heterozygous for a teosinte segment (derived originally from either Florida or Nobogame teosintes in separate experiments), then the trivalent frequency shot up abruptly to a range of 60 to 70 percent (MNL 45 and 46).

In order to resolve the question as to whether the sudden increase in trivalency involving Tr7 was due to heterozygosity for the fourth chromosome bivalent or due solely to the introduction of the teosinte segment, a control addition monosomic for Tr7 was developed in which the teosinte segment was homozygous, again involving the fourth chromosome segment from Florida teosinte in one family and from Nobogame teosinte in another family.

At pachytene Tripsacum chromosome 7 was usually found as a univalent folding back on itself. It showed a very feeble association with the homozygous teosinte bivalent. More often it was found sticking to the terminal region of one or the other of the corn chromosomes. In a few instances it was in close proximity to the long arm of corn chromosome 4 although the common Su_1 locus is in the short arm, but it did not show any chiasmatic association. In one case the Tripsacum univalent was found sticking to the terminal knob of chromosome 9 of maize. The trivalent frequency scored at Diakinesis and Metaphase I was about 20 percent in comparison with the 60 to 70 percent rate seen in the triple heterozygote.

On the basis of the preceding cytological observations it appears that Tr7 has not shown sufficiently greater affinity to teosinte chromosome 4 than to maize chromosome 4 to account for the high rate in the triple heterozygote. Perhaps a slightly heteromorphic condition in the maize-teosinte heterozygote releases cryptic affinity for Tr7 that enhances the trivalent frequency, thereby explaining its high rate in the triple heterozygote.

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5. Revision in a tentative identification of an extracted Tripsacum chromosome.

We had previously made a tentative (20 + 1) identification of an extracted Tripsacum chromosome (MNL 46:111) that had a partial ability to suppress expression of bm_2 as being Tr3, based on a length of 40.3 u

and an arm ratio of 3.1:1 in the monosomic condition. Since then, a change in the maize background and the derivation of the disomic condition for this Tripsacum chromosome requires a revision in this identification.

From the progenies derived by selfing the 20 + 1 plants we have now obtained three plants showing a 20 + 2 condition (72-445-5; 470-5, 471-8). From 31 observations on these three plants, the Tripsacum chromosome averaged 32.8 u with an arm ratio of 3.9:1 and, as previously evident, possessed a terminal knob in the long arm. This chromosome is more similar to Tr5 than to Tr3 in the idiogram of the original T. dactyloides prepared by Chandravadana et al. (1971). Because Tr5 had been assigned by us as the Tripsacum homeolog to maize chromosome 9, we have intercrossed this new Tr5 (?) to the old Tr5 as well as to the maize marker gene stock for M9.

In any case, it is clear that the new Tr5 (?) is not a partial homeolog to M1 as we had tentatively reported. Under the growing conditions of 1973, the expression of bm_2 in the presence of the extra Tripsacum chromosome was undeniable. Some plants carrying this extra Tr chromosome showed the multiple recessives, sr_1, br_1 and bm_2 loci marking almost the entire length of M1.

We shall check the synaptic behavior of the new Tr5 (?) with our original extraction of Tr5 in a hybrid made for this purpose. Also we shall check the capacity of new Tr5 (?) to cover the M9 markers known to be present on the old Tr5.

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6. On the relation of Tr9, a Tripsacum partial homeolog to M2, to maize M10.

Because Tr9, which carries the Ws_3, Lg_1, Gl_2, b, Sk, Fl_1 loci in common with the short arm of M2 occasionally associates with the short arm of M10 and may even transfer its terminal knob to M10 (MNL 44:117-119), this Tripsacum chromosome was tested for its capacity to cover the nl and g_1 markers on M10. For this purpose, these chromosome 10 recessives were added to the multiple recessive marker stock for chromosome 2. Within