

Table 1
Data from the crosses of $Y_9 \underline{bf}_2/++$ hypoploid TB-10a plants
with $Y_9 Y_9 \underline{bf}_2 \underline{bf}_2$.

$++$	$+\underline{bf}_2$	$Y_9 +$	$Y_9 \underline{bf}_2$	Total	% $++$	% $+\underline{bf}_2$
80	68	0	323	471	17.0%	14.4%

The data from Table 1 indicate that Y_9 is distal to \underline{bf}_2 with respect to the TB-10a breakpoint. Crossing over between \underline{bf}_2 and the breakpoint results in the $++$ class while crossovers between Y_9 and \underline{bf}_2 result in the $+\underline{bf}_2$ class. In order to get $Y_9 +$ a double crossover would have to occur--one between Y_9 and \underline{bf}_2 and the other between \underline{bf}_2 and the breakpoint. Such double crossovers were not observed. These data indicate the order of $Y_9-\underline{bf}_2-\underline{g}_1$ in chromosome 10. This order was confirmed by a three-point test involving Y_9 , \underline{bf}_2 and \underline{g}_1 . The results of this testcross are given in Table 2; they indicate a linkage map of $Y_9-3.6-\underline{bf}_2-18.2-\underline{g}_1$.

Table 2
Testcross results from the trihybrid $++ \underline{g}_1/Y_9 \underline{bf}_2 +$.

	$++ \underline{g}_1$	$Y_9 \underline{bf}_2 +$	$+\underline{bf}_2 +$	$Y_9 + \underline{g}_1$	$+++$	$Y_9 \underline{bf}_2 \underline{g}_1$	$+\underline{bf}_2 \underline{g}_1$	$Y_9 ++$	Total
No.	229	257	14	5	52	57	1	2	617
%			3.1		17.7		0.5		

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3. Linkage relationships of chlorophyll defective mutants on chromosome 6.

As part of a study of luteus seedling mutants, six ($\underline{w}8896$, \underline{l} -Brawn #1, \underline{l} -Blandy #3, $\underline{l}4120$, $\underline{l}10$ and $\underline{l}4920$) were found which showed close linkage with Y_1 on chromosome 6. Allele tests of the mutants demonstrated allelism only between \underline{l} -Brawn #1 and \underline{l} -Blandy #3. The linkage relationships of the

mutants were investigated to determine if there might be a cluster of closely linked luteus mutants on chromosome 6.

Phenotype

The basic phenotype of all these mutants was yellow (luteus). However, considerable variation of the basic luteus phenotype was observed in some of the mutants. Some of this variation is undoubtedly due to environmental differences, such as temperature, and differences in the genotypic background of the plants. The following is a brief phenotypic description of each mutant:

- (1) w₈₈₉₆: In the original stock obtained from the Maize Genetics Cooperation, this was a dark yellow mutant. However, on crossing into our stocks the mutant was found to vary in its expression from a strong, to light, to very pale luteus, to an off-white. No obvious chlorophyll is present in this mutant.
- (2) l₄₁₂₀-A: Dark yellow mutant that sometimes shows some greening of the leaf tips.
- (3) l₁₀: The darkest yellow of the five mutants with no obvious chlorophyll present.
- (4) l_{Brawn #1} and l_{Blandy #3}: Moderately dark yellow mutants that frequently but not always show considerable greening.
- (5) l₄₉₂₀: This mutant shows variation in the amount of yellow, from a moderate degree of yellowing, to pale yellow, to off-white. Frequently the tips of the leaves will be green and occasionally chlorophyll is observed elsewhere on the leaf.

Table 1 gives the chlorophyll, carotene, and xanthophyll content of these mutants. For these analyses, seedlings were grown under conditions of 27°C and 2,000 foot candles of light. The phenotype indicated in the table is that observed for the seedlings before they were harvested for extraction.

Table 1

Chlorophyll, carotene, and xanthophyll determinations for a series of luteus mutants on chromosome 6.

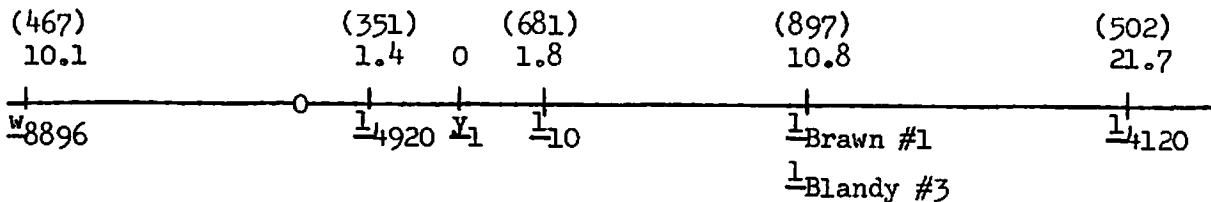
(From M.G.C.N.L. 42:85-88, 1968.)

Mutant	Phenotype	chlorophyll mg/gm	carotene mg/gm	xanthophyll mg/gm
$\underline{w}8896$	pale yellow	Trace	.006	.0090
$\underline{l}4120$	yellow, green leaf tips	.0935	.0021	.0175
$\underline{l}10$	good yellow	Trace	.0029	.0140
\underline{l} -Brawn #1	yellow-green	.5939	.0222	.0800
\underline{l} -Blandy #3	yellow with some green	.3115	.0176	.0432
$\underline{l}4920$	pale yellow, green leaf tips	.0486	.0021	.0117
Normal	green	1.674	.0980	.1140

Linkage

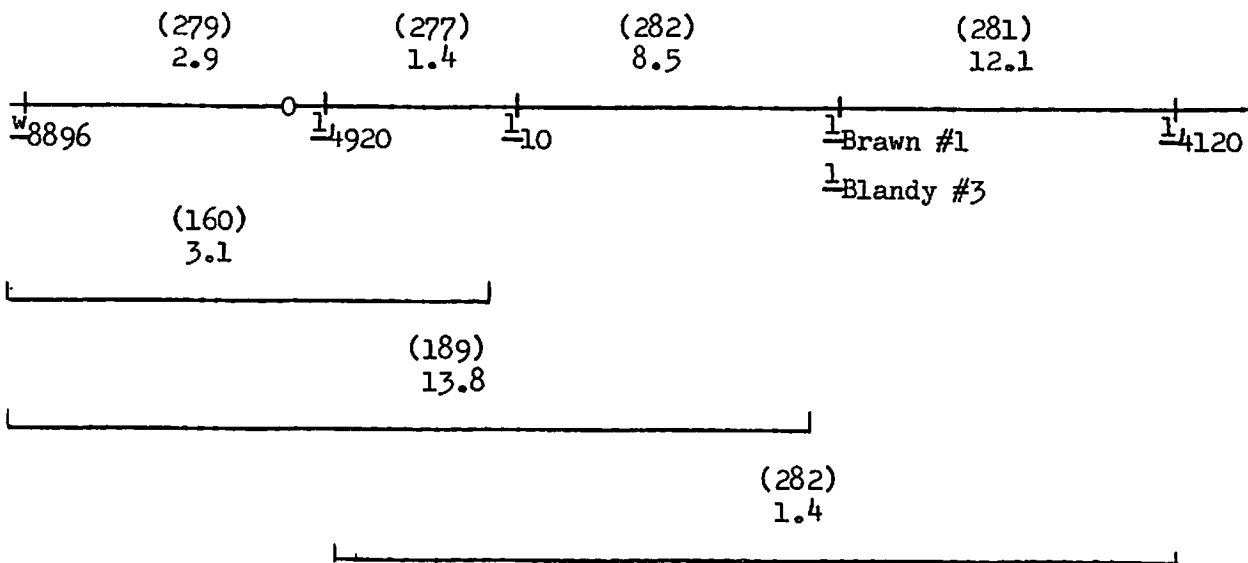
Each of the mutants was involved in three-point tests with \underline{y}_1 and one or more translocations. These tests permitted the placement of the genes on the linkage map with respect to \underline{y}_1 . Tests of $\underline{w}8896$ with T 1-6₄₄₅₆ (6L.30) and T 1-6a (6L.54) indicated a map of $\underline{w}8896 - \underline{y}_1 - T$. Crosses of $\underline{l}4120$ with T 1-6₄₄₅₆ (6L.30) and T 1-6a (6L.54) indicated an order of $\underline{y}_1 - T - \underline{l}4120$ for T 1-6₄₄₅₆ and an order of $\underline{y}_1 - \underline{l}4120 - T$ for T 1-6a. When $\underline{l}10$ was tested with the same two translocations the order was determined to be $\underline{y}_1 - \underline{l}10 - T$ for both. Tests of \underline{l} -Blandy #3 with T 1-6a (6L.54) gave a map of $\underline{y}_1 - \underline{l}$ -Blandy #3 - T, while crosses of T 6-9₄₇₇₈ (6S.80) with \underline{l} -Brawn #1 indicated a map of T - $\underline{y}_1 - \underline{l}$ -Brawn #1. The map for $\underline{l}4920$ was determined to be $\underline{l}4920 - \underline{y}_1 - T$ from crosses with T 1-6a (6L.54) and T 1-6₄₄₅₆ (6L.30). These tests placed $\underline{w}8896$ and $\underline{l}4920$ to the left and $\underline{l}10$, \underline{l} -Brawn #1 (\underline{l} -Blandy #3) and $\underline{l}4120$ to the right of \underline{y}_1 .

Two-point tests of these genes with \underline{y}_1 established the following map. (Figures in parentheses indicate the total number of individuals in the testcross populations):



This map does not reveal a tight clustering of the five loci but rather a wide distribution extending over 30 map units.

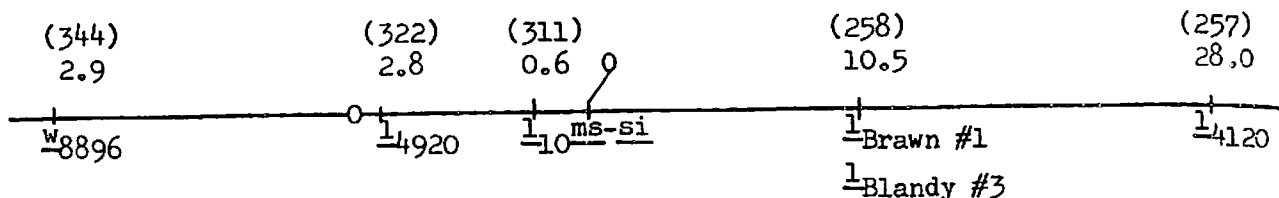
Seven intercrossovers were made between these five loci and the crossover values determined for each cross. The following map summarizes the results of these crosses. (The genes are placed on this map in the positions determined by the y_1 linkage tests above):



Two discrepancies are obvious when this map is compared with the y_1 map. First, all linkage data of w_{8896} with other mutants would suggest that this gene should be closer to l_{4920} than the y_1 data indicated. The linkage values with l_{4920} , l_{10} , and $l_{Brawn \#1}$ are consistent in indicating this. Other linkage data to be presented below are in agreement with the location of w_{8896} closer to l_{4920} . Second, the $l_{4920} - l_{4120}$ distance is much too short and is not in agreement with the y_1 data or the $l_{10} - l_{Brawn \#1}$ and $l_{Brawn \#1} - l_{4120}$ distances. The latter two agree with the y_1 data. The distance indicated by the $l_{4920} - l_{4120}$ test probably is in error.

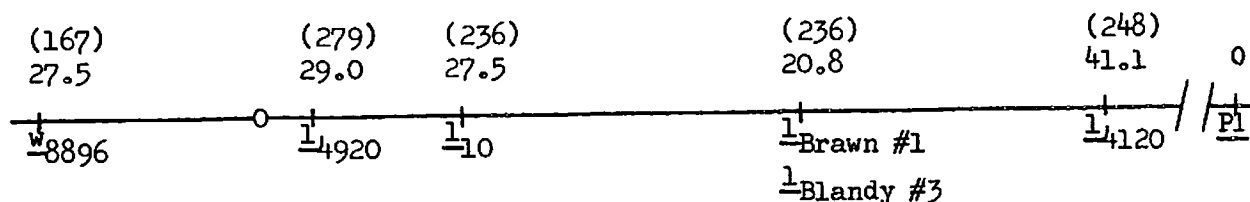
Linkage data were obtained for these five genes with ms-si (2 units to the right of y_1). These are presented on the following map. (The

genes are again placed in accordance with the y_1 data.)



All linkage data are in agreement with the y_1 data except for w_{8896} . Again the data indicate w_{8896} should be closer to l_{4920} . In this regard, the data agree with the intercross values.

Linkage tests were made between P_1 and the five luteus genes. The linkage values obtained are indicated on the following map (gene position as determined by the y_1 data):



Except for l_{4120} , the data are consistent with the previous linkage tests. It is possible that a new mutant had occurred in the stocks used for this test and the new mutant was confused with l_{4120} . Again notice that the data suggest w_{8896} should be closer to l_{4920} ; in fact, the data, in this instance, would place w_{8896} to the right of l_{4920} .

Linkage data with ms_1 were obtained for w_{8896} and l_{4120} . We have obtained values that indicate ms_1 is 2.8 units from y_1 , direction unknown. The $ms_1 - l_{4120}$ distance was 23.2 (177 plants tested), which is in close agreement with other linkage data for this locus. The $w_{8896} - ms_1$ distance was 3.7 (294 plants tested). Again the linkage data indicate that w_{8896} should be closer to l_{4920} than the y_1 data had indicated.

Also linkage of su_2 with l_{4920} and $l_{Blandy \#3}$ was determined. The crossover values were 28.1 for l_{4920} (235 plants tested) and 21.4 for $l_{Blandy \#3}$ (214 plants tested). Although the reliability of these data is in doubt, because of the difficulty in classifying su_2 in our stocks, they are in general agreement with other linkage values for these loci.

As was mentioned above, these luteus genes were crossed with several translocations involving chromosome 6. In addition to the translocations previously mentioned, tests were made involving 6-9c (6L.15) and 6-9e (6L.18). In general, the crossover values obtained with translocations were lower than those with genes. This is as expected, since translocations are known to frequently interfere with crossing over. However, in most instances where more than one gene was tested against a given translocation, the comparative magnitudes of the crossover values were as expected for the placement of genes from the y_1 linkage data. As was indicated earlier, \underline{l}_{4120} mapped to the right of T 1-6 \underline{l}_{4456} (6L.30) and to the left of T 1-6a (6L.54). The crossing over was 1.9% (322 plants tested) with T 1-6 \underline{l}_{4456} and 26.5% (298 plants tested) with T 1-6a. This places \underline{l}_{4120} between 6L.30 and 6L.54, and probably close to 6L.30.

Table 2 presents a summary of the distances between these five genes as determined by the four two-point tests that were made.

Table 2

A summary of the distances determined between the five luteus genes on chromosome 6 as determined by four two-point tests.

Two-point test with:	$\underline{w}_{8896} - \underline{l}_{4920}$	$\underline{l}_{4920} - \underline{l}_{10}$	$\underline{l}_{10} - \underline{l}_{\text{Brawn \#1}}$	$\underline{l}_{\text{Brawn \#1}} - \underline{l}_{4120}$
y_1	8.7	3.2	9.0	10.9
Intercrosses	2.9	1.4	8.5	12.1
<u>ms-si</u>	0.1	2.2	11.1	17.5
<u>Pl</u>	-1.5	1.5	6.7	----

The data are fairly consistent for each interval except $\underline{w}_{8896} - \underline{l}_{4920}$, which shows considerable variation between tests and even reversal in order in the case of the Pl crosses. The weight of the evidence would suggest that \underline{w}_{8896} is closer to \underline{l}_{4920} than indicated by the y_1 data.

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