Family 67-14 was planted from an ear with 26% non-sugary kernels (598u: 168 su); family 67-16 was planted from an ear with 25% non-sugary kernels (598u: 177 su). On the assumption that only Ga_1-carrying pollen functioned in these crosses, the percentage of non-sugary kernels measures Ga_1 - su_1 recombination. It is known, however, from previous work that in similar crosses, Ga_1-carrying pollen may function with a frequency of perhaps 2 to 5%.

Both families above were planted with non-sugary kernels. All plants were pollinated by a homozygous fl_2 source, and ears were classified for presence or absence of floury kernels.

In each of the above crosses, about one-third of the assumed Ga_1 - su_1 recombination occurred in the fl_2 - su_1 segment. This yields an estimated value of about 8% recombination between fl_2 and su_1, which is in good agreement with the data in (b) and (c), above. In the absence of other information, these results could be interpreted as indicating either the gene order Ga_1 - fl_2 - su_1 or the order Ga_1 - su_1 - fl_2; in the latter instance, su_1 - fl_2 recombination would be about 30-35%. From the other data above, however, it is clear that the first gene order is correct.

Combined data indicate that fl_2 - su_1 recombination is about 8%. On the current linkage map of Chromosome 4, fl_2 might therefore be assigned tentatively to position 63. Incidentally, the la - su_1 recombination value of 10.6% in (c), above, is in good agreement with the current tentative assignment of la to position 60 on the genetic map:

<table>
<thead>
<tr>
<th>Ga_1</th>
<th>st Ts_5</th>
<th>la</th>
<th>fl_2</th>
<th>sp_1</th>
<th>su_1</th>
</tr>
</thead>
<tbody>
<tr>
<td>35</td>
<td>(55) 56</td>
<td>(60)</td>
<td>(63)</td>
<td>66</td>
<td>71</td>
</tr>
</tbody>
</table>

E. B. Patterson

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Urbana, Illinois
Departments of Agronomy and Plant Pathology

1. Linkage relations of Ht.

In previous reports in the Maize News Letter (1963, 1965), data were presented which indicated that the dominant gene, Ht (chlorotic-lesion resistance to Helminthosporium turcicum), is located in the central region of the long arm of Chromosome 2. Additional data have now been accumulated on its position relative to w_2, and on some linkage relations in stocks heterozygous or homozygous for Inversion 2a (25.7; 2L.8).

(a) Position of Ht relative to w_2 in normal stocks

Progeny from the crosses indicated below were classified for Ht, and all plants were self-pollinated. The harvested ears were classified for Ch and seedling tested for segregation of w_4 and/or w_5.
(1) Standard (++++) X + w₂ + Ch

\[
\begin{array}{lcr}
\text{Region} & 66-(8353-8356) & \\
+ w + Ch & 22 \\
\text{v + Ht +} & 13 & \frac{v_4 - w_3}{17/71} = 24\% \\
+ + Ht + & 3 & \frac{v_4 - Ht}{18/71} = 25\% \\
\text{v w + Ch} & 6 & \frac{v_4 - Ch}{28/71} = 39\% \\
+ w \text{ Ht +} & 1 & \frac{w_3 - Ht}{3/71} = 4\% \\
\text{v + + Ch} & 12 & \frac{w_3 - Ch}{27/71} = 38\% \\
\text{v + Ht Ch} & 5 & \frac{Ht - Ch}{24/71} = 34\% \\
+ + + Ch & 1 & \\
\text{v w Ht +} & 0 & \text{Order:} \\
\text{1,2} & & \\
+ + \text{ Ht Ch} & 5 & \\
\text{v w + +} & 2 & \\
\text{Total} & 71 & \\
\end{array}
\]

(2) Standard (+++ ) X + Ht +

\[
\begin{array}{lcr}
\text{Region} & 65-(6171-6178) & \\
+ \text{ Ht +} & 39 \\
\text{w + Ch} & 45 & \frac{w_3 - Ht}{19/143} = 13.3\% \\
+ + \text{ Ch} & 6 & \frac{Ht - Ch}{43/143} = 30.1\% \\
\text{w Ht +} & 10 & \frac{w_3 - Ch}{56/143} = 39.2\% \\
+ \text{ Ht Ch} & 24 & \text{Order:} \\
\text{w + +} & 16 & \\
\text{1,2} & + + + & 2 \\
\text{w Ht Ch} & 1 & \frac{w_3}{13.3} \frac{Ht}{30.1} \frac{Ch}{39.2} \\
\text{Total} & 143 & \\
\end{array}
\]
chromatids, but in the case of Inversion 2a, there has been no evidence that either type is transmitted to viable progeny. In the above cross, in particular, chocolate and colorless pericarp occurred in equal frequency among the progeny.

(c) **Linkage relations in plants homozygous for Inversion 2a**

(1) \[
\text{Inv 2a} + B + \xrightarrow{\text{Inv 2a Ht b Ch}} X + b + X gl_2 + +
\]

<table>
<thead>
<tr>
<th></th>
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<th>B</th>
<th>+</th>
<th>7</th>
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<th>+</th>
<th>18</th>
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<tbody>
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<td>Ht</td>
<td>Ch</td>
<td>19</td>
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<th>+</th>
<th>b</th>
<th>Ch</th>
<th>4</th>
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<tbody>
<tr>
<td>Ht</td>
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<td>+</td>
<td>13</td>
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<th>+</th>
<th>Ch</th>
<th>15</th>
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<th>Ch</th>
<th>7</th>
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<tbody>
<tr>
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<td>+</td>
<td>4</td>
<td></td>
<td></td>
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</tbody>
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<table>
<thead>
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<th>+</th>
<th>+</th>
<th>Ch</th>
<th>2</th>
</tr>
</thead>
<tbody>
<tr>
<td>gl</td>
<td>Ht</td>
<td>+</td>
<td>13</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

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<th>+</th>
<th>b</th>
<th>Ch</th>
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<tbody>
<tr>
<td>Ht</td>
<td>B</td>
<td>Ch</td>
<td>3</td>
<td></td>
<td></td>
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</tbody>
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<table>
<thead>
<tr>
<th></th>
<th>1,2</th>
<th>+</th>
<th>Ht</th>
<th>+</th>
<th>2</th>
</tr>
</thead>
<tbody>
<tr>
<td>gl</td>
<td>+</td>
<td>Ch</td>
<td>0</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

\[
\text{Ht - B} = \frac{25}{52}
\]

\[
\text{Ht - Ch} = \frac{28}{52}
\]

\[
\text{B - Ch} = \frac{19}{52} = 37\%
\]

Combined data from progenies of testcrosses of plants homozygous for Inversion 2a which were scored for various combinations of markers are as follows:

\[
\text{lg}_1 - \text{gl}_2 = \frac{33}{90} = 36.7\% \\
\text{gl}_2 - \text{Ht} = \frac{6}{82} = 7.3\% \\
\text{gl}_2 - \text{Ch} = \frac{102}{227} = 44.9\%
\]

\[
\text{Ht - B} = \frac{25}{52} = 48.1\% \\
\text{Ht - Ch} = \frac{58}{121} = 47.9\% \\
\text{B - Ch} = \frac{58}{182} = 31.8\%
\]

Summary of gene order and linkage in homozygous Inversion 2a:

\[
\begin{array}{cccccccc}
\text{Inv 2a} & \downarrow & \text{Inv 2a} \\
\text{lg}_1 & 36.7 \ (90) & \text{gl}_2 & 7.3 \ (82) & \text{Ht} & 48.1 \ (52) & \text{B} & 31.8 \ (182) & \text{Ch} \\
\hline
\end{array}
\]

\[
\begin{array}{cccccccc}
\text{44.9} \ (227) & \hline
\hline
\text{47.9} \ (121)
\end{array}
\]
Combined data from these and other linkage tests involving markers in the long arm of Chromosome 2 are as follows:

\[ \frac{v_4}{v_3} = \frac{134}{486} = 27.6 \quad \frac{w_3}{w_2} = \frac{22}{214} = 10.3 \]
\[ \frac{v_4}{Ht} = \frac{129}{506} = 25.5 \quad \frac{w_3}{Ch} = \frac{108}{297} = 36.4 \]
\[ \frac{v_4}{Ch} = \frac{233}{506} = 46.4 \quad \frac{Ht}{Ch} = \frac{191}{562} = 34.0 \]

The two progenies in which \( w_2 \) and \( Ht \) were classified simultaneously (the crosses tabulated above) involve small numbers but agree in the location of \( Ht \) to the right of \( w_2 \). On the basis of combined data, the gene order and distances are as follows:

\[ v_4 \quad 27.6 \quad (486) \quad w_3 \quad 10.3 \quad (214) \quad Ht \quad 34.0 \quad (562) \quad Ch \]

(b) **Linkage relations of Ht in plants heterozygous for Inversion 2a**

\[ + \quad \text{Inv} \quad 2a \quad \text{Ch} \]
\[ \text{Ht} \quad + \quad X \quad + \quad + \]

<table>
<thead>
<tr>
<th>Region</th>
<th>(2961-3010)</th>
</tr>
</thead>
<tbody>
<tr>
<td>P</td>
<td>+ Inv Ch</td>
</tr>
<tr>
<td></td>
<td>Ht + +</td>
</tr>
<tr>
<td>1</td>
<td>+ + +</td>
</tr>
<tr>
<td></td>
<td>Ht Inv Ch</td>
</tr>
<tr>
<td>2</td>
<td>+ Inv +</td>
</tr>
<tr>
<td></td>
<td>Ht + Ch</td>
</tr>
<tr>
<td>1,2</td>
<td>+ + Ch</td>
</tr>
<tr>
<td></td>
<td>Ht Inv +</td>
</tr>
<tr>
<td>Total</td>
<td></td>
</tr>
</tbody>
</table>

The data above, together with \( gl^+ - Ht \) recombination reported in the 1963 MNL, may be summarized as follows:

\[ \text{Inv} \quad 2a \quad \downarrow \quad \text{Ht} \quad 3.3 \quad (420) \quad \downarrow \quad 17.0 \quad (420) \quad \text{Ch} \]
\[ \text{---16.8 \quad (709)----} \quad \text{---18.3 \quad (420)----} \]

The indicated \( Ht \)-Inv 2a recombination is presumably a measure of the frequency of 2-strand double crossovers within the inversion loop in which one crossover is to the left and one to the right of the \( Ht \) locus. Crossing over within the inversion is expected to yield two types of duplicate-deficient
The breakpoints of Inversion 2a are thus between \( g_1 \) and \( B \) in the short arm and between \( Ht \) and \( Ch \) in the long arm. There is an indication that \( Lg_1 - g_1 \) recombination may be increased in stocks homozygous for Inversion 2a.

E. B. Patterson  
A. L. Hooker  
K. M. S. Saxena  
D. E. Yates

2. Mapping studies of \( Rp_3 \).

In the 1964 MNL (p. 66), Hooker and Russell reported that a dominant gene for resistance to \( Puccinia sorghi \) present in line 178 showed linkage with \( T 3-9c \) (3L.09; 9L.12). This gene later proved to be allelic to \( Rp_3 \). In the data they reported, in plants heterozygous for \( T 3-9c \), \( wx \) and \( Rp_3 \) showed 11.7% recombination (32/274).

Further efforts to determine the map position of \( Rp_3 \) yielded the following information:

(a) In greenhouse classifications: \( d_1 - Rp_3 = 51/288 = 17.7% \) recombination

(b) In field classifications (255 plants): \( d_1 \ 23.1 \ Lg_3 \ 7.1 \ Rp_3 \)

(c) In greenhouse classifications (244 plants):

\[
\begin{align*}
Rp_3 & \ 3.3 \ g_1 \ 25.8 \ Lg_2 \\
& \ 28.3 \\
\end{align*}
\]

(d) Progeny of the following cross were scored in the field in 1967:

\[
+ + + \times + + Rp_3 \\
\leftarrow Lg_3 \ Rg \ +
\]

<table>
<thead>
<tr>
<th>P</th>
<th>+</th>
<th>+</th>
<th>Rp</th>
<th>202</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lg</td>
<td>Rg</td>
<td>+</td>
<td>233</td>
<td></td>
</tr>
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<td>Rg</td>
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<td>7</td>
</tr>
<tr>
<td>Lg</td>
<td>+</td>
<td>Rp</td>
<td>10</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>Lg</td>
<td>Rg</td>
<td>Rp</td>
<td>4</td>
</tr>
<tr>
<td>Total</td>
<td>456</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

At right above are indicated the recombination values based on the data as recorded. However, the four wild-type plants tabulated as region 2 recombinants in the table may represent contaminants, since no contamination marker was present in the male parent and hence their origin could not be verified. The occurrence of \( Rg \ Rp_3 \) progeny would have established the