The inbred strain Oh45, which is not itself blotched, proved in test crosses to be homozygous for the Bh factors on chromosome 4, 6, and 9. This suggested that there must be at least one more Bh factor in the system and that this factor was absent in Oh45.

Since Oh45 is rr and the three Bh testers are RR we should expect 9:7 ratios in the F_2 generation of the crosses between these stocks if the crosses are heterozygous for only one Bh gene and 27:37 ratios if they are heterozygous for two Bh genes.

In the cross of Oh45 with the tester for the Bh gene on chromosome 6 the segregation was 773 blotched:1064 not blotched on three ears—almost a perfect 27:37 ratio indicating that two of the Bh genes in addition to the R gene are segregating. On a fourth ear the ratio was 261:252 which is significantly different from either a 27:37 or a 9:7 ratio.

In the F_2 of the cross of Oh45 with a tester for Bh on chromosome 4, four ears segregated alike producing 621 blotched:1340 non-blotched—a perfect 81:175 ratio—indicating that this cross is segregating for four factors: R and three Bh genes. Since only one of the recessive bh genes is contributed by the Bh tester, the other two must come from Oh45.

In the cross of Oh45 with the tester for Bh on chromosome 9, four ears were similar in their segregation producing 780 blotched: 1304 nonblotched seeds. This ratio differs significantly from either a 27:37 or an 81:175 ratio. The results may represent modifications due to linkage or the presence of a gametophyte factor.

The results, though in some respects somewhat inconsistent, indicate that at least four and possibly five factors are involved in this Bh system. The reasons for the modified ratios remain to be determined.

Additional data on linkage relations indicate that the Bh gene on chromosome 4 is located on the long arm since it shows almost no linkage with de^{t1} which is located on the short arm. Data presented in last year's News Letter indicated that the Bh gene on chromosome 9 is located on the long arm. More recent data showing 45.3% crossing over between Bh and Sh and 47.5% between Bh and Wx tend to confirm this.

<div align="right">P. C. Mangelsdorf</div>

11. Number of genes in the r-R blotching systems.

Previous data have indicated that the number of genes involved in this system might be as high as six or seven. For some reason it has not yet been possible to isolate testers for all of these. Data ob-

tained this year, however, confirm the earlier conclusions with re-
spect to the number of genes. An ear, known to be homozygous for one
Bh factor and apparently segregating for five or six others, produced
progenies segregating in ratios of 243:781, 81:175, 27:37, 9:7, and
3:1. The actual numbers were respectively for blotched and nonblotch-
ed seeds: 198:667, 203:418, 142:207, 141:103, 182:54. The results indi-
cate that there must be at least six factors in the system. The effort to
identify testers for all of these will continue.

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12. Vestigial glume modifiers.

Having finally obtained homozygous Vg Vg inbred strains in a back-
ground approaching that of sweet corn inbred P39, it became apparent
that two and possibly three modifying genes are essential to insure good
pollen production under adverse environmental conditions. Previously
we reported that the effect of a certain weak tunicate allele in re-
storing tassel glumes to Vg plants bearing "glumeless" ears was suffi-
cient to permit normal pollen production. But such restored Vg tassel
glumes are flattened rather than boat-shaped and consequently they do
not enclose the young anthers tightly enough to prevent shriveling of
the dehiscence pore under conditions of heat and drought. However, if
the young anthers are colored a cherry red by a certain R-allele, then
there is sufficient additional protection provided by light obstruction
within the walls of the anther to permit normal pollen production. At
the actual time of pollen shedding, this red color fades out to a pale
shade in contrast to the purple-anthered character which remains per-
manently dark.

All three of these genes (Vg, tu^W, R^r) are dominant to normal
and this facilitates back-crossing them into a quality-acceptable
inbred (P39) of sweet corn. The final selection of the homozygous
condition of these dominants following inbreeding may be accomplished
in F$_2$ by the following techniques. Since one of the effects of tu^W
is to cause the semi-liguleless expression of the Vg gene to become
recessive in our stocks, selection of the "liguleless" plants in seg-
regating stocks identifies the Vg Vg plants. Classification as Vg Vg
on a basis of ligulelessness may be accomplished in either the seedling
or mature plant. The R^{r}R^r plants in segregations may be identified by
progeny tests of seedlings grown in sand flats. The tu^W gene is incom-
pletely dominant so that the homozygotes may be recognized by comparison
of tassel glumes for a given Vg condition determined as mentioned pre-
viously.

The possibility of a third important modifying gene for Vg exists.
In some stocks which have the necessary tu^W and R-allele modifiers, the
filaments of Vg Vg anthers are slow to elongate and when they do length-
en they are less than one-half normal length. Sometimes these Vg Vg