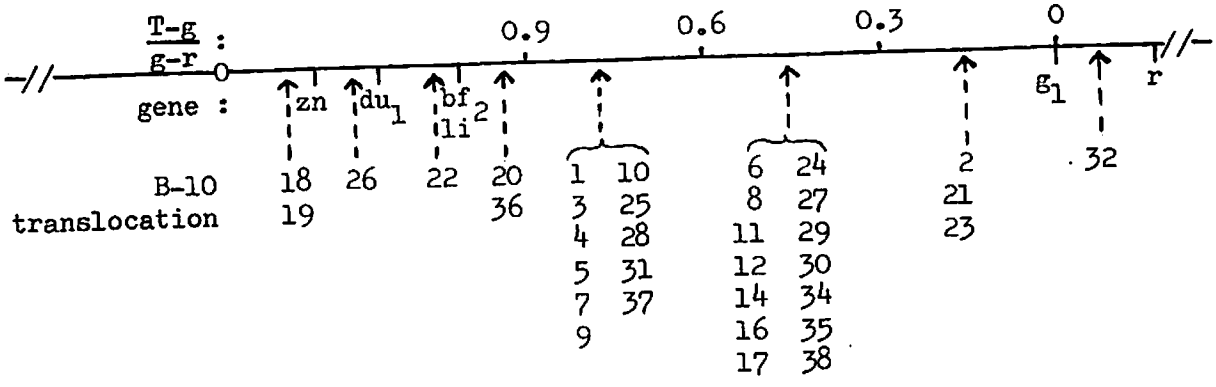
also for g to R. In part, the g-R variation can be attributed to the limited sample size for a given translocation. Agreement between subsamples was sufficiently good, however, to suggest differential effects associated with the translocation stocks. Accordingly, the T-g values have been normalized by dividing the percent T-g recombination in any given case by the percent g-R recombination recorded for that translocation.

The resulting T-g recombination index (right-hand column of the Table) bears a definite relationship to the translocation categories defined by marker genes. The three highest values, to cite an outstanding example, belong to the three translocations having breakpoints proximal to dull. A potential use of the index is to distinguish among translocations belonging to the same marker category. This is best illustrated in the present case by the 33 translocations categorized as having a breakpoint between g_1 and (bf_2 - li). For this group, the index ranged between 0.17 and 1.14.

Results of both studies are summarized in the following diagram.



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6. A seed-size effect associated with certain B-10 translocations.

In the course of establishing the set of 38 translocations whose breakpoints in the centromere-R segment of chromosome 10 are reported in the preceding note, a detrimental effect of six of them on seed development was observed. The effect is specific for kernels of the hypoploid endosperm class, produced following crosses of the translocation as pollen parent. The reduction is parallel, therefore, to effects

described by Roman and Ullstrup (1951) and Bianchi (1961) involving translocations B-1a, B-1b and B-4a. For the six TB-10 cases, consideration of the extent of reduction and the position of the breakpoint permits a tentative assignment of the minimum number and regional placement of the genetic factor involved.

Measurements of seed size were based on the cross, $10(\underline{r}^g)/10(\underline{r}^g)$ x $10(\underline{r}^g)/10^B/B^{10}(\underline{R}^{scm})/B^{10}(\underline{R}^{scm})$, where the female parent is inbred W23 and the translocation stock is a subline of inbred W22. With TB-10a, established by Roman, the weight of the hypoploid endosperm kernels (colorless aleurone, colored scutellum) was, on the average, 95% that of the euploid kernels (colorless aleurone and scutellum) formed by meiotic nondisjunction of the two B^{10} chromosomes. The hyperploid endosperm class, distinguished by colored aleurone but colorless scutellum, did not differ detectably from the control group. Thirty-two of the 38 additional B-10L translocations conform to the pattern set by TB-10a. Of the remaining six, reductions in weight of approximately 15% and 25% were observed in translocations TB-10(20) and TB-10(36), respectively, whereas a 50% reduction was characteristic of TB-10(18), TB-10(19), TB-10(22) and TB-10(26). Kernels of the hyperploid endosperm class did not differ significantly from the euploid control in any of the six cases. Likewise, kernels having both endosperm and embryo hyperploid, following functioning of 10 B^{10} microspores, were not subnormal. Thus, kernel size reduction may be attributed to segmental deficiency in the endosperm of that portion of chromosome 10 carried by B^{10}.

The slight reduction associated with 32 of the translocations suggests the presence of a factor of minor influence located beyond the point of break in the most distal case, i.e., TB-10(32). By similar reasoning, the four translocations associated with the most pronounced effect should have the most proximal breakpoints. Only these four of the 38, in fact, "uncovered" $\underline{bf}_2$ and $\underline{li}$. Translocations 20 and 36, the two with intermediate effects, are among the larger group that uncover golden but not $\underline{bf}_2$ or $\underline{li}$. They were, nevertheless, the two translocations of this group that mapped most distant from golden. The observations suggest then the presence of three factors of relatively major cumulative effects carried in a region distal to $\underline{du}_1$ or distal to

the breakpoint of TB-10(22) and a fourth factor of minor effect located distal to golden.

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ADDENDUM:

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1. Modulator as viewed through the pericarp.

Previous published works have stressed the importance of the conclusion that all transpositions of Modulator from the P locus result in only potential twin mutations. Potential in that a pair of differently mutant cells always arise from a transposition, but only sometimes do they condition pericarp phenotypes visibly definable as twin spots of red and light variegated tissue. While the pre-transposition cell has a P^{rr}Mp complex (medium variegated), the post-transposition pair of cells are altered, and one carries only P^{rr} with or without Mp somewhere within its nucleus but not at the P locus (potentially red-forming tissue), while the other member of the pair carries a P^{rr}Mp complex plus an Mp within its genome (potentially light variegated tissue).

The conclusion that there is equality in mutant frequency comes from a model of the mechanism of transposition rather than the published counts of equal red vs. light variegated frequencies. In fact, due to the effect of intervening events such as meiosis, only indirect evidence has been offered to support the model (Greenblatt, Genetics, 1968) which demands that mutant classes arise as equals since only in twin spots are they found in that ratio.

New data on untwinned mutant sectors and a reevaluation of previously published data derived from homozygous variegated pedigrees offer direct support for the contention of a 1 red: 1 lt. variegated ratio at the time of transposition. The two tables which follow are abstracted from a forthcoming publication in Genetics. Table 1 shows that mutant spots one kernel and larger in size in the pericarp tissue are most often twinned. Among those that are not twinned, the two mutant classes occur