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*₃ - ae - pr linkage

Five ears of the genotype \(+ ae + v₃ + pr\) were self-pollinated with the following results:

\[
\begin{array}{cccccccc}
+ + + + ae + & v₃ + + & v₃ ae + + & + + pr + & ae pr & v₃ + pr & v₃ ae pr \\
544 & 290 & 155 & 12 & 175 & 124 & 0 \\
\end{array}
\]

<table>
<thead>
<tr>
<th>colorless</th>
<th>Recombination %</th>
</tr>
</thead>
<tbody>
<tr>
<td>+ + v₃ + ae + ae v₃</td>
<td>(v₃ ae) 22 (\pm) 0.02 (colored or colorless)</td>
</tr>
<tr>
<td>290 112 102 5</td>
<td>ae - pr 14 (\pm) 0.03</td>
</tr>
<tr>
<td></td>
<td>v₃ - pr 34 (\pm) 0.02</td>
</tr>
</tbody>
</table>

The gene order is \(v₃ - ae - pr\). The data indicate the map positions to be

\[
\begin{array}{ccc}
10 & 32 & 14 \\
v₃ & ae & pr \\
\end{array}
\]

b. *bv* - ae - pr linkage.

Six ears of the genotype \(+ ae + bv + pr\) were self-pollinated with the following results:

\[
\begin{array}{cccccccc}
+ + + + ae + & bv + + & bv ae + + & + + pr + & ae pr & bv + pr & bv ae pr \\
269 & 123 & 41 & 7 & 39 & 121 & 2 \\
\end{array}
\]

<table>
<thead>
<tr>
<th>colorless</th>
<th>Recombination %</th>
</tr>
</thead>
<tbody>
<tr>
<td>+ + + ae bv + bv ae</td>
<td>(bv - ae) 25 (colored + colorless)</td>
</tr>
<tr>
<td>394 165 170 11</td>
<td>ae - pr 20</td>
</tr>
<tr>
<td></td>
<td>bv - pr 16</td>
</tr>
</tbody>
</table>
In general, these data agree with the \( v_3 - ae - pr \) 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 \( b \) and \( ae \) there tends also to be one between \( ae \) and \( pr \). This would result in a reduced recombination percentage between \( b \) and \( pr \) as is shown by the 10% 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. \( bm_1 - ae - pr \) linkages.

A cross of \( \frac{+ ae +}{bm_1 + pr} \times \frac{bm_1 ae pr}{bm_1 ae pr} \) gave the following results:

\[
\begin{array}{cccccccc}
+ + + & + ae + & + + pr & + ae pr & bm + + & bm ae + & bm + pr & bm ae pr \\
1 & 124 & 27 & 11 & 16 & 10 & 141 & 3
\end{array}
\]

Recombination %

\( bm_1 - ae \) 12.3

\( ae - pr \) 9.3

\( bm_1 - pr \) 19.2

Individual Gene Segregation

\( Ae \) 188: \( ae \) 148

\( Bm_1 \) 163: \( bm_1 \) 170

\( Pr \) 151: \( pr \) 182

* Significant deviation from 1:1 ratio.

These recombination values appear to be normal in that the \( bm_1 - pr \) recombination is what one expects from the \( bm_1 - ae \), \( ae - pr \) recombination observed. However, two things are aberrant in these data: (1) the recombination values are smaller than expected when they are compared with the \( v_3 - ae - pr \) and \( by - ae - pr \) data presented above, and (2) the \( Ae \) vs \( ae \) segregation deviates from a 1:1 ratio.

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

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 \( v_3 - ae - pr \) and \( by - ae - pr \).

-- J. N. Jenkins

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

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

-- Roy G. Creech