

problem of duplicate copies is eliminated; if by chance (one in 256, again assuming concordance) both gametes contribute the same mutant, it will be homozygous immediately and will be recognizable as such.

An equally efficient approach with some additional advantages over that just presented is to treat pollen; an investment of less than 100 plants for treatment plus a test by selfing of 2000 M_1 plants will produce 500 mutants for an efficiency of 0.25 (slightly less because of the plants needed for the original crosses with treated pollen). Pollen treatment has several advantages: (1) Each mutant seen is an independent event, so that except for normal attrition all mutants produced are saved--this allows easy comparison of mutation rates and of the relative frequencies of different mutant types. (2) Variations among different lines or between sexes in primordial cell number are not a concern in the estimation and comparison of mutation rates. (3) Dominant mutants are easily recognized as such and are ready for immediate testing.

The economic advantage described here for minimum sampling in mutation experiments applies equally well to the development of elite lines for breeding programs.

M.G. Neuffer

UNIVERSITY OF MISSOURI

and

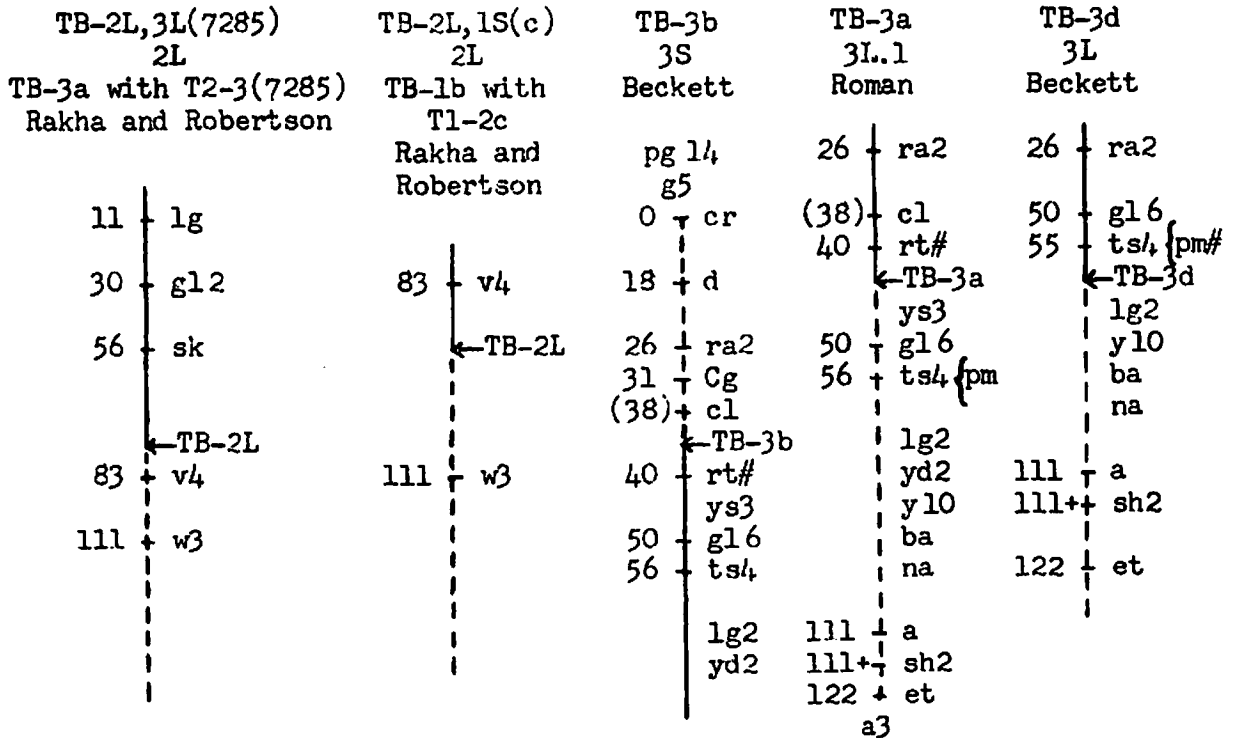
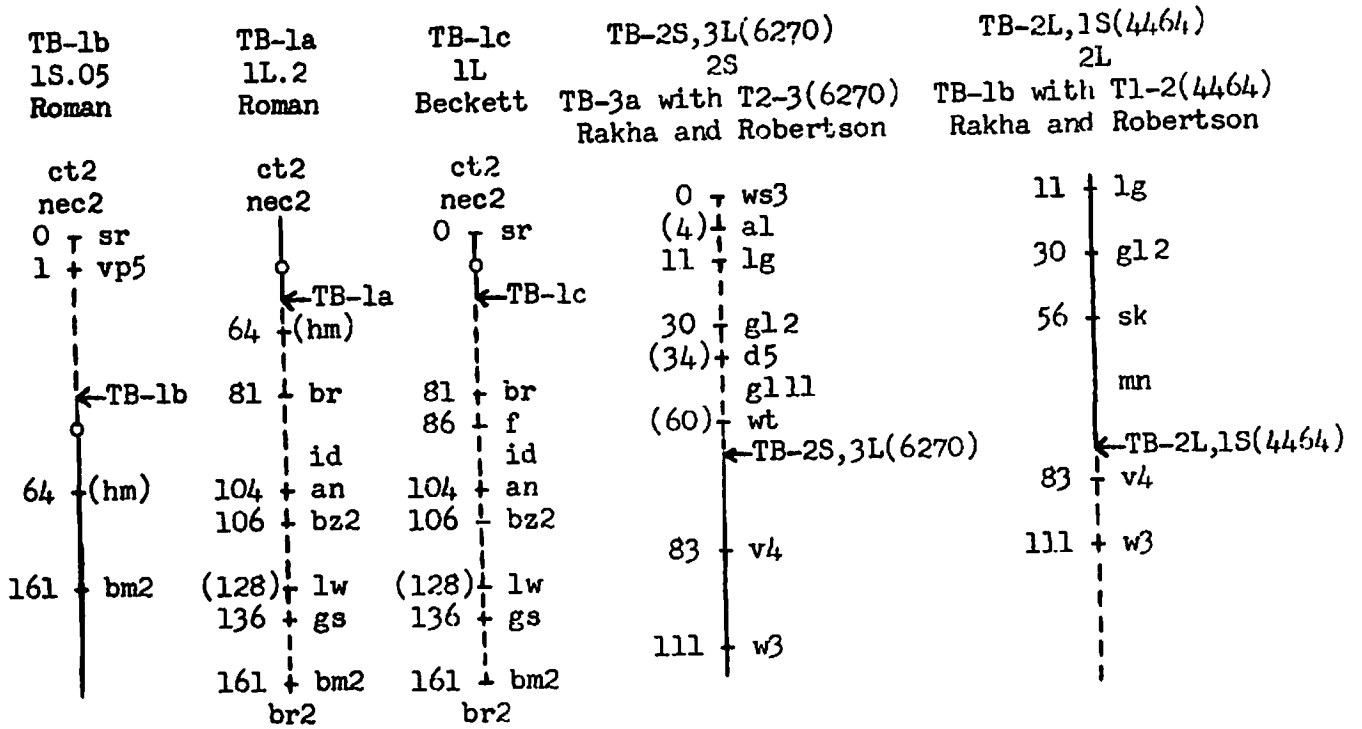
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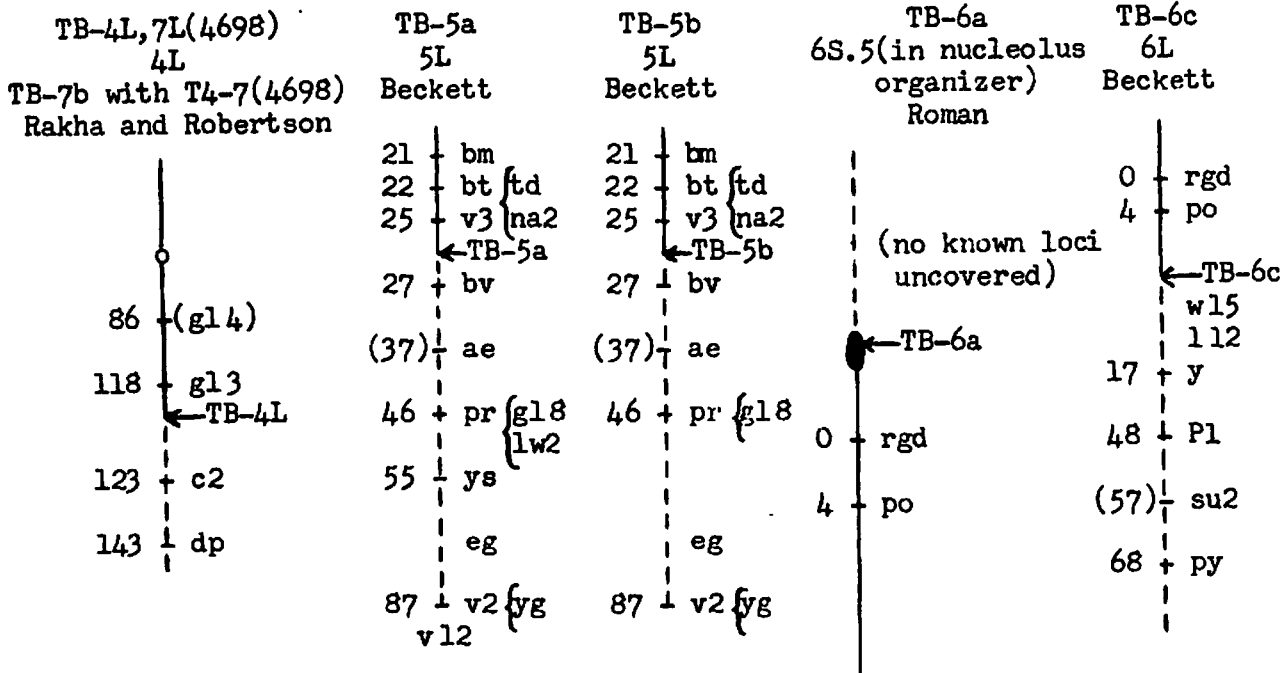
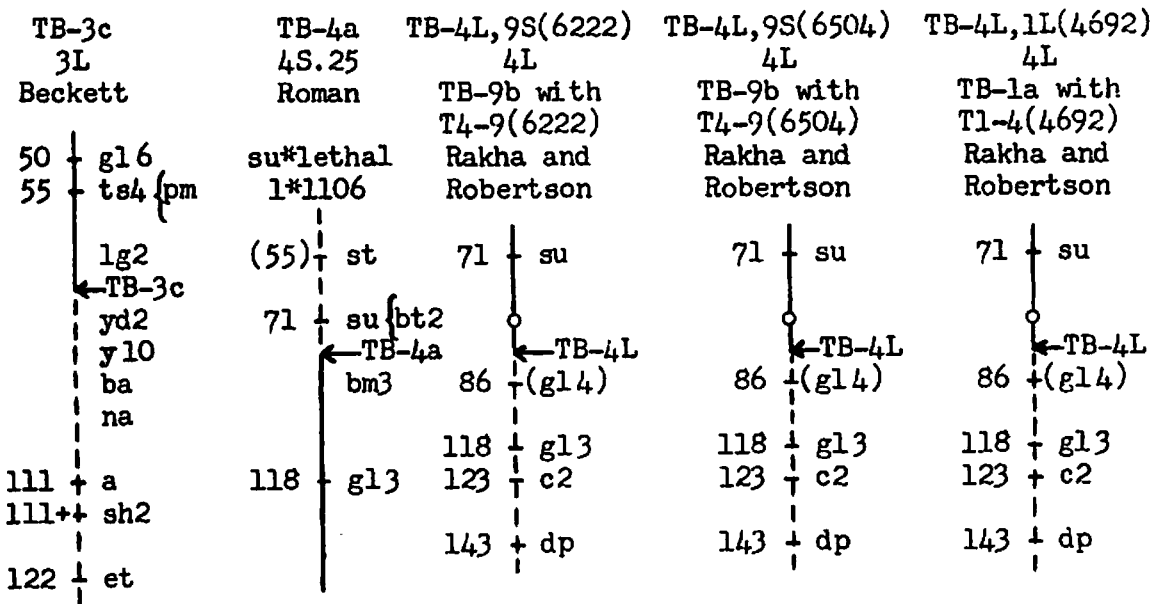
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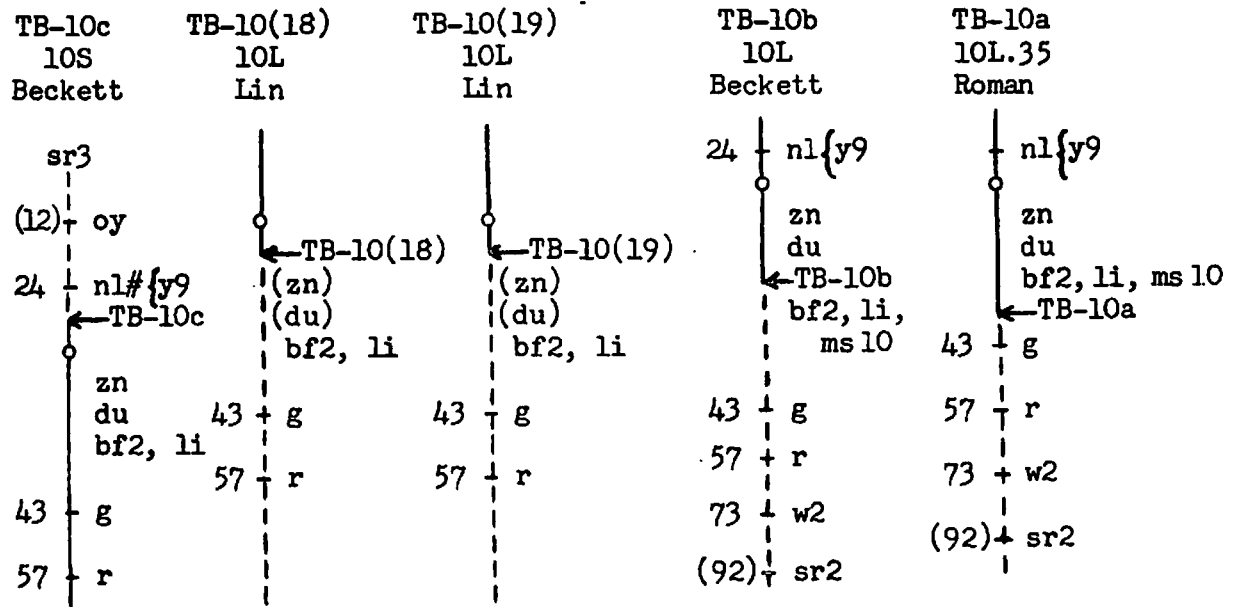
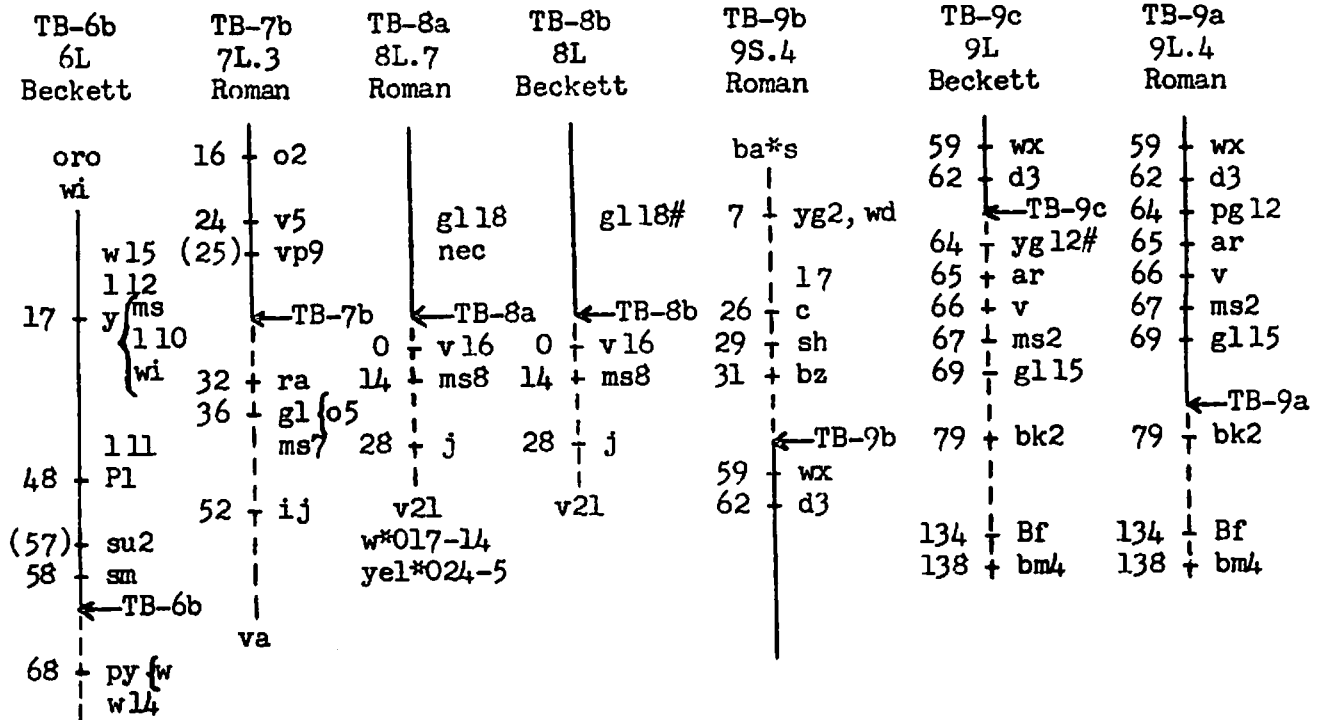
Genetic breakpoints of the B-A translocations of maize — The accompanying chromosome maps summarize the data I have collected on the genetic breakpoints of B-A translocations. The chromosome arm, cytological map position if known, and originator are given for each. The portion of each chromosome arm translocated to the centric segment of the B chromosome is shown as a broken line; therefore, all genes shown along the broken line were found to be "uncovered" by the translocation and all genes beside the solid portion were not uncovered.

I have tested all loci listed with the exception of hm (tested by Roman and Ullstrup, Agron. Jour. 43:450-454, 1951), gl4 (tested by Rakha and Robertson, Genetics 65:223-240, 1970) and, for TB-10(18) and TB-10(19), zn and du (tested by Lin, MGCNL 48:182-184). Loci that should be retested for confirmation of position with respect to the B-A translocation are marked by the symbol "#". Map positions of loci are usually given, if known, and other factors are inserted in what is believed to be the proper place or listed at the end of the arm.

GENETIC BREAKPOINTS OF B-A TRANSLOCATIONS







| segment attached to centric portion of B chromosome (genes in this region are uncovered by the B-A translocation)

| segment to which the distal portion of the B chromosome is attached (genes in this region are not uncovered by the B-A translocation)

o-centromere

●-nucleolus organizer

#-gene should be retested to confirm position

Herschel Roman's TB-7a (7L.95) is probably no longer extant. If anyone has viable seed, I would appreciate getting a small supply.

In addition to the translocations listed here, Lin (MGCNL 48:182-184) has reported 36 more B-A translocations on 10L.

Several changes in existing chromosome maps are required to accommodate the B-A translocation data; these changes are summarized as follows:

1. Although wt on chromosome 2 at map position 60 is uncovered by TB-2S,3L(6270), gs2 (position 54) is not, so the order of these 2 loci should be reversed. Tentative results indicate that sk may be uncovered, but the hypoploids produced by this translocation are often too weak to classify for this trait.
2. As reported in MGCNL 44:154-155, c1 is uncovered by TB-3b, so the centromere must lie to the right of c1.
3. TB-3c uncovers ba (72) and y10(75), but not lg2(83), so lg2 must lie to the left of ba and y10.
4. As reported in MGCNL 47:145-147, tests with TB-10b and TB-10c place li in the long arm of chromosome 10. Lin's data (MGCNL 48:182-184) from TB-10(18), -(19) and -(26), establish that the order is centromere, zn, du; my data from TB-10b (MGCNL 47:145-147) establish that bf2, li and ms10 are next (the order within this group is still not known). Data from TB-10a and TB-10(32)(Lin) establish that g comes next, followed by r, as previously determined by ordinary linkage tests.

Although unlikely, it is possible that inversions on the translocated chromosomes may be present in some cases, giving an improper gene order. Therefore, appropriate linkage tests are needed to confirm the above conclusions.

I wish to thank R. H. Whalen for calling to my attention the need for bringing together my data on the genetic breakpoints of the B-A translocations.

J.B. Beckett

Knotted leaf mutants — Five new knotted leaf mutants have been identified. These mutants have been given the temporary designation of K-2, K-3, K-4, K-5 and K-6. K-2 and K-3 occurred as spontaneous mutations in the inbred line Mo14W. Both are similar in expression to the original knotted leaf mutant on chromosome 1 except that the severity of the knotting is much less. K-3 differs from K-2 by leaving large holes in the leaf surrounding the knotted areas.

K-4 knots only the ligule and occurred in a commercial hybrid. K-2, K-3 and K-4 behave as dominant genes. Allelism tests with the original knotted mutant so far have been inconclusive due in part to varying expressivity and penetrance.

The K-5 and K-6 mutants have small "cup like" intrusions parallel to the midrib on the upper leaves at about the time of tasseling. K-5 was found by