

Family 67-14 was planted from an ear with 26% non-sugary kernels (59Su: 168 su); family 67-16 was planted from an ear with 25% non-sugary kernels (59Su: 177 su). On the assumption that only Ga<sub>1</sub>-carrying pollen functioned in these crosses, the percentage of non-sugary kernels measures Ga<sub>1</sub> - su<sub>1</sub> recombination. It is known, however, from previous work that in similar crosses, ga<sub>1</sub>-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<sub>2</sub> 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<sub>1</sub> - su<sub>1</sub> recombination occurred in the fl<sub>2</sub> - su<sub>1</sub> segment. This yields an estimated value of about 8% recombination between fl<sub>2</sub> and su<sub>1</sub>, 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<sub>1</sub> - fl<sub>2</sub> - su<sub>1</sub> or the order Ga<sub>1</sub> - su<sub>1</sub> - fl<sub>2</sub>; in the latter instance, su<sub>1</sub> - fl<sub>2</sub> 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<sub>2</sub> - su<sub>1</sub> recombination is about 8%. On the current linkage map of Chromosome 4, fl<sub>2</sub> might therefore be assigned tentatively to position 63. Incidentally, the la - su<sub>1</sub> 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:

<u>Ga</u> <sub>1</sub>	st Ts <sub>5</sub>	<u>la</u>	<u>fl</u> <sub>2</sub>	<u>sp</u> <sub>1</sub>	<u>su</u> <sub>1</sub>
35	(55) 56	(60)	(63)	66	71

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### 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<sub>3</sub>, and on some linkage relations in stocks heterozygous or homozygous for Inversion 2a (2S.7; 2L.8).

#### (a) Position of Ht relative to w<sub>3</sub> 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 v<sub>4</sub> and/or w<sub>3</sub>.

(1)

$$\text{Standard ( + + + + ) } X \frac{+ w_3 + \text{Ch}}{v_4 + \text{Ht} +}$$

Region		66-(8353-8356)
P	+ w + Ch v + Ht +	22 13
1	+ + Ht + v w + Ch	3 6
2	+ w Ht + v + + Ch	1 1
3	+ w + + v + Ht Ch	12 5
1,2	+ + + Ch v w Ht +	1 0
1,3	+ + Ht Ch v w + +	5 2
	Total	71

$$\frac{v_4}{v_4} - \frac{w_3}{w_3} = 17/71 = 24\%$$

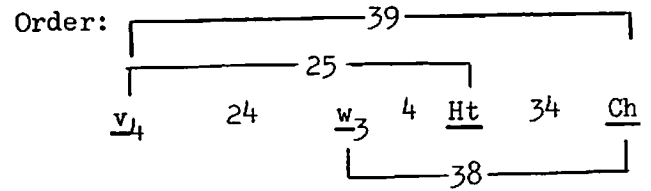
$$\frac{v_4}{v_4} - \frac{\text{Ht}}{\text{Ht}} = 18/71 = 25\%$$

$$\frac{v_4}{v_4} - \frac{\text{Ch}}{\text{Ch}} = 28/71 = 39\%$$

$$\frac{w_3}{w_3} - \frac{\text{Ht}}{\text{Ht}} = 3/71 = 4\%$$

$$\frac{w_3}{w_3} - \frac{\text{Ch}}{\text{Ch}} = 27/71 = 38\%$$

$$\frac{\text{Ht}}{\text{Ht}} - \frac{\text{Ch}}{\text{Ch}} = 24/71 = 34\%$$



(2)

$$\text{Standard ( + + + ) } X \frac{+ \text{Ht} +}{w_3 + \text{Ch}}$$

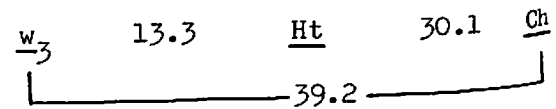
Region		65-(6171-6178)
P	+ Ht + w + Ch	39 45
1	+ + Ch w Ht +	6 10
2	+ Ht Ch w + +	24 16
1,2	+ + + w Ht Ch	2 1
	Total	143

$$\frac{w_3}{w_3} - \frac{\text{Ht}}{\text{Ht}} = 19/143 = 13.3\%$$

$$\frac{\text{Ht}}{\text{Ht}} - \frac{\text{Ch}}{\text{Ch}} = 43/143 = 30.1\%$$

$$\frac{w_3}{w_3} - \frac{\text{Ch}}{\text{Ch}} = 56/143 = 39.2\%$$

Order:



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) $\frac{\text{Inv 2a} \quad + \quad \underline{\text{B}} \quad +}{\text{Inv 2a} \quad \text{Ht} \quad \text{b} \quad \text{Ch}} \quad \text{X} \quad + \quad \text{b} \quad +$					(2) $\frac{\text{Inv 2a} \quad + \quad + \quad +}{\text{Inv 2a} \quad \underline{\text{gl}}_2 \quad \text{Ht} \quad \text{Ch}} \quad \text{X} \quad \underline{\text{gl}}_2 \quad + \quad +$				
P	+	B	+	7	P	+	+	+	18
	Ht	b	Ch	9		<u>gl</u>	Ht	Ch	19
1	+	b	Ch	4	1	+	Ht	Ch	1
	Ht	B	+	13		<u>gl</u>	+	+	1
2	+	B	Ch	7	2	+	+	Ch	15
	Ht	b	+	4		<u>gl</u>	Ht	+	13
1,2	+	b	+	5	1,2	+	Ht	+	2
	Ht	B	Ch	3		<u>gl</u>	+	Ch	0
				52					69

$$\frac{\text{Ht} - \underline{\text{B}}}{\text{Ht} - \underline{\text{Ch}}} = \frac{25/52}{28/52} = \frac{25}{28}$$

$$\frac{\underline{\text{B}} - \underline{\text{Ch}}}{\text{Ht} - \underline{\text{Ch}}} = \frac{19/52}{28/52} = 37\%$$

$$\frac{\underline{\text{gl}}_2 - \text{Ht}}{\underline{\text{gl}}_2 - \underline{\text{Ch}}} = \frac{4/69}{30/69} = 6\%$$

$$\frac{\underline{\text{gl}}_2 - \underline{\text{Ch}}}{\text{Ht} - \underline{\text{Ch}}} = \frac{30/69}{30/69}$$

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

$$\underline{\text{gl}}_1 - \underline{\text{gl}}_2 = 33/90 = 36.7\%$$

$$\text{Ht} - \underline{\text{B}} = 25/52 = 48.1\%$$

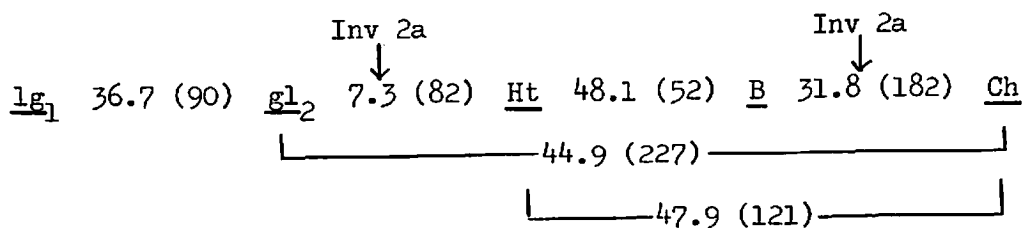
$$\underline{\text{gl}}_2 - \text{Ht} = 6/82 = 7.3\%$$

$$\text{Ht} - \underline{\text{Ch}} = 58/121 = 47.9\%$$

$$\underline{\text{gl}}_2 - \underline{\text{Ch}} = 102/227 = 44.9\%$$

$$\underline{\text{B}} - \underline{\text{Ch}} = 58/182 = 31.8\%$$

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



Combined data from these and other linkage tests involving markers in the long arm of Chromosome 2 are as follows:

$$\begin{array}{ll} \underline{v}_4 - \underline{w}_3 = 134/486 = 27.6 & \underline{w}_3 - \underline{Ht} = 22/214 = 10.3 \\ \underline{v}_4 - \underline{Ht} = 129/506 = 25.5 & \underline{w}_3 - \underline{Ch} = 108/297 = 36.4 \\ \underline{v}_4 - \underline{Ch} = 233/502 = 46.4 & \underline{Ht} - \underline{Ch} = 191/562 = 34.0 \end{array}$$

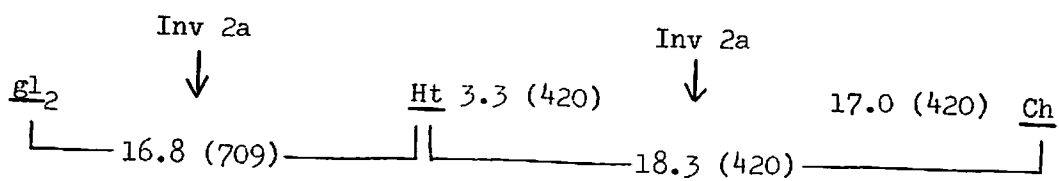
The two progenies in which  $\underline{w}_3$  and  $\underline{Ht}$  were classified simultaneously (the crosses tabulated above) involve small numbers but agree in the location of  $\underline{Ht}$  to the right of  $\underline{w}_3$ . On the basis of combined data, the gene order and distances are as follows:

$$\underline{v}_4 \quad 27.6 \quad (486) \quad \underline{w}_3 \quad 10.3 \quad (214) \quad \underline{Ht} \quad 34.0 \quad (562) \quad \underline{Ch}$$

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

				+ Inv 2a	Ch		
			Ht	+	+	X	+++
Region				(2961-3010)			
P	+	Inv	Ch	177			
	Ht	+	+	162		$\underline{Ht} - \text{Inv} = 14/420 = 3.3\%$	
1	+	+	+	10			
	Ht	Inv	Ch	0		$\underline{Ht} - \underline{Ch} = 77/420 = 18.3\%$	
						$\text{Inv} - \underline{Ch} = 71/420 = 17.0\%$	
2	+	Inv	+	34			
	Ht	+	Ch	33	Order:		
					$\underline{Ht} - \text{Inv} - \underline{Ch}$		
1,2	+	+	Ch	0			
	Ht	Inv	+	4			
		Total		420			

The data above, together with  $\underline{gl}_2$ - $\underline{Ht}$  recombination reported in the 1963 MNL, may be summarized as follows:



The indicated  $\underline{Ht}$ - $\text{Inv } 2a$  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  $\underline{Ht}$  locus. Crossing over within the inversion is expected to yield two types of duplicate-deficient

The breakpoints of Inversion 2a are thus between  $\underline{gl}_2$  and  $\underline{B}$  in the short arm and between  $\underline{Ht}$  and  $\underline{Ch}$  in the long arm. There is an indication that  $\underline{lg}_1$ - $\underline{gl}_2$  recombination may be increased in stocks homozygous for Inversion 2a.

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## 2. Mapping studies of $\underline{Rp}_3$ .

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  $\underline{Rp}_3$ . In the data they reported, in plants heterozygous for T 3-9c,  $\underline{wx}$  and  $\underline{Rp}_3$  showed 11.7% recombination (32/274).

Further efforts to determine the map position of  $\underline{Rp}_3$  yielded the following information:

(a) In greenhouse classifications:  $\underline{d}_1 - \underline{Rp}_3 = 51/288 = 17.7\%$  recombination

(b) In field classifications (255 plants):  $\underline{d}_1$  23.1  $\underline{Lg}_3$  7.1  $\underline{Rp}_3$   
└────────── 27.1 ─────────┘

(c) In greenhouse classifications (244 plants):

$\underline{Rp}_3$  3.3  $\underline{gl}_6$  25.8  $\underline{lg}_2$   
└────────── 28.3 ─────────┘

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

	+	+	+	X	+	+	$\underline{Rp}_3$	
					└───	├───	├───	
					$\underline{Lg}_3$	$\underline{Rg}$	+	
P	+	+	$\underline{Rp}$	202				
	$\underline{Lg}$	$\underline{Rg}$	+	233				
								$\underline{Lg}_3 - \underline{Rg} = 17/456 = 4.1\%$
1	+	$\underline{Rg}$	+	7				
	$\underline{Lg}$	+	$\underline{Rp}$	10				
								$\underline{Lg}_3 - \underline{Rp}_3 = 21/456 = 5.0\%$
								$\underline{Rg} - \underline{Rp}_3 = 4/456 = 0.9\%$
2	+	+	+	4				
	$\underline{Lg}$	$\underline{Rg}$	$\underline{Rp}$	0				
								Order: $\underline{Lg}_3 - \underline{Rg} - \underline{Rp}_3$
			Total	456				

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  $\underline{Rg} \underline{Rp}_3$  progeny would have established the