Cytological analysis of the hybrid su gl3 x bt2 gl4 — There has been some evidence of duplicate genes in corn (Rhoades, 1951), and their bearing on chromosome repatterning and evolution has thus far been only a matter of speculation; the following experiment was carried out in the hope of obtaining some concrete evidence in this direction.

The progeny from a cross between the \underline{su} $\underline{g13}$ and $\underline{bt2}$ $\underline{g14}$ chromosome 4 marker gene stocks was cytologically analyzed. The F_1 plants were all non-glossy and were studied at pachytene for possible chromosomal aberrations. An attempt was made to determine if the similar genes, $\underline{g13}$ and $\underline{g14}$, were separated by an inversion or if there was any indication of a duplication of a segment. In all the observations meiosis was regular. Chromosome 4 at pachytene was normal and did not show any heteromorphic structural differences.

The presence of duplicate genes is usually attributed to certain chromosomal aberrations in some ancestral generation. But in the above experiment where similar genes were introduced into the hybrid plant there was no indication of any such abnormalities. Therefore in this case there is now, at least, no evidence for a common origin of these two glossy loci.

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Fertilization ability of four inbred lines — Variability of male gametophyte competition in maize appears to be a widespread phenomenon not limited to the effects of the well known <u>Ga</u> genes (Pfahler, Genetics 52:513, 1965 and Genetics 57:513, 1967; Mulcahy, Nature 249:491, 1974). It has been observed that this character shows a variability which is typical of quantitative traits and that the differences between genotypes, at least in the case of pollen grown on synthetic medium, depend on genes that are expressed in the gametophytic phase (Sari Gorla et al., in press).

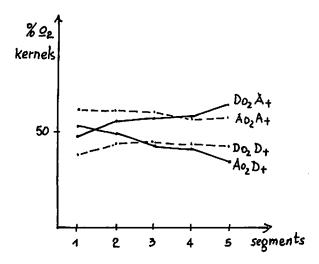
Competitive ability of pollen can be measured as the relative fertilization frequency of pollen of two different genotypes on the same ear; the competitive ability of four inbred lines was studied in this way.

The inbred lines RNY, B37, WF9 and C123 (which, for the sake of brevity, will be indicated as A, B, C and D, respectively) were compared, two by two, in all possible combinations. Mixtures were made with equal quantities of two different types of pollen, each marked for the presence of the normal or mutant allele

of the opaque-2 gene, which can be recognized on the kernels. The mixture was used to pollinate a hybrid obtained from two opaque-2 inbred lines.

For each line-pair tested four pollen mixtures were made: A+ Ao2 and B+ Bo2 (i.e., opaque and normal versions of the same line), which would test the effect of the marker gene and also the ability of both pollen types to reach the base of the ear; and A+ Bo2 and Ao2 B+, which would test the competitive ability of A versus B. The ears obtained were divided transversely into five segments in which the relative frequency of normal and opaque kernels was computed; the increase in fertilization frequency from the apex to the base of the ear (where the styles are the longest) by one of the two pollen types is an index of its relatively greater rate of growth. The results obtained for each pair can be expressed as the percentage of opaque kernels in the segments of ear from the apex (first segment) to the base (fifth segment). Figure 1 gives the A versus D comparison as an example.

Figure 1. A comparison of the competitive ability of pollen from two inbred lines.



The A+ $\underline{Ao2}$ and D+ $\underline{Do2}$ mixtures did not show any significant differences in the frequencies of the two kernel types in the different segments; this indicates that $\underline{o2}$ does not influence pollen tube growth. The same finding was obtained for lines C and D. In contrast, the A+ $\underline{Do2}$ combination revealed a significant increase of $\underline{o2}$ kernels from the first to the fifth segment, and when the $\underline{o2}$ version was the A line the opposite effect was observed. Thus, D line pollen has a greater competitive ability than that of the A line.

Results obtained from all line combinations are summarized in Table 1, in which A' and A" stand for normal and opaque versions of the same line, and the results of the comparisons are indicated in the conventional manner. The four lines included in this experiment revealed different fertilization abilities;

differences between these same lines were also observed with regard to pollen tube growth rates on artificial medium, which was in fact why they were chosen.

Table 1. Summary of the competitive abilities of pollen from four inbred lines.

	A	В	С	D
Α	Al = Ah	A>B	A>C	D>A
в	ь—		C>B	
c		1	C¹ ≈ C"	C>D
D				D'= D!

If the direct comparison between C and D lines is not considered, it is possible to rank the four inbred lines according to their competitive ability (D, A, C, B). However, when the results obtained with a mixture of C and D pollen are taken into account, it is found that they do not conform to the linear order indicated. This fact is not very easy to explain, but since the same female genotype was used for every comparison, it may suggest that some kind of interaction exists between pollen tubes growing in the same silk.

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Spontaneous losses of dominant markers of chromosome 9 analyzed in maize endosperm—
The consequences of chromosome breakage can be phenotypically observed in maize endosperm, if a multiple recessive tester is pollinated by a stock having the corresponding dominant alleles. Loss of dominant factors in a portion of the endosperm tissue is often due to breakage of the paternal chromosome in the tested region. This method was described by A. C. Fabergé (Z.i.A. Vererb. 87:392-420, 1956), who studied the effects of various agents on induced breakage of chromosome 9. The present report concerns the spontaneous breakage of this chromosome.

Two sets of crosses were made, and a sample of the progenies was examined. In cross #1 a single locus was considered. The stocks were those developed by E. H. Coe, Jr., which yield a high rate of maternal monoploids and are of the following genotypes: