It appears as though the phenotype of $\underline{a}^{m-1}$ $\underline{p}^{mo}$, both with and without Spm, is also brown but the low color level mosaic allele used makes color identification difficult.

R. I. Brawn

UNIVERSITY OF MARYLAND
Baltimore, Maryland

1. On the origin of abnormal 10.

In spite of the considerable interest in abnormal 10 (K10) that has been generated by the studies of Rhoades, Dempsey, and others, the origin of this chromosome has not been established. Ting (Chromosoma 9:286, 1958) postulated that the extra segment of K10 arose by simple translocation between normal 10 and a B-chromosome. This hypothesis was tested by comparing meiosis in haploids with either K10 or normal 10 (k10) and carrying a single B-chromosome. The desired haploids were obtained from diploids of the constitution $\underline{gl_6}/\underline{gl_6}$ K10/k10. The glossy seedlings were selected as putative maternal haploids among the progeny of the glossy female parents crossed with normal males. The male parent used was "stock 6", a high haploid-inducer line discovered and supplied by Dr. E. H. Coe. Sixty-four glossy seedlings were found among a total of 7,100 progeny obtained from this cross. Of these glossy exceptions, 58 were verified as haploids by chromosome counts in root tip squashes prepared by the Feulgen procedure. This is a haploid frequency of 0.82% which is considerably higher than the normal frequency of 0.1%. The chromosome 10 constitution was also determined in each haploid during the examination of dividing root tip cells where K10 can be recognized at metaphase by the acrocentric position of its centromere. Microsporocytes at various stages of division were obtained in the greenhouse from two plants of each chromosome 10 constitution. First division cells were examined for the occurrence of bivalent configurations, that is, associations of two chromosomes joined by a chiasma. Since no metaphase plate is formed during first division in haploid pollen mother cells, it is difficult to distinguish anaphase I from metaphase I. Only those cells in which several univalents were seen passing to the poles were scored. At this stage the two chromosomes of a bivalent can be seen disjoining but connected by a bridge resembling a delayed chiasma. Normally, maize haploids possess ten chromosomes. However, all of the plants used in this study had eleven chromosomes including the normal complement of ten plus one B-chromosome also contributed by the maternal parent.

The frequency of bivalent configurations at metaphase I-anaphase I in k10 and K10 haploids was determined and the data are presented in Table 1. One bivalent occurred in approximately 14% of the microsporocytes from both k10 and K10 plants. Two cells from each type of haploid were found to have two bivalents while one cell from a k10 haploid had three bivalents. A total of 51 bivalents, or an average of 0.15 per cell, was observed among the cells from K10-carrying haploids. This is not

Table 1

The frequency of bivalent configurations at anaphase I in microsporocytes from k10 and K10 maize haploids containing one B-chromosome

Chromosome 10	Plant no.	No. cells with 11 uni.	9 uni. plus 1 biv.	7 uni. plus 2 biv.	5 uni. plus 3 biv.	Total
k10	167-3	120	18	1	1	140
	168-7	169	31	1	0	201
	Total	289	49	2	1	341
	%	84.75±1.88	14.37±1.90	0.59±0.41	0.29±0.29	
K10	167-4	100	20	0	0	120
	168-4	195	27	2	0	224
	Total	295	47	2	0	344
	%	85.76±1.81	13.66±1.86	0.58±0.41	0	

significantly different from the controls with a normal chromosome 10 where an average of 0.16 bivalents per cell was found.

Bivalent associations in haploids have usually been interpreted as resulting from crossing over between duplicate segments present in different chromosomes. If the B and K10 chromosomes had homologous regions that would pair with subsequent chiasma formation, bivalents would be expected to occur more frequently in haploids with K10 than in those carrying the normal chromosome 10. However, the similarity in bivalent frequencies in the two types of haploids fails to lend support to the hypothesis that the extra chromatin of the K10 chromosome came from a B type. Prophase associations have been observed to occur between the two chromosomes at meiosis in diploids (Ting MNL 33:37; Rhoades and Dempsey MNL 33:58). However, these adhesions may represent non-specific attraction of the heterochromatin present in both chromosomes.

A. J. Snope

UNIVERSITY OF MARYLAND
College Park, Maryland
Department of Horticulture

1. Transfer of ae wx to sweet corn by the translocation method.[1]

Dr. R. G. Creech has found that the amylose extender gene (ae), in addition to changing amylose content of the endosperm, causes a substantial increase in sugars and reduction in starch. He found also that ae combined with wx (waxy gene) and du (dull gene) wx, causes a very high increase in sugars and reduction in starch. Preliminary post harvest studies by Dr. E. V. Wann indicate that starch accumulation in the mutant gene types is much lower than that in normal su_1 corn. These findings were of sufficient promise to encourage the transfer of ae and wx to standard su_1 inbred lines.

The transfer of ae and wx requires that after the first backcross to the recurrent su_1 parent, each succeeding backcross must be selfed in order to isolate the Ae ae Wx wx genotype for further backcrossing. At the 5% probability level, at least 10 BC plants must be selfed to be certain of detecting the double heterozygote. In order to save time, paired selfs and backcrosses can be made simultaneously. The efficiency of this system based on the number of ears saved from the numbers of ears needed is 5%.

With the thought of increasing the efficiency of conversion, an ae wx homozygous translocation line was developed at the University of Maryland from an Ae wx translocation obtained from the Maize Genetics Coop. Linkage data show that ae is separated from wx by 11.5 ± 0.5 units.

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[1]Scientific Article No. A1343, Contribution No. 3903 of the Maryland Agricultural Experiment Station.