LINKAGE RELATIONS OF Curl, Orc, AND "Det" WITH MARKERS ON CHROMOSOME 7

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Plants possessing the EMS-induced recessive mutant curl (6) bear a clear and distinctive phenotype early in the seedling stage and throughout their ontogeny. Though curl segregants are weaker and less productive than Curl/- counterparts, the mutant is a favorable marker for genetic studies. Preliminary observations made several years ago indicated that curl might belong to chromosome 7 (data not shown).

In 1984-1985 I constructed populations to verify and refine the linkage relationship among curl, r, and bt. The results of these crosses, three in all, are given in Table 1. For one population the F1 seeds were separated into round (R/-) and wrinkled (r/r) classes before planting but each F2 plant was also classified for R-r again at the dry seed stage to ensure the accuracy of the classification.

The data argue persuasively that curl is linked with r and bt in what is still generally accepted as chromosome 7, the Indicated order being curl-r-bt. Since, however, there still is controversy concerning the placement of the r-tl-bt group (2,3) curl is an additional clear marker which may help to resolve the controversy. Another unsettled matter concerns the placement of wsp on chromosome 7. I have not succeeded in confirming the reported linkage relationship between wsp and chromosome 7 markers (4). The fact that curl appears to be located toward the wsp end of chromosome 7 on the current map should aid in the ongoing quest to settle this issue as well. The linkage relations of two other newly discovered markers may also contribute to a resolution.

Orc, described by Blixt and Swiecicki (1,7), is a dominant mutant that causes orange cotyledons containing high amounts of lutein (5). My own experience with Ore indicates that the lower leaves of mutant plants become orangy yellow about the time the plants begin to flower, thus providing another diagnostic criterion for scoring Orc plants in segregating populations. A moderate sized F2 segregating simultaneously for Bt-bt, Orc-orc, and R-r indicates that the three genes are linked (Table 2). Accordingly, Orc and curl should show strong linkage, a supposition we are in the process of testing.

Another mutant that has recently come into my possession, and which I will provisionally designate det— , also shows linkage with R and Bt. Seed of the mutant was provided through the courtesy of Dr. Peter Matthews; the mutant line is maintained in the John Innes Institute Pisum collection under the number J.I. 1358/B. The mutant behaves as a monogenic recessive (Table 3a) and is distinguished from normal, wild type plants by its determinate reproductive behavior. The term "determinate" has been used in

1/ It falls to Drs. Matthews and Blixt to accept or reject the gene name and symbol.

various contexts in the pea literature so it is important to make clear that the present mutant confers a determinate habit in the botanical sense i.e. reproductive growth is terminated with an inflorescence. These plants typically produce two sets of inflorescences on the main stem. The first peduncle is borne in the leaf axis of the first reproductive node but the second and final reproductive node bears two peduncles. Further reproductive activity may occur but, if so, it arises from axillary branches lower down the stem.

Analysis of various crosses between J.I. 1358 and several marker lines revealed evidence of linkage between det and r and bt (Table 3b,c).

The det mutant may have important implications for applied breeding as a means to regulate the balance of reproductive and vegetative growth. There may be an advantage associated with the limits imposed on the maximal number of pods at the top of the main stem axis. As a result, photosynthates may be preferentially partitioned to the fruits and seeds because there is no longer a commitment, or even a potential, to continued apical development. Because pods borne above the third or fourth reproductive node on conventional varieties rarely, if ever, contribute significantly to crop yield under commercial field conditions, continued pod and seed formation puts a drain on plant metabolites but that drain is not translated into economic yield. Pods produced on det plants tend to be borne within a relatively narrow time span and consequently the pods and seeds are relatively uniform in maturity. Pods and seeds borne on axillary branches may or may not contribute to field yield depending on the level of intra- and inter-plant competition and on the level of available environmental resources. It may be possible to enhance yield potential still more by incorporating genes for multiple podding. Finally, the trait may facilitate hand harvesting in lines intended for the home and market garden. The validity, if any, of these speculations must await extensive breeding, selection, and evaluation.

1. Blixt, S. and W. K. Swiecicki. 1983. PNL 15:9-10.
2. Folkeson, D. 1985. PNL 17:14-15.
3. Lamm, R. 1978. PNL 10:32-33.
4. Lamprecht, H. 1954. Agri Hort. Genet. 12:115-120.
5. Ludwicki, J. and w". K. Swiecicki. 1985. PNL 17:51-53.
6. Sidorova, K. K. and L. P. Uzhlntzeva. 19/5. PNL 7:56.
7. Swiecicki, W. K. and S. Blixt. 1984. PNL 16:70-72.

Table 1. (a-c) Analysis of joint segregation in F2, for genes Curl, R, and Bt in three different three-point crosses (Curl r bt x curl R Bt); (d) Segregation for Curl and curl in F_2 of a population not segregating for linked markers.

(a)

Curl	R	Bt	No.	Gene pair	Chi-square X	Chi-square Y	Linkage	Recomb. fract.	S.E.
+	+	+	102						
+	+	-	39						
+	-	+	28	Curl R	1.49	0.01	11.30**	27.1	5.7
+	-	-	33	Curl Bt	1.49	10.47**	1.54ns	-	-
-	+	+	40	R Bt	0.01	10.47**	18.25**	33.5	3.7
-	+	-	0						
-	-	+	1		(Population: B285-358-369)				
-	-	-	3						
			258						

(b)

Curl	R	Bt	No.	Gene pair	Chi-square X	Chi-square Y	Linkage	Recomb. fract.	S.E.
+	+	+	49						
+	+	-	16						
+	-	+	15	Curl R	0.74	0.18	5.53*	21.5	8.8
+	-	-	11	Curl Bt	0.74	2.25	0.24ns	-	-
-	+	+	15	R Bt	0.18	2.25	1.53ns	-	-
-	+	-	9						
-	-	+	1		(Population: B285-370-373)				
-	-	-	0						
			116						

(c)

Curl	R	Bt	No.	Gene pair	Chi-square X	Chi-square Y	Linkage	Recomb. fract.	S.E.
+	+	+	183						
+	+	-	47						
+	-	+	67	Curl R	3.73	0.18	24.64**	21.3	4.6
+	-	-	39	Curl Bt	3.73	0.18	0.04ns	-	-
-	+	+	63	R Bt	0.18	0.18	10.56**	39.7	3.2
-	+	-	22						
-	-	+	2		(Population: B285-374-387)				
-	-	-	2						
			425						

(d)

	Curl	curl	
B285-388	22	7	
389	29	8	
390	15	4	
391	28	12	
392	28	7	
393	16	8	
394	25	10	
395	38	10	
396	21	9	
397	32	8	
	254	83	337

Table 2. Analysis of an F_2 population derived from a three-point cross: bt orc r x Bt Orc R.

Bt	Orc	R	No.	Gene pair	Chi-square X	Chi-square Y	Linkage	Recomb. fract.	S.E.
+	+	+	115						
+	+	-	13						
+	-	+	17	Bt Orc	5.19*	0.01	2.10ns	-	-
+	-	-	19	Bt R	5.19*	0.62	15.59**	34.3	3.9
-	+	+	34	Orc R	0.01	0.62	38.29**	26.4	3.4
-	+	-	18						
-	-	+	8		(Population: B285-404-412)				
-	-	-	15						
			239						

Table 3. (a) Single gene segregation for indeterminate (Det) and determinate (det) in two F2 populations; and (b) analysis of joint segregation of Det with Bt and with R.

(a) Number of normal (Det) and determinate (det) segregants reproductive habit in two segregating F2 populations.

	Det	det			Det	det	
B285-541	11	4		B285-568	5	3	
542	12	6		569	10	2	
543	8	3		570	9	6	
544	11	3		571	8	3	
545	8	3		572	16	7	
546	12	4		573	14	6	
547	14	6		574	14	5	
548	7	2		575	16	11	
549	1	1		576	15	7	
550	14	2		577	12	4	
	98	34	132	578	12	8	
				579	9	5	
				580	9	2	
					149	69	218

(b) Analysis of F2 populations derived from three two-point crosses involving Det, Bt, and R.

Gene pair	XY	Xy	xY	xy	Tot.	Chi-square X	Chi-square Y	Chi-square Linkage	Recomb. fract.	S.E.
Det Bt	36	19	17	1	73	0.00	0.22	6.04*	22.2	11.0
(Population: B285-552-559)										
Det R	101	1	16	22	140	0.34	5.49*	65.32**	6.9	2.2
(Population: B285-560-567)										
Det R	43	0	4	12	59	0.14	0.68	34.25**	<7.2	3.5

EDITOR'S NOTE:

Four articles submitted by W. K. Swlecickl arrived too late to be included in the present volume. Although the articles were posted on 19 February, they did not arrive in Geneva until 24 April, at which time the volume had already been delivered to the printer. The envelope containing the manuscripts was marked "Air Mail", "express", "Certified", so clearly Dr. Swiecicki was not responsible for the extraordinary delay in getting the manuscript to me.

In one article Dr. Swiecicki provides good evidence for linkage between det and r and tl. He therefore rightfully shares equal credit for being first to establish the linkage relations or det. Moreover, his article also takes note of the possible applied implications of the det mutant.

In another article, Swiecicki's data led him to conclude that Orc is located on chromosome 1 and that the yellow orange foliage is caused by a separate but linked gene, designated orl. However, my evidence (above) suggests linkage of Orc on chromosome 7 and that the foliage color is a pleiotropic effect of Orc. Thus, in this case, our conclusions conflict. If Swiecicki's view prevails then he deserves priority.

The third and fourth articles, co-authored with B. Wolko, consider the use of isozyme markers in identifying cultivars and confirm the linkage of Aat-p and A on chromosome 1.