In the first case, crossing over has no genetically detectable effect (fig. a); in the second case crossing over is limited to a region of effective pairing (fig. b). Any exchange occurring in this region gives rise to a crossover strand missing the entire R locus and to another carrying it in duplicate. Assumption (b) does not account for the pale mutants. Rather, their low frequency of production suggests that they are associated with a mutational event of a regulatory component (see 2a). Even though the data do not allow us to make a definite choice among these plausible assumptions, the working hypotheses proposed are easily amenable to experimental tests that should resolve the problems of the structural organization of R^{ch}.

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2. Effects of the "opaque-2" gene in maize: quantitative variations.

The quality of protein in the corn kernel can be genetically modified by the action of the gene opaque-2 (o_2) when homozygous. The main effect of this gene is an increase of lysine and tryptophan content (Mertz, Bates and Nelson, 1964).

In addition to this variation, some negative effects are correlated with the same genotype; the most important characters involved are kernel weight and kernel texture (Alexander et al. 1969; Salamini et al. 1969).

Some experimental results obtained during the last few years have shown that most of the effects of the o_2 gene can vary in intensity in relation to the genetical background. Therefore, it has been suggested that it should be possible to select genetical backgrounds in which the negative effects of o_2 would be minimized. Following the same reasoning, it should also be possible to select for high Tryptophan/Protein and Lysine/Protein ratios. The experiment described in this report was designed to evaluate all these possibilities, studying the genetical variability of those characters in a segregating population to which the selection could be applied.

An F_2 population segregating for o_2 was the material used for this research. The parent o_2/o_2 was an inbred line selected by Prof.

Bianchi from an Italian population and as the $+/+$ parent the line W 64 A was used. Plants from phenotypically normal F_2 kernels ($+/+$ and $+/o_2$) were crossed according to the design N.C.M.1 in order to produce progeny families from heterozygote parents ($o_2/+$). On the basis of the progeny test, all the families in which one parent was homozygous $+/+$ were discarded. After this operation, 45 full-sib families from 15 pollen parents, each mated to three seed producing plants, were left. This material was sown in an isolated field in three randomized blocks, each one including 15 full-sib families from a set of five pollen parents. Each family was replicated twice within the block. Each plot consisted of three 10-plant rows: the central one from the opaque-2 progeny (o_2/o_2) and the two lateral ones from the phenotypically normal progeny ($o_2/+$ and $+/+$). Plants of the lateral rows of each plot were detasseled and, in order to insure a sufficient amount of pollen, the field was bordered with o_2/o_2 plants of the same population. In order to obtain information about the variations of the differences between opaque-2 kernels and their normal counterparts in individual plants, observations were made on only the segregating ears of the plants in the lateral rows. On the average, 8 plants per family (four plants per plot) were considered; the family size was less than 8 only in few cases.

Opaque-2 and normal kernels from these segregating ears were separated and 40 kernels of each were weighed. Six samples of both phenotypical classes taken from six different plants of each family, making a total of 270 individuals, were analyzed for protein, tryptophan and oil content.

Total nitrogen content of each sample was determined by the "Technicon Autoanalyzer" following the method of Andress-Ferrari. The results were multiplied by 6.25 to obtain protein percent. Tryptophan content was assessed adopting the method suggested by Hernandez and Bates and using the "Technicon Autoanalyzer" for the colorimetric reading. A Soxhlet apparatus with hexane extraction was used for the oil content analysis.

The results obtained expressed as mean values for each class are given in Table 1. Clearly the weight is reduced in opaque-2 kernels. However, the degree of this effect varies according to the family

Table 1

Mean values and differences of normal and opaque-2 kernels from segregating ears

Characters		Normal ($++o_2$)	Opaque ($o_2o_2o_2$)	Differences: ($o_2o_2o_2$)-($++o_2$)	
				absolute	% of normal
40 - Kernel wt., g.	mean range	9.75 9.15 - 10.74	8.51 7.94 - 9.08	-1.24** 0.92 - 1.56	-12.67 -10.22 - -15.97
Protein g/100	mean range	13.22 12.66 - 13.74	12.50 12.08 - 12.88	-0.72** -0.55 - -1.01	-5.43 -4.11 - 7.34
Tryptophan g/100	mean range	0.099 0.089 - 0.114	0.166 0.141 - 0.183	0.067** 0.051 - 0.078	66.70 56.49 - 79.23
Tryptophan % of protein	mean range	0.75 0.70 - 0.87	1.33 1.17 - 1.48	0.58** 0.51 - 0.67	76.28 64.68 - 90.74
Oil g/100	mean range	5.57 4.91 - 6.42	5.83 5.25 - 6.65	0.26** 0.09 - 0.47	4.74 1.73 - 8.72

** : indicates significant differences ($P<0.01$)

Ranges are evaluated considering half-sib family means.

considered; the range of the variation between full-sib families is wider than that shown in Table 1 and in only a few plants is the weight of opaque kernels the same as that of their normal counterparts.

The genetical control of this variation was studied by means of variance analysis of the absolute differences taking into account the family (full-sib and half-sib) classifications of the plants. As the correlation between these differences and the weight of normal kernels showed a high degree of association ($\underline{r}$ estimated within half-sib families varied around 0.75), this variation might be the result of the scaling effect. Therefore, an unbiased estimate of the genetical variance of this character can be obtained either by changing the scale or by reducing the variances of the part associated with the weight of normal kernels. Adopting this second procedure it was possible to show that there exist genes which modify the phenotypical expression of opaque-2 with mainly additive-type effects.

Protein percent in the normal and opaque phenotypes was 13.22 and 12.50, a significant difference.. This difference is not very great and some plants were found in which the difference was reversed. The variability of this reduction was not correlated with protein content of normal kernels and resulted mainly from genetical effects of the non-additive type.

As expected tryptophan content of opaque-2 kernels was higher than that of their normal counterparts. Of great interest for our study was the evaluation of this character as the Tryptophan/Protein ratio. From the variability of this ratio it is possible to obtain information on the changes of the biochemical expression of opaque-2 and to determine whether this character can be genetically modified.

The results of the analysis of variance showed that the differences observed should be easily fixed in inbred lines. It is important to point out that the variation of this effect was not correlated with the value of the Tryptophan/Protein Ratio in phenotypically normal kernels.

Oil percent in normal and opaque kernels was 5.56 and 5.83 and the difference between these values is significant. This difference

can easily be explained by the increase of the germ/total weight ratio of the opaque kernels. The analysis of the data did not show that this effect was conditioned by the genetical background.

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E. Ottaviano

3. Non-random transmission of chromosomes in trisomic plants.

Trisomy is an abnormal situation which would be easily eliminated in nature unless it is selected for. One of the homologous chromosomes may be lost as a univalent during meiotic divisions. Moreover, spores with eleven chromosomes sometimes abort and, in the male gametophyte, they suffer a severe competition with the normal ones. Nevertheless, we would expect these events to involve each of the three chromosomes at random unless the chromosomes differ from each other with respect to pairing, disjunction or otherwise.

Trisomic plants whose three homologous chromosomes are marked by three different alleles of the same locus offer a convenient genetic material whereby the transmission of individual chromosomes or chromosome regions can be followed. This is the case in trisomic 10 plants with the markers $\underline{R}^{st}$, $\underline{R}^{nj}$ and $\underline{r}$. Some of these plants were pollinated by an $\underline{r}$ tester and their progenies examined. Four phenotypical classes are expected ($\underline{R}^{nj}\underline{R}^{st}$, $\underline{R}^{st}$, $\underline{R}^{nj}$ and $\underline{r}$) but their relative frequencies are not readily predictable since segregation of three homologous chromosomes, as well as of the $\underline{R}$ alleles, is affected by a number of factors such as: pairing configurations, frequency and location of crossing over with respect to the centromeres, frequency of crossing over between the markers and the centromere, and frequency of loss of a chromosome as a univalent with different phenotypic consequences depending on whether a dominant or a recessive marker is lost.

However, in spite of any complication, two phenotypical classes ($\underline{R}^{st}$ and $\underline{R}^{nj}$) are expected to appear with the same frequency if the three chromosomes do not differ in any regard.

Thirteen ears were obtained from the cross: $\underline{R}^{nj}\underline{R}^{st}\underline{r}$ x $\underline{rr}$ and, after classifying their progeny, they were ordered according to the departure of the $\underline{R}^{st}$ and $\underline{R}^{nj}$ classes from the expected 1 : 1 ratio (Table 1). The series starts with a significant deficiency of $\underline{R}^{nj}$ (ear