5. **TB-10 breakpoints and marker genes on the long arm of chromosome 10.**

Entered in the accompanying Table are results based on intercrossing as male 38 TB-10 translocation stocks with strains carrying the chromosome 10 marker genes, golden-1 (g_1), lineate (li), blue fluorescent-2 (bf_2), dull-1 (du_1), and zebra necrotic (zn). The translocation stocks all have breakpoints between R and the centromere of 10 since R was used as a selective marker in their derivation (MGCNL 46:193). The hypoploid offspring, generated through use of the translocation lines as male, are deficient for segments of 10L extending from its tip through R to the translocation breakpoint. Presence of the mutant phenotype among plants of the intercross progenies (recessive mutant x TB-10 stock) is indicated by a "+" and absence of mutant offspring by a "-".

The pattern of mutant gene "uncovering" in hypoploid plants defines five translocation categories which form the following nierarchical ranking: one translocation, TB-10(32), failed to uncover any of the five mutants; 33 expressed only golden-1; one expressed bf_2 and li as well as g_1; one gave dull kernels as well as g_1, bf_2 and li plants; and two gave zn plants in addition to expressing the four other markers. Beckett's evidence (MGCNL 47:145) concerning two previously established B-10L translocations places TB-10a in the second category and TB-10b in the third. The 200 combinations involving the five mutants and 40 translocations are without exception in indicating a gene order of centromere-zn - du_1 - (bf_2 - li) - g_1 - R. None of the 40 breakpoints separates bf_2 from li.

A sixth marker, white-tip, was tested against the translocations since it had shown linkage with T2-10 (6061) but not with two other chromosome 2 translocations (Burnham, MGCNL 44:145). No plants of white-tip phenotype were observed, however, in the F_1 progenies obtained following crosses with the 38 TB-10 translocation stocks.

Three-point linkage data involving the breakpoint (T), golden, and R are available for 36 of the translocations. Testcrosses involved g r^g/g r^g as female parents with N g R^r/T G R^{scm} as male. Kernels lacking aleurone color and therefore inheriting the translocation were classified for golden and seedling root color after sprouting.

The level of recombination varied widely. Not only was this true for the T-g interval, which is of variable length from case to case, but
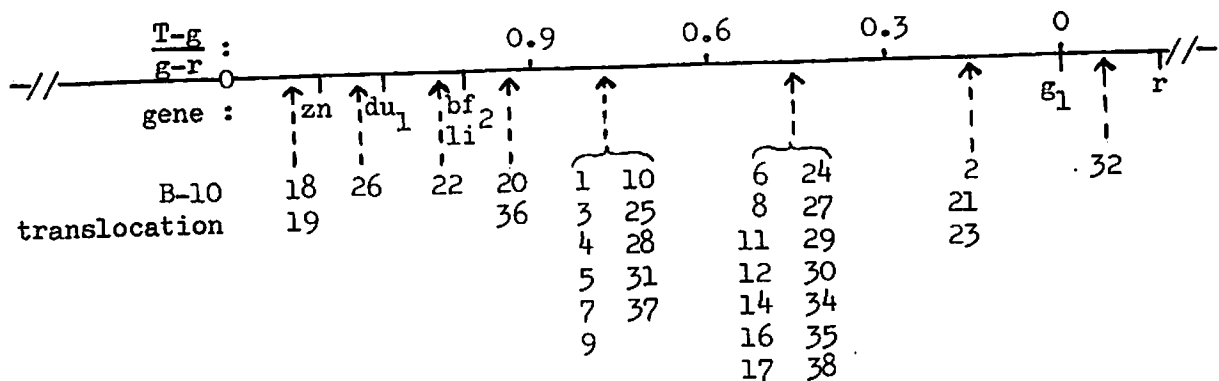
Table 1

Tests for marker uncovering and three-point linkage
analysis involving 38 B-10 translocations

B-10 trans-location	Marker genes					T-g-R recombination		
	zn	du_1	bf_2	li	g_1	Population	g-R c.o (%)	$\dfrac{T\text{-}g}{g\text{-}R}$
1	−	−	−	−	+	239	16.7	0.80
2	−	−	−	−	+	261	6.5	0.17
3	−	−	−	−	+	241	16.2	0.61
4	−	−	−	−	+	362	16.0	0.89
5	−	−	−	−	+	261	20.7	0.61
6	−	−	−	−	+	278	13.6	0.32
7	−	−	−	−	+	342	15.2	0.77
8	−	−	−	−	+	86	23.2	0.50
9	−	−	−	−	+	115	15.6	0.61
10	−	−	−	−	+	298	18.1	0.65
11	−	−	−	−	+	274	19.7	0.33
12	−	−	−	−	+	189	11.6	0.41
13	−	−	−	−	+	...	−	...
14	−	−	−	−	+	305	12.6	0.45
15	−	−	−	−	+	188	0	...
16	−	−	−	−	+	218	13.7	0.40
17	−	−	−	−	+	251	23.1	0.42
18	+	+	+	+	+	335	25.3	1.35
19	+	+	+	+	+	417	21.6	1.30
20	−	−	−	−	+	315	15.5	1.04
21	−	−	−	−	+	385	12.7	0.30
22	−	−	−	−	+	305	21.3	0.98
23	−	−	+	+	+	270	15.5	0.29
24	−	−	−	−	+	189	15.3	0.34
25	−	−	−	−	+	215	18.1	0.67
26	−	+	+	+	+	510	22.9	1.21
27	−	−	−	−	+	204	5.4	0.45
28	−	−	−	−	+	226	17.7	0.82
29	−	−	−	−	+	577	19.9	0.39
30	−	−	−	−	+	76	22.3	0.35
31	−	−	−	−	+	186	15.6	0.86
32	−	−	−	−	−	240	9.6	...
33	−	−	−	−	+	−	−	−
34	−	−	−	−	+	206	19.4	0.47
35	−	−	−	−	+	441	18.6	0.41
36	−	−	−	−	+	498	20.5	1.14
37	−	−	−	−	+	216	10.2	0.63
38	−	−	−	−	+	230	10.4	0.54
TB-10a	−	−	−	−	+	−	−	−

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

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 outstand-ing example, belong to the three translocations having breakpoints proxi-mal to dull. A potential use of the index is to distinguish among trans-locations belonging to the same marker category. This is best illustra-ted in the present case by the 33 translocations categorized as having a breakpoint between g_1 and $(\underline{bf}_2 - \underline{li})$. For this group, the index ranged between 0.17 and 1.14.

Results of both studies are summarized in the following diagram.

	0.9	0.6	0.3	0	
T-g :					
g-r : 0					r
gene : zn du$_1$ bf$_2$ li				g$_1$	

| B-10 translocation | 18 19 | 26 | 22 | 20 36 | 1 3 4 5 7 9 | 10 25 28 31 37 | 6 8 11 12 14 16 17 | 24 27 29 30 34 35 38 | 2 21 23 | 32 |

<div style="text-align:right">Bor-yaw Lin</div>

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-$\underline{R}$ segment of chromosome 10 are reported in the preceding note, a detrimental effect of six of them on seed develop-ment 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