HARVARD UNIVERSITY Cambridge, Massachusetts

1. The blotching system involving the c locus.

Three of the four genes involved in the blotching system which causes color to develop in the aleurone in the presence of recessive conversed have now been located on the chromosomes through backcross linkage tests. The data follow:

			Number of Individuals					Recombinations	
Row	Genes	X¥	Ху	Υx	ху	Total	No.	Percent	
184	Bh Su	169	148	130	198	645	278	43.1	
186	Bh Y	378	168	158	304	1008	326	32.3	
181	Bh Wx	248	306	300	245	1099	493	44.8	

The Bh gene on chromosome 4 shows very weak linkage with Det-1. Since this locus appears to be on the short arm of chromosome 4 (Bianchi) it is probable that Bh is on the long arm. Rhoades (MNL, 1948) has already shown that the Bh on chromosome 6 is closely linked to Pl and, therefore, is on the long arm of that chromosome. Since the Bh locus on chromosome 9 shows 44.9 per cent of crossing over with Wx, it could be on either arm and, if on the short arm, is probably near Yg. If this is true, then the experiment reported by Rhoades (MNL, 1945), in which he found less blotching in the aleurone of kernels carrying a chromosome 9 deficient for the c locus than in kernels with normal chromosomes, may involve the loss of the Bh factor on chromosome 9 and thus represents a case of dosage differences with respect to Bh factors rather than an indication that c is mutating to C.

2. The blotching system affecting the r locus.

Three of the five or more loci involved in the system in which blotches of color appear in the aleurone in the presence of recessive r have been located through backcross linkage tests. Two of the genes are linked with Su. Earlier data had indicated that two of the genes in this system were linked with each other. This occurred in modifications of 9:7 ratios as follows:

Ear	Total	No. Bh	Percent Bh
241A-1	582	401	68, 9
2	513	317	61.8
3	546	366	67.0
4	372	249	66.9
243-3	409	267	65.3
4	425	258	60.7
5	340	226	66.5
Totals	3187	2084	65.4

This deviation from the 56.75 percent of <u>Bh</u> seeds expected in a normal 9:7 ratio can be explained in terms of linkage between two <u>Bh</u> factors on the same chromosome with crossing over of the order of 25 percent.

There is no doubt that one of these \underline{Bh} loci is on chromosome 4, as the following data from backcross linkage tests show:

Row		Number of Individuals					Recombinations	
	Genes	XY	Ху	Ϋ́χ	ху	Total	No.	Percent
188	Bh Su	262	205	204	261	932	409	43.9
189	Bh Su	325	211	156	322	1014	367	36.2
	Totals	587	416	360	583	1946	776	39.9

Since the two <u>Bh</u> loci are linked, and one is definitely on chromosome 4, the other must also be on chromosome 4 and may show strong linkage or weak linkage with <u>Su</u> depending on the sequence of the genes. The data from two ears in which <u>Bh-bh</u> segregated in a 1:1 ratio, and <u>Su-su</u>, in a 3:1 ratio, follow:

Ear	Su Bh	Su bh	su Bh	su bh	Totals
178-1	95	116	35	54	300
1-2	153	157	45	53	408
Totals	248	273	80	107	708

tions rcent

ich sive <u>c</u>

43.1 32.3

t-l.
(Bianchi)
has
l and,
locus
could
If this
which
romosome
nes,

epresents han an

ich ssive genes genes lificaThe deviation from independent inheritance is not significant, although there is in both ears a higher percentage of <u>Su</u> seeds in the <u>Bh</u> class than in the <u>bh</u> class.

The data so far available indicate that the sequence is <u>Bh</u>, <u>Bh</u>, <u>Su</u>, and that it involves a total map distance of the order of 80 units. This suggests that both <u>Bh</u> genes occur in the long arm of chromosome 4.

The third <u>Bh</u> gene in this system appears to be linked with <u>Fl</u>. Following are the data from three backcross ears:

		Recombination				
Row	Bh Fl	Bh fl	bh Fl	bh fl	Total	No. Percent
190	241	295	275	261	1072	502 46.8

If the <u>Fl</u> gene is the one on chromosome 2, then <u>Bh</u> is almost certainly on the short arm of this chromosome, near the \underline{lg} locus. Crosses have been made to test this possibility.

3. Bh genes in common in the two blotching systems.

Since the two blotching systems involving the <u>c</u> and <u>r</u> genes are similar in their manifestations, and since both involve a locus on chromosome 4 with 40-45 percent crossing over between <u>Bh</u> and <u>Su</u>, the question arises whether the two systems have loci in common. In preliminary tests in 1955, stocks lacking one <u>Bh</u> gene in the <u>c</u> system were crossed with stocks lacking one <u>Bh</u> in the <u>r</u> system. The F₁ seeds were, of course, completely colored because of the complementary action of <u>C</u> and <u>R</u>. Blotched seeds appeared in the F₂ in about one half of the progenies. This indicated that stocks from one system were carrying <u>Bh</u> genes of the other, but did not prove that the <u>Bh</u> genes themselves were identical since many stocks which have no blotching do carry one or more <u>Bh</u> genes.

A more critical test was made in 1956. Fifteen different stocks of the composition <u>cc</u> <u>rr</u> but carrying all four of the <u>Bh</u> genes of the <u>c</u> system, were pollinated by two stocks of the <u>r</u> system, each lacking one <u>Bh</u> gene. It was assumed that if only part of the fifteen stocks carrying the four <u>Bh</u> genes of the <u>c</u> system were capable of producing blotches in crosses with stocks lacking one <u>Bh</u> gene in the <u>r</u> system, then it could not be concluded that the two systems had genes in common. But if <u>all</u> of the stocks carrying the four <u>Bh</u> genes of the <u>c</u> system were capable of completing the <u>r</u> system, then there would be at least a strong indication, if not final proof, that one of the four genes in the <u>c</u> system is identical with one of the five or more in the <u>r</u> system.