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

the F_2 of an outcross of the M2 tester carrying Tr9 to the compound tester for M2 and M10, an equal number of Tr9 plants showed nl g_1 (16) as did not show nl g_1 (17 plants). We can only conclude that if Tr9 does have any true homeology to M10, it does not include the nl and g_1 loci. Because the nl and g_1 loci mark both arms of M10, the possibility of any true relationship to Tr9 seems slight.

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1. Selection of lines in relation to the effect of the opaque-2 gene on kernel weight in maize.

In order to reduce the negative effect on yield associated with the conversion of normal strains into the opaque-2 endosperm type, it has been suggested that material be selected in which the expression of the opaque-2 gene on kernel weight would be modified (Alexander, 1966; Sreeramulu and Bauman, 1970). This suggestion is based on experimental results showing that the effects of opaque-2 on the physical traits of the endosperm vary with the genetical background. The phenomenon has been studied by comparing different hybrid combinations (Lambert et al., 1969; Salamini et al., 1970) and analyzing the variation within F_2 (Ottaviano and Cabulea, 1971) and synthetic varieties (Ottaviano, unpublished data).

This note gives a brief account of the results obtained by a selection experiment. The material used was derived from F_2 plants of the previous study; it consisted of half-sib families open pollinated by homozygous (o_2o_2) plants of the same population. Selection was made taking into account kernel weight differences between normal and opaque-2 endosperm types. To evaluate these differences using segregating kernels of the same ear, only heterozygous (o_2+) plants were used. The same procedure was adopted in the successive generation in which homozygous (++) plants were discarded on the basis of progeny testing. In each