

# RECENT LINKAGE STUDIES IN MAIZE

## MAIZE GENETICS COOPERATION

*Ithaca, New York*

Received October 13, 1938

**M**AIZE geneticists in different parts of the United States and in other countries have been cooperating very closely with each other since 1932 through the Maize Genetics Cooperation. In addition to freely exchanging seed stocks through the central repository, they freely exchange new methods, hypotheses, suggestions, and unpublished linkage data by means of an annual circular letter. This mimeographed Co-op News Letter does not constitute publication and none of the material in it may be quoted except by permission of the author.

The rapid progress in the genetics of maize may be largely attributed to this liberal exchange of unpublished material among maize workers. Some of the linkage data presented in the Co-op News Letter, however, are complete and should be published so that they will be more readily available to other geneticists. It is hoped that a group of short linkage papers can be published collectively each year in the same manner as they are presented in this article. Each paper must be considered a separate entity and any reference to the data in it must include the name of its respective author.

For further information on the genetics of maize the reader is referred to "A Summary of Linkage Studies in Maize," Cornell Memoir 180, June, 1935.

### I. Virescent seedling-16 ( $v_{16}$ ).

H. K. HAYES and M. S. CHANG, Minnesota Agricultural Experiment Station.

A virescent seedling in Minn. #13 corn was found to be linked with japonica and given the symbol  $v_{21}$ . RHOADES (Co-op News Letter, March 23, 1937) has found  $v_{16}$  and  $v_{21}$  to be allelic after trisomic tests had placed  $v_{16}$  also in chromosome VIII. Further linkage data of  $j$ ,  $ms_8$  and  $v_{16}$  are as follows:

| GENES<br>XY    | LINKAGE<br>PHASE | NUMBER OF INDIVIDUALS* |     |     |     | TOTAL | RECOMBI-<br>NATION<br>PERCENTAGE |
|----------------|------------------|------------------------|-----|-----|-----|-------|----------------------------------|
|                |                  | XY                     | Xy  | xY  | xy  |       |                                  |
| $J_1V_{16}$    | RB               | 82                     | 565 | 542 | 71  | 1260  | 12.1 ± 0.9                       |
| $J_1V_{16}$    | RS               | 354                    | 149 | 154 | 4   | 661   | 16.9 ± 3.7                       |
| $J_1M_{58}$    | CS               | 464                    | 39  | 23  | 135 | 661   | 9.5 ± 1.2                        |
| $M_{58}V_{16}$ | RS               | 337                    | 150 | 171 | 3   | 661   | 13.9 ± 3.8                       |

\* Dr. F. R. Immer supervised the taking of these data.

The order of the genes appear to be  $v_{16}-ms_8-j$ .

(Paper No. 1510 of the Journal Series of the Minnesota Agricultural Experiment Station.)

## II. Zebra striped-6 ( $zb_6$ ).

H. K. HAYES and M. S. CHANG, Minnesota Agricultural Experiment Station.

Emerson et al. list five cases of zebra striping that have been reported. There are two types, one that is expressed in the seedling stages and which may completely disappear as the plants approach maturity and the other that first appears in partly grown plants. The type reported here was obtained from an inbred line of Del Maiz sweet corn furnished by J. D. BARNARD of the Minnesota Valley Canning Company. The season in 1936 was very hot and dry. Germination of sugary seeds was much lower than normal. Zebra striping could not be classified until late summer when the weather was cooler. Classification was difficult in some cultures. The results given in the summary indicate Zebra striped is located in group 4.

| GENES<br><i>XY</i>                  | LINKAGE<br>PHASE | NUMBER OF INDIVIDUALS |           |           |           | TOTAL | RECOMBI-             |
|-------------------------------------|------------------|-----------------------|-----------|-----------|-----------|-------|----------------------|
|                                     |                  | <i>XY</i>             | <i>Xy</i> | <i>xY</i> | <i>xy</i> |       | NATION<br>PERCENTAGE |
| <i>Zb<sub>6</sub>Tu</i>             | CS               | 410                   | 64        | 64        | 90        | 628   | 23.3 ± 2.0           |
| <i>Zb<sub>6</sub>Gl<sub>3</sub></i> | RS               | 326                   | 148       | 135       | 19        | 628   | 33.9 ± 3.5           |
| <i>TuGl<sub>3</sub></i>             | RS               | 314                   | 160       | 147       | 7         | 628   | 20.5 ± 3.8           |
| <i>Zb<sub>6</sub>Su<sub>1</sub></i> | CS               | 4227                  | 259       | 175       | 361       | 5022  | 13.3 ± 0.5           |

The order of the genes appears to be  $su_1-zb-Tu-gl_3$ .

(Paper No. 1510 of the Journal Series of the Minnesota Agricultural Experiment Station.)

## III. Zebra seedling-4 ( $zb_4$ ).

H. K. HAYES, Minnesota Agricultural Experiment Station.

Zebra seedling,  $zb_4$ , has been located in chromosome 1 by the following studies:

| GENES                               | PHASE | <i>XY</i> | <i>Xy</i> | <i>xY</i> | <i>xy</i> | TOTAL | PERCENTAGE         |
|-------------------------------------|-------|-----------|-----------|-----------|-----------|-------|--------------------|
|                                     |       |           |           |           |           |       | RECOMBI-<br>NATION |
| <i>Zb<sub>4</sub>Br</i>             | RS    | 448       | 142       | 152       | 12        | 754   | 31.1               |
| <i>Zb<sub>4</sub>F<sub>1</sub></i>  | RS    | 455       | 135       | 158       | 9         | 757   | 28.0               |
| <i>Zb<sub>4</sub>Bm<sub>2</sub></i> | RS    | 487       | 103       | 144       | 23        | 757   | 46.0               |
| <i>Zb<sub>4</sub>P</i>              | CS    | 266       | 24        | 5         | 64        | 359   | 6.9                |

Progeny of one ear indicated that the *P* parent was heterozygous, giving the following segregation:

|    |    |    |   |    |     |     |
|----|----|----|---|----|-----|-----|
| CS | 63 | 30 | 2 | 24 | 119 | 6.7 |
|----|----|----|---|----|-----|-----|

(Paper No. 1510 of the Journal Series of the Minnesota Agricultural Experiment Station.)

IV. *Ramosa ear-2* ( $ra_2$ ).

H. K. HAYES, Minnesota Agricultural Experiment Station.

A culture of  $ra_2$  received from Dr. BRINK at Wisconsin proves to be similar to the one I have studied for many years. There is some variability in type of ear, some cultures showing rudimentary male flowers on the tips of some ears, irregularity of rows on the cob but no division of the cob as in  $ra_1$ . Other cultures have a divided cob on the tip of the ear but a solid cob at the basis.  $Ra_1$  can be separated from  $ra_2$  in the  $F_2$  of a cross.

(Paper No. 1510 of the Journal Series of the Minnesota Agricultural Experiment Station.)

V. *Opaque endosperm-2* ( $o_2$ ).

W. RALPH SINGLETON, Connecticut Experiment Station, New Haven.

Opaque endosperm is a character in which the endosperm has very little or no corneous starch. It is phenotypically indistinguishable from floury. Opaque, however, gives 25 percent recessive seeds on segregating ears, while floury gives the gametic ratio of 50 percent. Classification of opaque is good in flinty stocks. Separation can be facilitated by placing over a light. Normal seeds are translucent while the recessives are opaque. Opaque 2 is located on chromosome VII, probably beyond  $v_5$ , as is shown by the following data. (Opaque 1 has not yet been located in any linkage group.)

Linkage of  $o_2$ ,  $ra_1$ ,  $gl_1$ , and  $ij$ :

| GENES     | PHASE | XY   | Xy   | xY   | xy  | TOTAL | NO. | PERCENT |
|-----------|-------|------|------|------|-----|-------|-----|---------|
| $O_2Ra_1$ | RB    | 116  | 597  | 554  | 109 | 1376  | 225 | 16      |
| $O_2Ra_1$ | CB    | 127  | 15   | 15   | 112 | 269   | 30  | 11      |
| $O_2Gl_1$ | RS    | 3148 | 1595 | 1487 | 64  | 6294  |     | 20      |
| $O_2Ij$   | RS    | 405  | 169  | 184  | 30  | 688   |     | 37      |

A three-point test involving  $o_2$ ,  $gl_1$ , and  $ij$  gave the following counts:

| $F_1$ GENOTYPE | 0       | 1       | 2      | 1, 2  | TOTAL |
|----------------|---------|---------|--------|-------|-------|
| $o_2 + +$      | 467 513 | 115 150 | 94 123 | 28 23 | 1513  |
|                | 980     | 265     | 217    | 51    |       |
| $+ gl_1 ij$    |         | 17.5%   | 14.3%  | 3.4%  |       |

The recombination percentages of  $o_2$  and  $ra_1$  (repulsion phase), also  $o_2$  and  $gl_1$  indicate that  $o_2$  is to the left of  $v_5$  and within 2 or 3 units of  $v_5$ . The percentages between  $o_2$  and  $ij$  indicate that  $o_2$  is 2 or 3 units to the right of  $v_5$ .

VI. White sheath-3 ( $ws_3$ ).

M. M. RHOADES, U. S. Department of Agriculture, Washington, D. C.

The recessive mutant character white sheath<sub>3</sub> is characterized by the partial absence of chlorophyll in the culm and sheaths of the plant. The character can be readily classified both in the seedling and in later stages of development. The expression of the white sheath character is determined by a single recessive gene which has been designated  $ws_3$ . It is not allelic with the  $ws_1$  and  $ws_2$  factors reported by KEMPTON (1921) and CLARK (1932). The  $ws_3$  gene was first placed in chromosome II by trisomic tests. Linkage data to be presented here confirm this location.  $F_2$  data from

the selfing of  $\frac{ws_3 \ lg_1 \ Gl_2}{Ws_3 \ Lg_1 \ gl_2}$  plants are as follows:

| GENES      | LINKAGE PHASE | NUMBER OF INDIVIDUALS |           |           |           | TOTAL | RECOMBINATION PERCENT |
|------------|---------------|-----------------------|-----------|-----------|-----------|-------|-----------------------|
|            |               | <i>XY</i>             | <i>Xy</i> | <i>xY</i> | <i>xy</i> |       |                       |
| $Ws_3Lg_1$ | <i>CS</i>     | 1593                  | 103       | 114       | 431       | 2241  | 11                    |
| $Ws_3Gl_2$ | <i>RS</i>     | 1167                  | 529       | 505       | 40        | 2241  | 27                    |
| $Lg_1Gl_2$ | <i>RS</i>     | 1158                  | 549       | 514       | 20        | 2241  | 19                    |

The order is  $ws_3$ - $lg_1$ - $gl_2$ .

The linear order, with the intervening crossover percentages of the genetic factors in chromosome II as determined from the summary of data in EMERSON, et al (1935), is  $lg_1$  19  $gl_2$  19 *B* 7 *sk* 12 *fl\_1* 6 *ts\_1* 8 *v\_4*. MCCLINTOCK (1931) has shown that both  $lg_1$  and *B* lie in the short arm of chromosome II with  $lg_1$  occupying a more distal position. Studies of a reciprocal translocation involving chromosomes II and V (RHOADES, 1933) indicate that *ts\_1* is very close in terms of crossover units to the spindle fiber attachment region of chromosome II. Since the data presented here show that  $ws_3$  is to the left of  $lg_1$ , which has been placed cytologically near the end of the short arm, it follows that  $ws_3$  lies close to the distal end of the short arm. The map distance from  $ws_3$  to *ts\_1* is 74 units. There is an unknown amount of crossing over between  $ws_3$  and the distal end of the short arm so this value represents an estimate of the minimum length of the short arm of chromosome II. The length of the long arm of chromosome II used in these studies is 1.4 times that of the short arm. If the assumption is made that the amount of crossing over per unit of physical length is of the same order in the two arms it is possible to arrive at the estimate of 178 units as the total length of the genetic map of chromosome II. This estimate is in all likelihood less than the true map length of this chromosome but may closely approximate it.

## LITERATURE CITED

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