Ramosus loci *rms-3* and *rms-4* are in pea linkage groups 1 and 7, respectively

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Arumingtyas et al. (1) recently identified several new *ramosus* loci including *rms-3* and *rms-4*. We present here evidence that *rms-3* is in linkage group 1 and *rms-4* in linkage group 7.

The data for *rms-3* were obtained from crosses between line WL6042 (*rms-3 a i*) and Hobart lines 63 (*Rms-3 A I*) and 111 (*Rms-3 A i*). The data for *rms-4* are from crosses between line K164 (*rms-4 Pgd-p*^{F} *Wa Aat-m*^{F} *Aldo*^{F} *Gal-2*^{S}) and Hobart lines 6 (*Rms-4 Pgd-p*^{F} *wa Aat-m*^{S} *Aldo*^{S} *Gal-2*^{S}) and 111 (*Rms-4 Pgd-p*^{S} *Wa Aat-m*^{S} *Aldo*^{S} *Gal-2*^{F}). K164 is the type line for *rms-4* and WL6042 is a representative line for *rms-3* (1). The plants were grown in the glasshouse under an 18 h photoperiod following the procedures previously described (1). The joint segregation χ^2 values and recombination fractions were calculated using the LINKAGE-1 program (2). All crosses were fully fertile.

Rms-3 showed significant evidence of linkage with group 1 marker *A* in two crosses (Table 1). The combined data generate a linkage $\chi^2 = 21.17$ ($P = 0.000004$) and a recombination fraction of 25 ± 8%. There was no evidence of linkage between *Rms-3* and marker *I* in the lower section of group 1 (Table 1). The map position of the *Rms-3* locus remains to be determined and we have made crosses involving several additional group 1 markers.

Table 1. Segregation data obtained from F_2 populations for *rms-3* and markers *a* and *i* in linkage group 1.

Genes	Cross	Phenotype					Chi-square			Recomb.	SE
		DD	DR	RD	RR	Total	Locus 1	Locus 2	Joint	Fract.	
Rms-3 A	6042x111	39	5	12	8	64	1.33	0.75	6.97*	30.9	11.1
	6042x63	46	7	3	8	64	2.08	0.08	17.98**	18.8	12.0
	Combined	85	12	15	16	128	0.04	0.67	21.17**	25.0	8.2
Rms-3 I	6042x63	37	16	8	3	64	2.08	0.75	0.04		
A I	6042x63	32	17	13	2	64	0.08	0.75	2.51		

*,** $P < 0.01$ and 0.0001, respectively; all other cases $P > 0.05$.

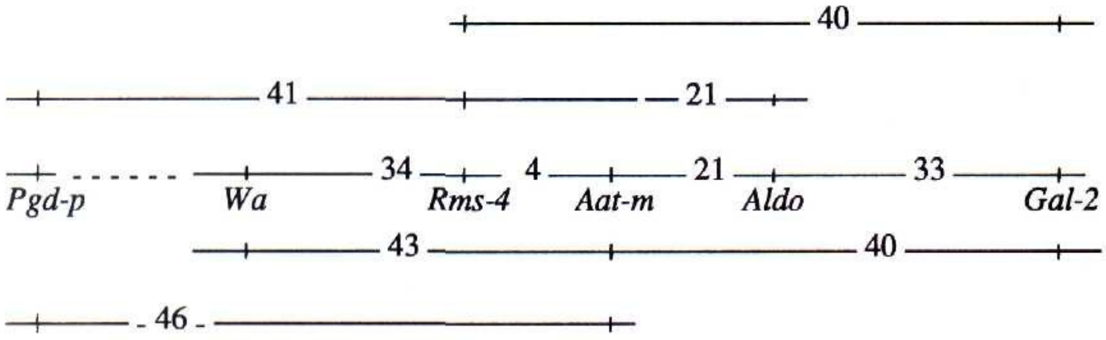
Table 2. Segregation data obtained from F_2 populations for *rms-4* and several markers in linkage group 7.

Genes	Cross	Phenotype [a]										Chi-square			Recomb. Fract.	SE
												Locus 1	Locus 2	Joint		
		DD	DR	RD	RR						Total					
Rms-4 Wa	164x6	39	**10**	**14**	1						64	0.08	2.08	1.52	34.0	10.9
		DF	DH	DS	RF	RH	RS									
Rms-4 Pgd-p	164x111	23	50	**27**	**11**	12	5				128	0.67	0.19	3.15	40.8	5.3
Rms-4 Aat-m	164x111	3	26	**22**	**11**	0	0				62	1.74	3.68	45.85*	5.8	3.0
	164x6	1	31	**16**	**14**	1	0				63	0.05	0.05	52.51*	3.3	2.3
	Total	4	57	**38**	**25**	1	0				125	1.18	1.94	98.10*	4.4	1.9
Rms-4 Aldo	164x111	7	43	**21**	**11**	8	1				91	0.44	1.68	21.15*	21.0	4.7
	164x6	9	21	**16**	**11**	4	0				61	0.01	2.51	16.19*	21.7	5.9
	Total	16	64	**37**	**22**	12	1				152	0.32	0.00	37.23*	21.3	3.7
Rms-4 Gal-2	164x111	**25**	54	15	4	16	**7**				121	0.47	3.79	2.37	40.0	5.4
Wa Aat-m	164x6	**14**	26	13	1	6	**3**				63	2.80	0.05	1.25	42.9	7.6
Wa Aldo	164x6	**19**	19	14	1	6	**2**				61	3.42	2.51	3.28	43.7	7.7
		FF	FH	FS	HF	HH	HS	SF	SH	SS						
Pgd-p Aat-m	164x111	**4**	7	3	9	9	8	4	11	**7**	62	1.06	3.68	2.37	45.5	6.3
Pgd-p Aldo	164x111	**6**	5	7	15	26	10	4	13	**7**	93	0.29	1.65	5.23	47.6	5.2
Pgd-p Gal-2	164x111	4	15	**10**	21	39	15	**8**	7	7	126	0.14	5.35	6.34	42.9	4.3
Aat-m Aldo	164x111	**8**	2	2	5	19	8	0	3	**12**	59	4.80	0.73	30.78*	20.7	4.3
	164x6	**12**	8	0	3	16	6	0	7	**9**	61	0.02	2.51	28.66*	21.5	4.3
	Total	**20**	10	2	8	35	14	0	10	**21**	120	2.18	0.32	56.83*	21.1	3.0
Aat-m Gal-2	164x111	1	4	**7**	8	16	10	**4**	6	4	60	3.20	1.20	4.07	39.8	6.1
Aldo Gal-2	164x111	1	12	**8**	10	37	11	**7**	13	2	101	5.42	2.25	9.14	32.8	4.2

[a] D = dominant, R = recessive, F = homozygous fast, H = heterozygous, and S = homozygous slow. The first named locus is shown first.
Numbers in bold face indicate the parental phenotypes.
* P <0.001; all other cases P >0.05.

Rms-4 showed significant evidence of linkage with group 7 isozyme markers *Aat-m* and *Aldo* in two crosses (Table 2). The combined data indicate strong linkage between *Rms-4* and *Aat-m* with a distance of about 4 cM. Unfortunately, the map position of *Rms-4* relative to the other group 7 loci is not clear as the distances *Rms-4* to *Aldo* and *Aat-m* to *Aldo* both work out at 21 cM and the distances *Rms-4* to *Gal-2* and *Aat-m* to *Gal-2* both work out at 40 cM. The results for *Pgd-p*, *Wa*, *Rms-4* and *Aat-m* indicate the order shown but these data are far too weak to permit a definite conclusion. The relative position of *Rms-4* therefore remains to be determined.

The data from Table 2 may be plotted as follows:



This map is, in general, consistent with the latest pea map (3) but more recombination occurred between *Wa* and the *Rms-4* and *Aat-m* loci than might be expected; neither joint segregation χ^2 is significant (P > 0.05). However, the sample size (n = 64 and 63) is fairly small for a morphological marker and larger numbers are necessary to properly establish these relationships.

In summary, *Rms-3* is in linkage group 1 about 25 cM from *A,* and *Rms-4* is in linkage group 7 about 4 cM from *Aat-m*, but the map position of both loci remains to be determined.

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1. Arumingtyas, E.X., Floyd, R.S., Gregory, M.J. and Murfet, I.C. 1992. Pisum Genetics 24:17-31.
2. Suiter, K.A., Wendel, J.F. and Case, J.S. 1983. J. Hered. 74:203-204.
3. Weeden, N.F., Swiecicki, W.K., Ambrose, MJ. and Timmerman, G.M. 1993. Pisum Genetics 25: Cover.