

length 24.4). The longer segments involved in the TB-4L translocations may result in more effective pairing (in spite of the complex configuration) and thus allow for more crossing over than is possible in the TB-9b translocation. Higher crossing over would result in a higher percentage of recessive c2 seeds.

In the crosses of each of the TB-4L translocations one or two ears with off ratios were observed. These were not included in Table 2 but are listed in Table 3.

Table 3. Off ratio types from the cross of compound TB-4L translocations.

Translocation	No. of <u>C2</u> seeds	No. of <u>c2</u> seeds	Total	% <u>C2</u>	% <u>c2</u>
TB-1La-4L4692	84	75	159	52.8	47.2
TB-1La-4L4692	63	27	90	70.0	30.0
TB-7Lb-4L4698	125	95	220	56.8	43.2
TB-9Sb-4L6222	110	74	184	59.8	40.2
TB-9Sb-4L6504	93	62	155	60.0	40.0
TB-9Sb-4L6504	165	129	294	56.1	43.9
Total	640	462	1102	58.1	41.9

The 41.9% c2 seed is very close to the 41.8% c seeds observed when euploid heterozygous female TB-9b plants ($9c\ 9^B B^9 C$) are pollinated by c c plants (Robertson, Genetics 55:433-449, 1967). Thus, it is possible that the TB-4L plants that gave off ratios were not hyperploid for the translocation but euploid. An analysis of the TB-9b euploid ratios indicated that the B^A element moved at random with respect to the 9 and 9^B chromosomes. If the off ratios are from euploid TB-4L plants they would suggest that the compound B^A elements in these translocations also are moving at random with respect to the other elements.

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The cytological localization of bm on the short arm of chromosome 5

Last year I reported (M.G.C.N.L. 49:79-81, 1975) on the production of the new compound translocation TB-1La-5S8041. This translocation had 90% of the short arm of chromosome 5 attached to a proximal portion of B^1 segment of TB-1a. In 1974 plants carrying this translocation (genotype $a2\ 1^B\ B^5, 1A2\ B^5, 1A2\ 5l$) were crossed to a homozygous $a2\ bm\ bt$ stock. Last summer I grew out large purple seeds and large yellow seeds from this cross and obtained the following plants:

Large purple seeds			Large yellow seeds		
Tall Plants	Small green midrib plants	Very small, brown midrib	Tall plants	Small green midrib plants	Very small, brown midrib
10	1	5	18	5	0

Two classes of small plants were observed in this cross. In one, the plants were about 3 feet tall and had green midribs and in the other the plants were about 2 feet tall and had brown midribs. The taller of these small plants were similar to deficient TB-1a plants and are probably produced following crossing over that reconstituted the original B^1 chromosome. The smaller brown midrib plants probably represent those that are deficient for the new compound translocation. Because of the genotype of the cross, these small brown midrib deficient plants would only be expected from purple seeds while the B^1 deficient plants could occur from both purple and yellow seeds. Five small brown midrib plants were observed from the purple seeds and none from the yellow seeds while the taller small green midrib

plants were produced by both classes of seeds. These results would place bm distal to 5S.10, the breakpoint of T1-5(8041) in chromosome 5.

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Genetic systems for the production of hybrid corn seed without detasseling

True genetic systems to eliminate detasseling (in contrast to cytogenetic systems that require translocations and deficiencies for gamete selection) are possible if man takes a physical part in selection for certain seed or plant characters associated with male sterility. Two such systems are described here.

A y ms system based on the close linkage of yellow-white endosperm and the male sterile gene on chromosome 6 was described by Singleton and Jones in 1930. The system was never put to use because the problem of contamination by the five percent of recombinant plants was not resolved. A modification in this system by applying the electronic eye seed sorters can make it practical. The y ms kernels that give male sterile plants are electronically sorted from a sib to heterozygous yellow endosperm, male fertile (Y y Ms ms) counterparts. When these white kernels are planted as the female in a crossing field with a normal yellow male, damage from selfing and sibbing by the five percent fertile recombinants appears as white kernels. Here again the electronic seed sorters are used but this second time to remove the white seed. Thus, the result is 100% hybrid bicolor seed. The farmer's crop will segregate ca. 25% white kernels on each ear.

A ts2 sk system is based on the female development of the tassel and its modifying genes. The ts2 gene raises the level of femaleness, resulting in tassel seed as well as ears with irregular rows from the development of both florets. But when the ts2 gene is combined with the silkless (sk) gene on chromosome 2, the tassels become at least partially male fertile, depending on the environment and other modifying genes. In contrast to the ts2 gene, the sk gene raises the level of maleness, resulting in stamens developing in both tassels and ears. Thus, when both the ts2 and sk genes are combined in the double recessive some sort of a male-female balance is once again established. A line cross between plants that are homozygous for ts2 and Sk with plants that are homozygous for ts2 and sk yields a progeny that is 100% tassel seed male sterile (ts2 ts2 Sk sk) because the recessive silkless gene is heterozygous. When this line cross is used as the female in crossing fields, detasseling is unnecessary. The ts2 ts2 Sk sk parent of this line cross must be maintained by the backcross-sib technique. In producing the line cross, the normal segregants may be cut out of the female rows long before pollen shedding. The tassel silks on the plants to remain in the field appear in the plant-whorl stage two weeks or more before the plant elongates and exposes ear silks.

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Further notes on the use of Tr7 in the production of bisweet hybrids

In last year's MNL we mentioned that Tripsacum chromosome 7 (Tr7), which carries the Su locus also found on corn chromosome 4, may facilitate the practical production of bisweet hybrids. When the double recessive of sugary-shrunken-2 with an extra pair (20+2) of Tr7 chromosomes is line-crossed to su sh2 without the extra pair, the 20+2 condition is reduced to the 20+1 state. Then if the sh2 gene is also covered in the final crossing field involving a normal sugary seed parent, the hybrid seed crop is normal sugary with about 10% starchy kernels from Tr7. These starchy kernels may be eliminated from hybrid seed by the proper combination of