LINKAGE RELATIONSHIPS AMONG SIX GENES IN CHROMOSOME 6

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Genes na (9,4), .sbm. (1,2), E (7,8), Arg (3,4), and art (5) recently have been found to reside in ohromosome 6, along with well-established markers such as wlo, p, and Pl. Most of the known markers appear to be clustered at one (wlo-p) or the other (Pl-Arg-Fl) end of the chromosome.

This is a record of an attempt to establish and/or verify the order of the following six genes: na., wlo, art, Pl, and Arg. Two separate series of crosses are reported, supplemented by data from a four-point linkage analysis referred to in the previous article (6). In the first series, four of the markers, Arg. Pl, na, wlo were associated together in one parent, while art and p were combined in the other parent. Thus the genetic constitution of the cross was:

Arg Pl na wlo. Art P

x

arg pl Na Wlo art p.

The F1's of this series of crosses therefore segregated for six genes simultaneously. A second set of crosses involved only three markers: wlo p, and art. The genetic formula in this case was:

Wlo-p-Art

x

wlo-P-art

In the populations segregating simultaneously for six genes the presence of na. presented some difficulties since a disproportionate share of the na plants succumbed before producing pods and seeds. Their short stature rendered the .na. segregants relatively less competitive in relation to the Na/- segregants, the latter shading out the former. This situation dictated that the gene analysis be carried out by pairs or by three's or by four's (Table 1). Thus, depending on which genes were involved, the total number of plants involved differed. For example, the na-wlo pair was analyzed separately from the rest because the plants were easily and accurately scored in the seedling stage, before the onset of severe competition.

A pair-wise analysis was also made for genes Arg and Pl. The genes art, p, and wlo were analyzed together but because wlo is closely linked with na and since some of the na segregants did not survive to maturity, the three-point analysis reveals a deficiency of wlo segregants. This, however, was not the sole reason for the deficiency of wlo segregants, since the deficiency was evident even in the seedling stage, before shading became a factor.

The second series of crosses, in which na was not involved, also showed a deficiency of wlo segregants (Table 2).

The available data, including the four-point analysis of Arg-Pl-Wlo-Na from a previous study (6) (Table 3), suggest the following gene order:

art —— na —— wlo —— p —— Pl —— Arg

Because certain single gene ratios were disturbed, some measure of doubt is cast on the gene order as presented, i.e, there still is some question as to which side of wlo the na gene is located. Note that the

distance separating Arg and Pl from Art is such that the linkage chi-squares were non-significant. Also, the location of Arg raises anew the possibility that Arg is an allele at the Fl locus.

1. Gritton, E. T. and D. J. Hagedorn. 1975. Crop Sci. 15:447-448.
2. Hampton, R. 0. and G. A. Marx. 1981. PNL 13:16-17.
3. Marx, G. A. 1978. PNL 10:34-37.
4. Marx, G. A. 1981. PNL 13:35-37.
5. Marx, G. A. 1981. PNL 13:38-39.
6. Marx, G. A. 1982. PNL 14:47-49.
7. Murfet, I. C. 1971. Heredity 27:93-110.
8. Murfet, I. C. 1980. PNL 12:59.
9. Wellensiek, S. J. 1972. PNL 4:60.

Table 1. Linkage analyses of a cross in which six genes segregated simultaneously in F_2. Because of differential survival, the population was subjected to separate two-(A), three-(B), and four-point (C) analyses.

A. Two-point analyses

Arg	Pl	Total
+	+	741
+	pl	15
arg	+	15
arg	pl	242
		1013

Na	Wlo	
+	+	930
+	wlo	21
na	+	51
na	wlo	258
		1260

Gene pair	Chi-squares X	Chi-squares Y	Linkage	Recomb. fract.
Arg-Pl	0.07	0.07	877.84	3.0 ± 0.5
Na-Wlo	0.15	5.44	893.88	5.5 ± 0.7

B. Three-point analysis

Na	Wlo	Arg	
+	+	+	654
+	+	arg	265
+	wlo	+	16
+	wlo	arg	2
na	+	+	27
na	+	arg	32
na	wlo	+	192
na	wlo	arg	22
			1210

Gene pair	Chi-squares X	Chi-squares Y	Linkage	Recomb. fract.
Na-Wlo	3.84	21.91	797.65	6.0 ± 0.7
Na-Arg	3.84	1.51	8.24	43.2 ± 2.3
Wlo-Arg	21.91	1.51	38.57	31.9 ± 2.5

C. Four-point analysis

Arg	Pl	Art	P	
+	+	+	+	480
+	+	+	p	70
+	+	art	+	96
+	+	art	p	87
+	pl	+	+	9
+	pl	+	p	2
+	pl	art	+	0
+	pl	art	p	4
arg	+	+	+	13
arg	+	+	p	0
arg	+	art	+	2
arg	+	art	p	0
arg	pl	+	+	117
arg	pl	+	p	64
arg	pl	art	+	11
arg	pl	art	p	48
				1003

Gene pair	Chi-squares X	Chi-squares Y	Linkage	Recomb. fract.
Arg-Pl	0.10	0.10	870.37	3.0 ± 0.6
Arg-Art	0.10	0.04	0.12	49.2 ± 2.4
Arg-P	0.10	3.13	46.80	36.1 ± 2.0
Pl-Art	0.10	0.04	0.00	50.0 ± 2.4
Pl-P	0.10	3.13	61.10	34.3 ± 1.9
Art-P	0.04	3.13	135.71	27.7 ± 1.7

Table 2. Three-point linkage analysis of a cross: Wlo p Art x wlo P art (cross distinct from that summarized in Table 1).

Wlo	Art	P	Total
+	+	+	146
+	+	p	97
+	art	+	31
+	art	p	6
wlo	+	+	32
wlo	+	p	0
wlo	art	+	41
wlo	art	p	1
			354

Gene pair	Chi-squares X	Y	Linkage	Recomb. fract.
Wlo-Art	3.17	1.36	64.01	23.7 ± 2.5
Wlo-P	3.17	3.62	35.42	10.7 ± 5.2
Art-P	1.36	3.62	20.63	27.2 ± 4.9

Table 3. Analysis of a four-point linkage test of a cross Arg Pl wlo na x arg pl Wlo Na. Data taken from experiment described in preceding article (6).

Arg	Pl	Wlo	Na	Total
+	+	+	+	102
+	+	+	na	20
+	+	wlo	+	4
+	+	wlo	na	37
+	pl	+	+	4
+	pl	+	na	0
+	pl	wlo	+	0
+	pl	wlo	na	0
arg	+	+	+	3
arg	+	+	na	0
arg	+	wlo	+	1
arg	+	wlo	na	2
arg	pl	+	+	45
arg	pl	+	na	0
arg	pl	wlo	+	0
arg	pl	wlo	na	2
				220

Gene pair	Chi-squares X	Y	Linkage	Recomb. fract.
Arg-Pl	0.10	0.39	156.13	4.7 ± 1.5
Arg-Na	0.10	1.96	4.65	34.3 ± 5.9
Arg-Wlo	0.10	0.87	14.94	25.8 ± 6.2
Pl-Na	0.39	1.96	9.34	22.6 ± 6.3
Pl-Wlo	0.39	0.87	19.40	18.7 ± 6.5
Na-Wlo	1.96	0.87	101.37	10.0 ± 2.2