SUPPLEMENTAL LINKAGE DATA FOR CHROMOSOMES 1 AND 7

Marx, G. A.
NYS Agricultural Experiment Station
Geneva, NY 14456 USA

Although aeromaculata (aero) was found to be situated in chromosome 1 in close proximity with I and Af (3), the population sizes used to make that determination were smaller than desired to fix the linkage intensity with confidence. Therefore, new crosses were made to generate segregating populations of larger size.

plants from crosses between af and aero were grown in the field in 1986 where they produced abundant seed. Nearly 1900 F2 seeds were then planted in flats in the greenhouse. The resulting seedlings were scored in the 6-8 node stage of development, at which time the phenotypes were clearly manifest and reliably distinguished. It is evident from the data in Table 1 that the linkage between af and aero is unusually tight, for not a single recombinant was recovered.

Table 1. Joint segregation in F2 from crosses: Af aero x af Aero.

Gene Pair	XY	Xy	xY	xy	Tot.	Chi-square X	Chi-square Y	Chi-square Linkage	Recomb. fract.	S.E.
Af-Aero	942	484	465	0	1891	0.138	0.406	211.112**	<4.6	2.3

(Pops. C286-506-521;675-692;752)

A, Au, and Af are known to reside in chromosome 1. Unfortunately, few favorable markers are located between A, which is near one end of the chromosome, and the cluster of genes which includes Af. An analysis of an F2 in which the three genes segregated simultaneously is given in Table 2. Whereas A and Au show moderately strong linkage, neither mutant showed linkage with Af.

Table 2. F2 analysis of a three-point cross:
A au Af x a Au af.

A	Au	Af	No.
+	+	+	115
+	+	-	49
+	-	+	2
+	-	-	1
-	+	+	17
-	+	-	5
-	-	+	28
-	-	-	11
		Total	228

Gene Pair	Chi-square X	Chi-square Y	Chi-square Linkage	Recomb. fract.	S.E.
A-Au	0.37	5.26*	114.80**	8.2	1.9
A-Af	0.37	1.89	0.28	-	-
Au-Af	5.26*	1.89	0.00	- -	

(Pops. B286-673-676; 680,681,694-696)

Table 3A,B,C provides additional data relating to the linkage of *Det* and *Curl* in chromosome 7. These results together with those presented previously (2) and those reported by other investigators (1,4,5) establish rather convincingly that *Det*, *Curl*, R, and Tl are all linked on the same chromosome. While the estimates of linkage intensity for *Curl* between years and between investigators are rather consistent, the estimates involving *Det* and R and Tl are less uniform. The recombinant fraction for *Det-Tl* in Table 3A is 27 + 4, which agrees reasonably well with Swiecicki's data (4), but the estimated distance between *Pet* and *R* shown in Table 3B and C is 1 unit and in 1986 7 units. This tight linkage is unexpected in light of the fact that Tl and R are so tightly linked.

The paper by Makasheva and Drozd (page 31, this volume) reveals not only that the gene for determinate habit was discovered in 1975 but also that the symbol *det* was proposed that year by Popova. It would appear that the same mutant was induced in experiments conducted independently in USSR (1) and in Poland (4) and that the mutant arose spontaneously sometime before that. The spontaneous mutant is the source of the accession held by the John Innes Institute.

1. Makasheva, R. Kh. and A. M. Drozd. 1987. PNL 19:31.
2. Marx, G. A. 1986. PNL 18:45-48.
3. Marx, G. A. 1986. PNL 18:42-44.
4. Swiecicki, W. K. 1987. PNL 19:72.

Table 3. Linkage analyses of a dihybrid cross (A) and two four-point crosses (B and C) involving genes on chromosome 7.

A. Joint segregation in F2 of Tl and Det

						Chi-square			Recomb	
Gene Pair	XY	Xy	xY	xy	Tot.	X	Y	Linkage	fract.	S.E.
Tl-Det	207	112	86	8	413	1.10	3.62	26.69**	26.8	4.5

(Pop. B286-624-641)

B. F2 analysis of cross segregating simultaneously for curl, tl, r, and bt

Curl	Tl	R	Bt	No.
+	+	+	+	97
+	+	+	-	30
+	+	-	+	0
+	+	-	-	0
+	-	+	+	1
+	-	+	-	1
+	-	-	+	57
+	-	-	-	13
-	+	+	+	40
-	+	+	-	7
-	+	-	+	1
-	+	-	-	0
-	-	+	+	0
-	-	+	-	0
-	-	-	+	3
-	-	-	-	0
			Total	250

	Chi-square			Recomb.	
Gene Pair	X	Y	Linkage	fract.	S.E.
Curl-Tl	2.82	3.33	18.86**	22.1	6.0
Curl-R	2.82	2.82	15.38**	25.7	5.8
Curl-Bt	2.82	2.82	0.94	-	-
Tl-R	3.33	2.82	300.30**	1.1	0.6
Tl-Bt	3.33	2.82	0.40	-	-
R-Bt	2.82	2.82	0.78	-	-

(Pop. B286-642-651)

C. F2 analysis of cross segregating simultaneously for curl, det, r, and bt

Curl	Tl	R	Bt	No.
+	+	+	+	96
+	+	+	-	30
+		-	+	1
+	+	-	-	0
+	-	+	+	3
+	-	+	-	0
+	-	-	+	54
+	-	-	-	8
-	+	+	+	32
-	+	+	-	7
-	+	-	+	0
-	+	-	-	0
-	-	+	+	0
-	-	+	-	0
-	-	-	+	1
-	-	-	-	0
			Total	232

	Chi-square			Recomb.	
Gene Pair	X	Y	Linkage	fract.	S.E
Curl-Det	7.45**	1.47	15.99**	15.4	6.4
Curl-R	7.45**	0.82	15.23**	15.7	6.4
Curl-Bt	7.45**	3.88*	0.11	-	-
Det-R	1.47	0.82	248.28**	1.4	0.8
Det-Bt	1.47	3.88*	3.12	-	-
R-Bt	0.83	3.88*	2.69	-	-

(Pop. B286-652-660)