

PROPOSED ORDER OF MARKERS IN CHROMOSOME 3

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Some of the data collected for the previous article (18), while only indirectly applicable to the linkage relations of creep, bear directly on the linkage relations of markers on chromosome 3. Many good markers have been mapped to chromosome 3 but their order has yet to be clarified. Besides presenting the analysis of a linkage experiment conducted in 1981, this article attempts to coordinate evidence collected previously.

Table 1 shows the analysis of a three-point coupling phase cross involving genes St., B, and Chi-6.

The present results accord with results from two other experiments heretofore not reported. The first was a small greenhouse population segregating simultaneously for M, St, B, and Chi-6 (Table 2) and the second a field population grown in 1973 (Table 3). All are consistent in showing that b lies between st and chi-6. Thus for the three experiments the results can be summarized as follows:

M — 37 —	St — 25 —	B — 21 —	Chi-6	N=527
	St — 30 —	B — 18 —	Chi-6	N=152
	St — 25 —	B — 14 — Twp — 3 —	Chi-6	N=412

Additional linkage data involving the Wilty (wil) gene were collected subsequent to the original report of linkage in 1976 (12). The results of four three-point linkage analyses are given in Tables 4-6. Since wil is distal to b, wil is expected to be close to chi-6. Two hitherto unreported two-point testcross populations and a two-point F2 show the linkage between st. and wil to be 23, 28, and 30% respectively (data not presented).

Since bulf was shown (16, 17) to be situated between st and chi-6, bulf presumably lies between b and chi-6. This, however, has not yet been experimentally verified; there is some small possibility that bulf lies between b and st.

By combining all available evidence, my own best estimate of the order of markers on chromosome 3 that I have worked with is as follows:

uni-M-alt-wel-F-Pu-st-la-b-(yp)-b-bulf-wil-twp-chi-6

It is quite possible that bulf and wil actually occur in reverse order from that given. There is still insufficient data to propose the placement of genes dp, ch4, Dpo, Gty, er, En, or och. My tests for linkage of rb with st and chi-6 have been negative. The possibility remains that rb is located at the M end of the chromosome.

Not all the references given below, although pertinent to the discussion, were specifically cited in the text.

1. Blixt, S. 1968. Agri. Hort. Genet. 26:100-106
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4. Blixt, S. 1978. Agri. Hort. Genet. 36:23-47.
5. Gritton, E. T. 1971. PNL 3:15-16.
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7. Marx, G. A. 1971. PNL 3:18-19.

8. Marx, G. A. 1972. PNL 4:30-31.
 9. Marx, G. A. 1973. PNL 5:25-26.
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 11. Marx, G. A. 1974. PNL 6:30-31.
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 13. Marx, G. A. 1977. PNL 9:29-30.
 14. Marx, G. A. 1978. PNL 10:41-42.
 15. Marx, G. A. 1978. PNL 10:46.
 16. Marx, G. A. 1980. PNL 12:47-48.
 17. Marx, G. A. 1981. PNL 13:29-30.
 18. Marx, G. A. 1982. PNL 14:41-42.
 19. Monti, L. and F. Saccardo. 1971. PNL 3:28.
 20. Murfet, I. C. 1967. Heredity 22:602-607.

Table 1. Distribution of phenotypes and linkage analysis of a coupling phase cross:
St B Chi-6 x st b chi-6.

<u>St</u>	<u>B</u>	<u>Chi-6</u>	<u>Total</u>	Chi-squares			Recomb. fract.
				<u>Gene pair</u>	<u>X</u>	<u>Y</u>	
+	+	+	282	<u>St-B</u>	0.03	0.08	<u>91.56</u>
+	+	chi-6	59	<u>St-Chi-6</u>	0.03	4.60*	<u>2.61</u>
+	b	+	7	<u>B-Chi-6</u>	0.08	4.60*	<u>21.46</u>
+	b	chi-6	49				
st	+	+	51				
st	+	chi-6	6				
st	b	+	34				
st	b	chi-6	<u>39</u>				
			<u>527</u>				
				(B281-648-682)			

Table 2. Distribution of phenotypes and analysis of a four-point linkage test from a cross:
st b chi-6 m x St B Chi-6 M.

<u>St</u>	<u>Chi-6</u>	<u>B</u>	<u>M</u>	<u>Total</u>	Chi-squares			Recomb. fract.
					<u>Gene pair</u>	<u>X</u>	<u>Y</u>	
+	+	+	+	76	<u>St-Chi-6</u>	1.72	0.88	<u>2.29</u>
+	+	+	m	15	<u>St-B</u>	1.72	0.32	<u>11.98</u>
+	+	b	+	6	<u>St-M</u>	1.72	0.32	<u>4.68</u>
+	+	b	m	1	<u>Chi-6-B</u>	0.88	0.32	<u>39.34</u>
+	chi-6	+	+	7	<u>Chi-6-M</u>	0.88	0.32	<u>2.29</u>
+	chi-6	+	m	3	<u>B-M</u>	0.32	0.32	<u>0.75</u>
+	chi-6	b	+	9				
+	chi-6	b	m	4				
st	+	+	+	8				
st	+	+	m	7				
st	+	b	+	5				
st	+	b	m	1				
st	chi-6	+	+	1				
st	chi-6	+	m	0				
st	chi-6	b	+	5				
st	chi-6	b	m	<u>4</u>				
					(C280-210-212)			

Table 3. Distribution of phenotypes and linkage analysis of a cross:
st b twp chi-6 x St B Twp Chi-6

St	B	Twp	<u>Chi-6</u>	<u>Total</u>	Chi-squares			Recomb. fract.	
					Gene pair	X	Y		
+	+	+	+	250	<u>St-B</u>	0.83	1.05	60.08	25.2 ± 2.5
+	+	+	chi-6	5	<u>St-Twp</u>	0.83	4.67*	23.31	33.7 ± 3.0
+	+	twp	+	2	<u>St-Chi-6</u>	0.83	1.29	19.37	34.6 ± 3.0
+	+	twp	chi-6	17	<u>B-Twp</u>	1.05	4.67	163.16	14.2 ± 1.9
+	b	+	+	10	<u>B-Chi-6</u>	1.05	1.29	159.07	13.2 ± 1.8
+	b	+	chi-6	4	<u>Twp-Chi-6</u>	4.67*	1.29	329.30	3.2 ± 0.9
+	b	twp	+	0					
+	b	twp	chi-6	29					
st	+	+	+	42					
st	+	+	chi-6	0					
st	+	twp	+	0					
st	+	twp	chi-6	2					
st	b	+	+	14					
st	b	+	chi-6	3					
st	b	twp	+	1					
st	b	twp	chi-6	33					
				414	(B273-494-516)				

Table 4. Distribution of phenotypes and analysis of a three-point coupling phase cross: st b wil x St B Wil.

Wil	B	St	<u>Total</u>	Chi-squares			Recomb. fract.	
				Gene pair	X	Y		
+	+	+	158	<u>Wil-B</u>	0.02	0.08	171.68	6.9 ± 1.7
+	+	st	22	<u>Wil-St</u>	0.02	0.19	48.60	24.2 ± 3.2
+	b	+	3	<u>B-St</u>	0.08	0.19	76.30	19.4 ± 2.8
+	b	st	7					
wil	+	+	6					
wil	+	st	1					
wil	b	+	19					
wil	b	st	36					
			252	(B278-422-445)				

Table 5. Distribution of phenotypes and analysis of a three-point cross:
St B wil x st b wil

<u>St</u>	<u>B</u>	<u>Wil</u>	<u>Total</u>	Chi-squares			Recomb. fract.
				<u>Gene pair</u>	<u>X</u>	<u>Y</u>	
+	+	+	55	<u>St-B</u>	2.54	0.01	31.19
+	+	-	28	<u>St-Wil</u>	2.54	0.01	3.17
+	-	+	13	<u>B-Wil</u>	0.01	0.01	10.58
+	-	-	0				16.1 ± 3.8
-	+	+	4				30.8 ± 8.2
-	+	-	1				18.0 ± 8.8
-	-	+	16				
-	-	-	<u>1</u>				
			<u>118</u>	(B275-410-415)			

Table 6. Distribution of phenotypes and linkage analyses of two three-point crosses:
A. St b Wil x st B wil. B. st b Wil x St B wil

A.	<u>St</u>	<u>B</u>	<u>Wil</u>	<u>Total</u>	Chi-squares			Recomb. fract.	
					<u>Gene pair</u>	<u>X</u>	<u>Y</u>		
	+	+	+	76	<u>St-B</u>	1.39	1.39	4.17	30.8 ± 6.5
	+	+	-	35	<u>St-Wil</u>	1.39	1.02	6.39	36.9 ± 4.6
	+	-	+	37	<u>B-Wil</u>	1.39	1.02	20.01	10.3 ± 35.4
	+	-	-	0					
	-	+	+	19					
	-	+	-	18					
	-	-	+	3					
	-	-	-	<u>0</u>	(B277-423-437)				
				<u>188</u>					
B.	<u>St</u>	<u>B</u>	<u>Wil</u>	<u>Total</u>	<u>Gene pair</u>	<u>X</u>	<u>Y</u>	Recomb. fract.	
					<u>St-B</u>	0.49	1.23	12.00	27.0 ± 5.2
					<u>St-Wil</u>	0.49	0.20	4.21	32.6 ± 8.5
					<u>B-Wil</u>	1.23	0.20	9.48	23.6 ± 20.4