The mapping of *Pea-2* supports the assignment of *Vc-5* and *rb* to a specific region of chromosome 3

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The establishment of linkage between *Vc-5* and *rb* (5) is an important step in the process of mapping both genetic loci in the pea genome. *Vc-5* is one member of the small multigene family that encodes vicilin, a major seed storage protein. The *rugosus* gene, *rb,* affects several traits, including the lipid content of mature seeds. The tentative assignment of the pair to chromosome 3 (1) originated with a loose linkage between *rb* and *st* reported by Gritton (4). Marx (6) was unable to confirm this finding, however, using *st* and *chi-6* markers from the "*b* end" of chromosome 3; but, he did demonstrate another loose linkage between *rb* and *tac,* located at the opposite (*M*) end of the chromosome (7). The absence of linkage between *rb* and *apu,* which is located between *st* and *tac*, further suggested that *rb* is located distal to *tac,* and much nearer the end of chromosome 3.

Ellis et al. (3) have recently assigned a small *Vc-5* gene cluster that is linked with *rb* to one end of their chromosome 3 RFLP linkage group; but, the absence of accompanying standard marker loci disallows direct comparison and integration with the extant pea linkage map (10). Thus, Weeden et al. (10) still tentatively place *rb,* and now *Vc-5,* near the *b* end of chromosome 3.

Data obtained in this study for the F_2 progeny from two independent, reciprocal crosses, A1078-234 x 82-14n and A1078-234 x PI179449, verify that *Vc-5* is, in fact, linked to *st* and isozyme marker *Lap-1* (see Table 1 and Fig. 1), both located in chromosome 3. The genetic locus *Vc-5,* defined by cDNA clone pDUB2 (2), is the same RFLP marker found linked with *rb* (5), thereby establishing the location of the *rugosus* gene on chromosome 3 by association.

Further evidence supporting the assignment of the *Vc-5–rb* gene pair to chromosome 3 involves the RFLP marker *Pea-2*, a putative light-regulated gene which corresponds to pea cDNA clone pEA2 (9). In the A1078-234 x 82-14n cross, it exhibits linkage with both *Vc-5* and *st* (see Fig. 1). In the A1078-234 x PI179449 cross, in which *Vc-5* was not scored, *Pea-2* displays linkage with *st* and *Aat-c,* the cytosolic isozyme of aspartate aminotransferase, which is unambiguously located at the *M* end of chromosome 3 (10, 11).

These findings support both the proposal by Gritton (4) that *rb* is linked with *st* and the subsequent study by Marx (7) establishing the location of the *rb* gene near the *M* end of chromosome 3.

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Table 1. Joint segregation analyses for chromosome 3 genetic loci.

Loci	Number of F_2 progeny in each genotypic class[a]									n	χ^2	P	Recombinant fraction[e]
	11,11	11,12	11,22	12,11	12,12	12,22	22,11	22,12	22,22				
					A1078-234 x 82-14n[d]								
Pea2, Vc-5[b]	14	0	0	2	16	8	0	11	l	52	47.1	<<0.001	22.6 ± 4.8
Vc-5, st[c]	21		4	37		4	9		14	89	22.1	<<0.001	25.6 ± 5.2
Pea2, st[c]	12		2	17		10	12		0	53	7.3	<0.05	44.9 ± 8.3
Lap-1, st[c]	22		2	38		8	10		14	94	18.9	<<0.001	24.8 ± 5.0
Vc-5, Lap-1[b]	5	11	8	17	24	0	1	8	14	88	32.6	<<0.001	38.2 ± 4.9
					A1078-234 x PI 179449[d]								
Aat-c, Pea2[b]	6	1	0	2	24	1	0	2	8	44	52.2	<<0.001	7.1 ± 2.9
Pea2, st[c]	6		4	24		4	3		6	47	9.6	<0.01	37.0 ± 8.4

[a] Genotypic designations: 11 = 82-14n or PI 179449 homozygotes, 22 = A1078-234 homozygotes, and 12 = heterozygotes (for *Vc-5*, 1 and 2 represent haplotypes).

[b] 1:2:1:2:4:2:1:2:1 expected ratio.

[c] 3:1:6:2:3:1 expected ratio; due to dominance, *st* heterozygote listed as 11.

[d] Reciprocal cross.

[e] Calculated using the LINKAGE-1 computer program (8).

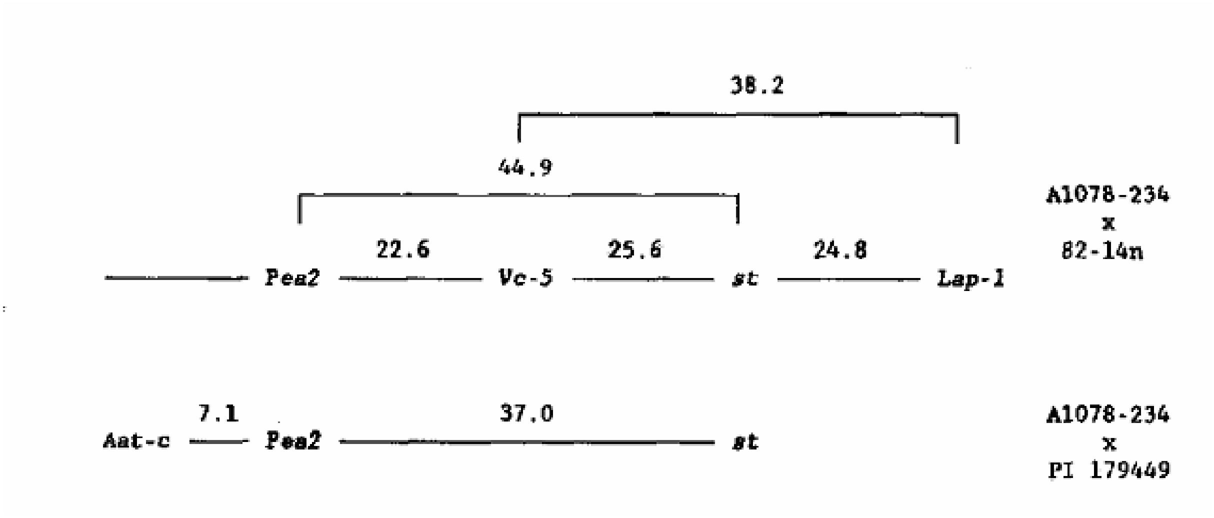

Fig. 1. Linkage relationships among *Vc-5, Pea-2* and associated marker loci for chromosome 3. The linkage maps show intrachromosomal arrangements among a group of genetic loci segregating in F_2 progeny from reciprocal crosses A1078-234 x 82-14n and A1078-234 x PI 179449. *Aat-c* was not scored in the former cross, while neither *Vc-5* nor *Lap-1* were scored in the latter cross.

1. Blixt, S. 1974. *In* Handbook of Genetics, Ed. R.C. King, Plenum Press, pp. 181-221.
2. Ellis, T.H.N., Domoney, C., Castleton, J., Clearly, W. and Davies, D.R. 1986. Mol. Gen. Genet. 205:164-169.
3. Ellis, T.H.N., Turner, L., Hellens, R.P., Lee, D., Harker, C.L., Enard, C., Domoney, C. and Davies, D.R. 1992. Genetics 130:649-663.
4. Gritton, E.T. 1971. Pisum Newsl. 3:15-16.
5. Lee, D., Turner, L., Davies, D.R. and Ellis, T.H.N. 1988. Theor. Appl. Genet. 75:362-365.
6. Marx, G.A. 1982. Pisum Newsl. 14:43-46.
7. Marx, G.A. 1987. Pisum Newsl. 19:40-41.
8. Suiter, K.A., Wendel, J.F. and Case, J.S. 1983. J. Heredity 74:203-204.
9. Thompson, W.F., Everett, M., Polans, N.O., Jorgensen, R.A. and Palmer, J.D. 1983. Planta 158:487-500.
10. Weeden, N.F., Ambrose, M. and Swiecicki, W.K. 1991. Pisum Genet. 23:cover.
11. Weeden, N.F. and Wolko, B. 1990. *In* Genetic Maps, Ed. S. O'Brien, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, pp. 6106-6112.