

the hybrid maize breeding program. It was found that a plot of about 14 square yards gave a coefficient of variation of about 10%. An increase in the size gave no reduction in the coefficient of variation while smaller plots showed a considerably increased C.V. The shape of the plots had no material effect on the coefficient of variation. Thus, under these circumstances where the plants were spaced 3 ft. x 2 ft., one plant per hill, and where the commercial maize variety "Improved Potchefstroom Pearl" was used, a plot of about 14 sq. yds. was found the most efficient size and nothing was gained by using larger plots.

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1. Linkage studies on chromosome 5 with special reference to ae.

a. v<sub>3</sub> - ae - pr linkage

Five ears of the genotype  $\frac{+ ae +}{v_3 + pr}$  were self-pollinated with the following results:

+++	+ ae +	v <sub>3</sub> ++	v <sub>3</sub> ae +	++ pr	+ ae pr	v <sub>3</sub> + pr	v <sub>3</sub> ae pr
544	290	155	12	175	5	124	0

colorless			
++	v <sub>3</sub> +	ae +	ae v <sub>3</sub>
290	112	102	5

Recombination %

v<sub>3</sub>-ae 22 ± 0.02 (colored or colorless)

ae-pr 14 ± 0.03

v<sub>3</sub>-pr 34 ± 0.02

The gene order is v<sub>3</sub> - ae - pr. The data indicate the map positions to be

10	32	46
v <sub>3</sub>	ae	pr

b. bv - ae - pr linkage.

Six ears of the genotype  $\frac{+ ae +}{bv + pr}$  were self-pollinated with the following results:

+++	+ ae +	bv ++	bv ae +	++ pr	+ ae pr	bv + pr	bv ae pr
269	123	41	7	39	4	121	2

colorless			
++	+ ae	bv +	bv ae
394	165	170	11

Recombination %

bv - ae 25 (colored + colorless)

ae - pr 20

bv - pr 16

In general, these data agree with the  $v_3 - \underline{ae} - \underline{pr}$  data presented above. There seems to be a high frequency of associated crossovers in these data. It appears that whenever a cross over occurs between  $\underline{bv}$  and  $\underline{ae}$  there tends also to be one between  $\underline{ae}$  and  $\underline{pr}$ . This would result in a reduced recombination percentage between  $\underline{bv}$  and  $\underline{pr}$  as is shown by the 16% recombination.

These data indicate (1) an increase in the total number of double crossovers, as well as (2) an increase in the number of two-strand double crossovers.

c.  $\underline{bm}_1 - \underline{ae} - \underline{pr}$  linkages.

A cross of  $\frac{+ \underline{ae} +}{\underline{bm}_1 + \underline{pr}} \times \frac{\underline{bm}_1 \underline{ae} \underline{pr}}{\underline{bm}_1 \underline{ae} \underline{pr}}$  gave the following results:

+++	+ ae +	++ pr	+ ae pr	bm ++	bm ae +	bm + pr	bm ae pr
1	124	27	11	16	10	141	3

Recombination %

$\underline{bm}_1 - \underline{ae}$	12.3
$\underline{ae} - \underline{pr}$	9.3
$\underline{bm}_1 - \underline{pr}$	19.2

Individual Gene Segregation

$\underline{Ae}$ 185:	$\underline{ae}$ 148*
$\underline{Bm}_1$ 163:	$\underline{bm}_1$ 170
$\underline{Pr}$ 151:	$\underline{pr}$ 182

\* Significant deviation from 1:1 ratio.

These recombination values appear to be normal in that the  $\underline{bm}_1 - \underline{pr}$  recombination is what one expects from the  $\underline{bm}_1 - \underline{ae}$ ,  $\underline{ae} - \underline{pr}$  recombination observed. However, two things are aberrant in these data: (1) the recombination values are smaller than expected when they are compared with the  $v_3 - \underline{ae} - \underline{pr}$  and  $\underline{bv} - \underline{ae} - \underline{pr}$  data presented above, and (2) the  $\underline{Ae}$  vs  $\underline{ae}$  segregation deviates from a 1:1 ratio.

These data indicate differential transmission of the  $\underline{ae}$  and  $\underline{Ae}$  alleles through the female. A comparison of the reciprocal crossover classes supports differential transmission rather than misclassification of  $\underline{ae}$ .

Differential transmission would reduce the measurable recombination between the genes and could account for the observed differences between these recombination values and those mentioned above for  $v_3 - \underline{ae} - \underline{pr}$  and  $\underline{bv} - \underline{ae} - \underline{pr}$ .

-- J. N. Jenkins

2. A new locus for studying the fine structure of the gene.

A method for studying the fine structure of the  $\underline{ae}$  locus has been developed. By overstaining with an excess of iodine and destaining with 25% alcohol and slight heating, one is able to differentiate  $\underline{wx} \underline{ae}$  from  $\underline{wx} +$  pollen. The  $\underline{wx} \underline{ae}$  pollen stains black and the  $\underline{wx} +$  pollen stains red. This technique allows a study of recombination at the  $\underline{ae}$  locus in a  $\underline{wx}$  background when different sources of  $\underline{ae}$  are crossed and the  $F_1$  pollen is observed.

-- Roy G. Creech