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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When using this translocation for the *ae wx* transfer, semi-sterility of pollen and scattered kernel set on the ear will identify the *Ae ae Wx wx* genotype for subsequent backcrossing. Since each backcross progeny segregates 1 Fertile: 1 Semi-Sterile, only 4 plants are needed to be certain of obtaining a semi-sterile plant. The probability of not selecting a semi-sterile plant in which crossing over had occurred between *Ae-ae* and/or *Wx-wx* is approximately 9:1. The probability of selecting 2 semi-sterile plants, both having crossovers would be quite remote (1:81). Therefore 2 paired selfs and backcrosses are all that are required to obtain each succeeding backcross. Observation of the selfed ear serves as a check on semi-sterility and whether or not a crossover between the dominant and recessive allelles had occurred. If either *ae* or *wx* does not segregate, a crossover occurred and the paired backcross ear would be discarded. Based on the number of ears saved from the number of ears needed, this method is 5 times more efficient than the previous method.

The number of plants necessary to obtain each backcross generation in the first method of transfer would be 20 (10 backcross plants and 10 recurrent parent plants). The number of plants needed in the second method would be 10(8 backcross plants and 2 recurrent parent plants). The translocation method is twice as efficient in regard to the number of plants needed for obtaining backcross populations.

When the desirable number of backcrosses have been made by using either conversion method, the *ae wx* segregates are selected from the last selfed progeny. However, in the translocation method, the *ae wx* segregates will also be homozygous for the translocation. The significance of this is that normal inbreds developed by the first method cannot be utilized as parents with inbreds developed by the translocation method. Such hybrids would be translocation heterozygotes and would have semi-sterile pollen and scattered kernel set.

In one way development of homozygous *ae wx* and *ae wx* $su_1$ translocation inbreds would be advantageous to a seedsman. It would guarantee that his inbreds could not be used indiscriminately by other seedsmen and would prevent the introduction of large numbers of hybrids that for all practical purposes are similar.

If the breeder wishes to obtain the *ae wx* combination on normal chromosomes, this can be accomplished by further selection for the crossover type in the following manner. The probability would be very low for selecting a double crossover *ae wx* type in the first self population after backcrossing is complete. Frequency of this genotype would be .000025 or 1 in 40,000 kernels. The most promising method would be to select *wx* kernels in this population. Approximately 1 in 225 *wx* kernels will be of the $\frac{++wx}{ae+wx}$ genotype. In order to obtain this number of *wx* kernels, 23 self pollinated ears are required; however, at the 5% probability level, it would require 70 selfed ears to provide enough *wx* kernels (670) to insure obtaining the $\frac{++wx}{ae+wx}$ genotype.

The following year self all 670 wx plants. At seed harvest, throw out all ears not segregating ae wx and also those that are semi-sterile (this will eliminate 50% of the ears).

The following year cross 300 ae wx plants to a normal chromosome line and also self these 300 ae wx plants.

In the following year allow the 300 crosses to open pollinate. Save the seeds of the selfs whose test cross did not have scattered seed set. These plants should have the ae wx combination on normal chromosomes.

The advantages and disadvantages of using the ae wx translocation method have been presented. It can be concluded that if one is satisfied with obtaining the ae wx homozygous translocation, this method is a great deal more efficient in transferring ae and wx to normal $su_1$ lines. If however, one feels it necessary to select further for the ae wx combination on normal chromosomes, the translocation method is inferior and probably should not be used.

R. J. Snyder