

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

P. C. Mangelsdorf

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 .

P. C. Mangelsdorf

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.

P. C. Mangelsdorf
W. C. Galinat

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:

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

Plant No.	Su Gl_3	Su gl_3	su Gl_3	su gl_3	Totals	% Su	% Gl_3	% C. O. Su Gl_3
211-4	76	39	79	136	330	34.8	47.0	35.8
5	39	33	63	95	230	31.3	44.3	41.7
7	106	39	59	147	351	41.3	47.0	27.9
11	38	28	40	69	175	37.7	44.6	38.9
12	77	53	75	103	308	42.2	49.4	41.6
Totals	336	192	316	550	1394	37.9	46.8	36.4

Previous experiments have indicated that this Ga is not transmitted through the pollen. If this is true then the percentage of Su and Gl_3 represent respectively the percentages of crossing over between Ga and Su and between Ga and Gl_3 . On this basis the linear sequence must be Ga Su Gl_3 and Ga must be on the short arm of chromosome 4, perhaps fairly near the terminal end.

P. C. Mangelsdorf
S. M. Sehgal

5. The mutagenic effects of homozygous and heterozygous teosinte chromosomes in an isogenic stock.

There has been some indication from previous studies that the mutagenic effects of teosinte chromosomes incorporated into an inbred strain (A158) are greater when the introduced teosinte chromosomes are heterozygous than when they are homozygous. To test this possibility further we conducted the following experiment: Eight different modified strains of A158 each containing one or more introduced teosinte chromosomes in the homozygous condition were scored for seed and seedling abnormalities. These same eight strains were crossed with the original A158 and the F_2 ears were scored for seed and seedling abnormalities. The results are shown in the following table:

Stock	No. ears Scored	Percent with Abnormalities		
		Seed	Seedling	Total
Control, pure A158	100	0.0	0.0	0.0
A158 with homozygous teosinte chromosomes	876	10.0	6.6	16.6
A158 with heterozygous teosinte chromosomes	658	15.2	19.4	34.6

It is probable that some of the abnormalities found are phenocopies rather than inherited mutations. However the fact that the frequency of abnormalities is more than twice as great when the teosinte chromosomes are heterozygous than when they are homozygous is highly significant. It suggests that crossing over between maize and teosinte chromosomes may be involved in the production of abnormalities. Since maize and teosinte chromosomes are probably not completely homologous, crossing over between them may often be unequal. This could result in deficiencies and duplications.

W. C. Galinat

6. Genetic control of phytomer development.

Although different regions of the plant differ greatly in final form, despite their common genom, their initial repetitious design, the so-called "phytomer," is identical. The role of specific genes in modifying development of the phytomeric parts, an internode with attached leaf and an axillary bud with associated prophyll for specialized functions, is revealed by certain genetic variants. In the central region along the plant the leaves are greatly enlarged and widely separated by elongated internodes