investigated are somatic crossing over and a pre-disposition to high frequency of crossing over in certain sectors of the developing ear.

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11. High amylose starch.

It was reported in the Maize Genetics News Letter #30 that the cross between <u>hal</u> and one of the Missouri high amylose strains (<u>ham</u> 123) gave an amylose content of 27%, indicating the two factors were not allelic. When grown in Missouri, <u>hal</u> and <u>ham</u> 123 gave amylose contents of 49% and 37%, respectively. Selected samples of kernels from the F3 ears gave amylose contents from 60% to slightly more than 70%. It is possible

strains with higher amylose contents will be found in this or in later generations. The amylose was determined by potentiometric titration with iodine at the Northern Regional Utilization Branch, Peoria, Illinois.

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1. Distribution of transposed Modulator.

Modulator (\underline{Mp}) , the element postulated by Brink and Nilan as responsible for the suppression of $\underline{P^{TT}}$ (red pericarp, red cob) action to give the $\underline{P^{VV}}$ (variegated pericarp, variegated cob) allele, frequently undergoes transpostion from the \underline{P} locus. A transposed-Modulator $(\underline{tr}-\underline{Mp})$ when present in the genome with an unaltered $\underline{P^{VV}}$ allele $(\underline{P^{TTMp}})$ gives the light variegated phenotype.

An experiment was designed to study the distribution of these transposed Modulators. Independent transpositions of Mp (new mutations from medium variegated to light variegated) were collected, and the linkage relations of tr-Mp then studied.

It was found that <u>tr-Mp</u> could occupy positions both linked and non-linked to the <u>P</u> locus. Cases were observed in which <u>tr-Mp</u> showed linkage to reciprocal translocations marking chromosomes 4 and 5, and 5 and 9. In the majority of cases, however, <u>tr-Mp</u> shows some degree of linkage with the <u>P</u> locus on the first chromosome. Among 67 independent transpositions of <u>Mp</u> from the <u>P</u> locus, 64 per cent of the new positions were linked to the <u>P</u> locus. This percentage is much higher than would be expected if moves were at random. The frequency with which <u>tr-Mp</u> occupies any given position on chromosome l increases sharply as the distance from the <u>P</u> locus decreases. Modulator, after becoming transposed from the <u>P</u> locus, often undergoes further transposition. Limited data were obtained suggesting that <u>tr-Mp</u> is less likely to undergo secondary moves if the position first held is close to the <u>P</u> locus.

2. Cytological positions of reciprocal translocations involving chromosome 1 and linkage with the P locus.

During the course of an experiment in which various reciprocal translocations were used as markers, the data given below were collected showing the linkage between the \underline{P} locus and several reciprocal