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et al., 1970) and analyzing the variation within F_2 (Ottaviano and Cabulea, 1971) and synthetic varieties (Ottaviano, unpublished data).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

generation, plants were selfed and the kernels produced were used for the evaluation. Within each half-sib group a two-way selection was performed: one way to reduce and the other to enhance the differences between opaque and normal kernels. The lines produced will be referred to as (+)-lines and (-)-lines, respectively.

A very high positive association was found between the differences and the weight of normal kernels, indicating that most of the difference variability is due to a multiplicative effect of o_2. Therefore, in each group the values were adjusted to the mean weight of normals. This criterion should make it possible to utilize the variability due to genes interacting with o_2 rather than to select mainly for kernel weight. After two generations of selfing and selection 36 S_3 lines (18 for each way of selection), the parents of the population (P_1= Bianchi o_2o_2, P_2= W64A++) and the F_1 (P_1 x P_2) were crossed with two testers: WF9 o_2o_2 and R109B o_2o_2. As the selected lines were held in heterozygosis (o_2+) it was possible to produce homozygous (o_2o_2) and heterozygous (o_2+) progeny from each cross, so the effect of selection was evaluated considering both genotypical combinations.

The hybrids produced were planted together in two replications to form two complete blocks of 39 plots. Each plot consisted of two 10-plant rows: one formed by the normal progeny ($\pm$ o_2) and the other by opaque-2 progeny (o_2o_2). Homozygous plants and five heterozygotes were detasselled in order to ensure open pollination by only segregating plants.

Ears of five detasselled plants were harvested in each row. Opaque and normal kernels from these segregating ears were separated and 50 kernels of each were weighed. Statistical analysis was performed using mean values per row; however, since nonsignificant differences due to the plant genotype (o_2o_2 vs. ++) within crosses were found, the results are given in terms of mean values per plot.

The most significant results concerning differences in weight between normal kernels and their opaque-2 counterparts are given in the table.

Differences in 50 kernel weight (g.) between normal and opaque-2.

		observed	adjusted	% of normal
(WF9$\underline{o}_2$) x				
(+)-Lines	mean	0.54	0.59	4.0
	range	0.07 - 1.05	0.33 - 0.91	0.6 - 6.6
(-)-Lines	mean	0.73	0.69	5.3
	range	0.37 - 1.27	0.53 - 1.02	3.0 - 8.6
(-)-(+)		0.19*	0.10*	1.3*
P_1, F_1, P_2		0.27,0.62,1.08	0.32,0.64,1.32	1.9,4.6,8.8
(R109$\underline{o}_2$) x				
(+)-Lines	mean	1.01	1.05	7.1
	range	0.51 - 1.59	0.83 - 1.36	4.1 - 10.3
(-)-Lines	mean	1.25	1.20	8.5
	range	0.46 - 1.83	0.74 - 1.57	3.5 - 10.9
(-)-(+)		0.24	0.15*	1.4*
P_1, F_1, P_2		0.92,0.92,0.69	0.56,0.91,0.78	6.4,6.5,4.9

*significant differences (P < 0.05). Ranges are evaluated considering hybrid means.

Differences were linearly associated with kernel weight. Therefore, in order to evaluate selection response, the values were adjusted to the overall mean of normal kernels. Significant differences were found according to both criteria of comparison (original and adjusted means) and these results were the same with both testers. The values of the hybrids involving parental lines fell within the range of values of hybrids obtained crossing testers with selected lines; this shows that a recombination of genes interacting with $\underline{o}_2$ introduced by both parents of the original population took place. Mean differences between the two groups of lines obtained by two generations of selection, even though significant, were not very great. This fits in with the prediction

made on the basis of genetical analysis of the population; in fact, the variability in the reduction of kernel weight due to the effect of opaque-2 was found to be under genetical control ($h^2 = 0.52$), but its amount was not very large when the portion attributable to the multiplicative effect of the gene was removed. However, it must be remembered that the hybrids compared differed in only one parent. Therefore, the differences would probably have been larger if crosses were made between lines selected in the same direction. Moreover, since the pollen has effects on endosperm development, the differences between hybrid values might have been under-estimated because each combination was not pollinated by its own pollen.

In many cases it was observed that the reduction of differences between normal and opaque kernels was associated with modification of the endosperm phenotype, which shows visible translucent sectors. It re-mains to be seen whether this phenomenon changes the chemical composi-tion of the endosperm.

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2. **Nucleolar patterns in microspore quartets of trisomic 6, in relation to trisomic inheritance.**

Trisomic inheritance of the nucleolar chromosome (chromosome 6) was investigated. Microsporocytes collected from trisomic plants were examined in connection with the behavior of the three chromosome 6 units during meiosis. Root tips were collected, and their chromosomes counted, in a sample of individuals obtained from the cross: 2n+1 x 2n. Compari-sons were made of the trisomic 6 frequency (38%) found among the progeny of this cross with the meiotic behavior of the chromosomes present in triplicate. The data indicated that post-meiotic losses of n+1 spores and/or of 2n+1 zygotes or embryos may take place, in addition to meiotic losses, and may partially account for the failure of trisomic types to reach the theoretical frequency of 50% in the progeny.

The finding of post-meiotic losses in this trisomic 6 material contradicts Einset's statement (Genetics 28:349-364, 1943) that failure of the extra chromosome to be transmitted to 50% of the progeny through the egg apparently was due only to its elimination as a univalent during