

somes 4, 6, and 9 act upon the genotype $\underline{A}_1 \underline{A}_2 \underline{c} \underline{R}$ to produce blotches of color.

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2. The blotching system involving the R locus.

The previous data have indicated that there might be as many as six loci in this blotching system. Test crosses made in 1959 show that the 81:175 ratios repeatedly encountered involved segregation for both \underline{A}_2 and \underline{C} as well as for two blotching genes. Ratios suggesting segregation for five or more loci are now known, from studies made in 1959, to involve preferential segregation. Thus only two \underline{Bh} factors are now identified for this system. One of these is known from data previously reported to be located on chromosome 4; the other appears to be on chromosome 2. Previous data had shown linkage between \underline{Bh} and floury endosperm; recent data show that the floury endosperm gene involved is that on chromosome 2. The data available, since they involve an F_2 , are not satisfactory for determining a linear sequence but, since \underline{Bh} appears to be strongly linked with \underline{Fl} and \underline{V}_4 and only weakly linked with \underline{Lg} , \underline{Gl}_2 , and \underline{B} , it is tentatively assumed that this \underline{Bh} lies between \underline{Fl} and \underline{V}_4 .

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3. The gene for tunicate a compound locus?

Because the allele, \underline{tu}^h which originated in our cultures as a mutant of \underline{Tu} , has almost exactly half of the effect on various characters which \underline{Tu} exhibits, we have for some years suspected that the \underline{Tu} locus may be a compound one, similar to bar eye in *Drosophila*, resulting from the duplication through unequal crossing over of a more simple locus. We have for some years been developing stocks to test this possibility. A uniform inbred strain of the genotype $\underline{Su} \underline{Tu} \underline{Gl}$ was crossed with a uniform inbred strain of the genotype $\underline{su} \underline{tu} \underline{gl}_3$. The F_1 was backcrossed on a second uniform inbred of the genotype $\underline{su} \underline{tu} \underline{gl}_3$. In the population resulting from this backcross, approximately half of the plants should be $\underline{Tu} \underline{tu}$. Mutations to \underline{tu}^h in the previous generation would result in plants of the genotype $\underline{tu}^h \underline{tu}$ which should be distinguishable from $\underline{Tu} \underline{tu}$. In a population of 8134 plants, 4129 were tunicate. Of these two appeared phenotypically to be heterozygous half tunicate ($\underline{tu}^h \underline{tu}$). Both of these are crossovers between \underline{Su} and \underline{Gl} : one being the genotype $\underline{Su} \underline{gl}$, the other $\underline{su} \underline{Gl}$.

Progeny tests to determine whether these plants are mutants or phenocopies are being made in the Florida winter planting. If these prove to be mutants and are identical then it is possible that the \underline{Tu} locus is a compound one which has originated during domestication. But if the mutants are different it is probable that the compound locus is an ancient one characteristic of the genotype of wild corn.

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4. Linkage relations of an unstable gametophyte mutant.

The position on chromosome 4 of an unstable mutant originating in a maize-teosinte cross and affecting preferential segregation with respect to the \underline{Su} - \underline{su} locus has now been determined by a three-point test. The data from the back cross $\underline{ga} \underline{su} \underline{gl}_3 \times \underline{Ga} \underline{Su} \underline{Gl}_3$ follows:

$\underline{ga} \underline{su} \underline{gl}_3 \quad \underline{ga} \underline{su} \underline{gl}_3$