

Location of the *Lv* gene in pea linkage group VI

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Mutant *lv* plants are characterised by elongated internodes when grown under red or white light but are indistinguishable from wild type *Lv* plants in darkness or under far-red light (4, 11). Mutant plants also lack a normal elongation response to end-of-day far-red light and to a low red : far-red ratio (10) and are earlier flowering under short (non-inductive) photoperiods (11). Four recessive *lv* alleles have been identified from the mutant lines NEU3, R83, Wt10895 and L80m (5, 9), with each conferring a similar phenotype (9, 11). Because expression of the *Lv-lv* difference is restricted to certain light conditions, the *lv* mutants can be termed photomorphogenic. The syndrome of photomorphogenic abnormalities seen in the *lv* mutants is indicative of a reduction in the function of phytochrome B (phyB), one of several related photoreceptor proteins which play a major role in the control of plant development by light. Recent results have shown that lines R83, Wt10895 and L80m are all deficient in the phyB apoprotein while the NEU3 mutant has normal levels of phyB (11) suggesting that *Lv* may be a structural gene for phy B.

We report here data showing that the *lv* locus is in linkage group VI between *wlo* and *Prx3*, and close to *na* (within 2 cM).

F₂ segregation data for *lv* and group VI primary markers *wlo*, *na*, *Prx3*, *Arg* and *Pl* [see mapping guidelines (8)] were obtained from three crosses as detailed in Table 1. Parental marker lines 111 (A875-55-0) and 224 (A783-161) come from the Marx collection, line 107 is a selection from cv Torsdag, and the *lv* allele in line 232⁻ is derived from mutant line NEU3. Further details of the lines used are given in previous papers (9, 10).

Identification of the *Lv-lv* segregation was facilitated by growing the plants for the first 10 days in a growth chamber at 20°C under continuous white light (150 μmol m⁻²s⁻¹ at pot top) supplied by 40W cool white fluorescent tubes. The plants were then transferred to the glasshouse and grown to maturity under an 18 h photoperiod. All crosses were of normal fertility. Data were analysed using the programs LINKAGE-1 (6) and CROS (S.M. Rozov).

All individual segregations in Table 1 are in accordance with expectation (P>0.05). The joint segregation data reveal strong linkage of *lv* with *na* (<2 cM), *wlo* (4 cM) and *Prx3* (8 cM) and moderate linkage with *Arg* (26 cM) and *Pl* (26 cM) with P<0.000001 and <0.0001, respectively.

Our data for *wlo-Prx3* generate a map distance about one third that shown in the latest map (7). However, our data for *wlo-Pl* and *wlo-Arg* are consistent with the latest map and values obtained from very large data sets by Lamprecht (1) and Marx (2, 3). Based on a sample of 2797 plants, Lamprecht reported a recombination fraction of 31.6 ± 1.1% for *wlo* and *Pl*. Marx' data indicate a similar value for *wlo* and *Arg*. In the absence of multi-point data the map position of *na* remains unclear. Our 2-point data place *na* and *lv* in close proximity and imply that *na* may lie between *wlo* and *pl* as shown in Marx' (2) tentative map. However, the majority of Marx' 1981 (2) and 1982 (3) results in fact support the conclusion that *na* lies in the upper section of group VI above *wlo*. Likewise, our data do not indicate whether *Pl* lies between *Arg* and *wlo* as shown by Marx (2, 3) or the reverse arrangement as shown on the latest map (7). Our data for the *Arg-Pl* joint segregation are very similar to those of Marx and confirm tight linkage between these two loci.

Table 1. F₂ segregation data for *lv* and linkage group VI markers.

Loci	Cross ^a	Phenotype ^b						Total	Chi-squared			Linkage Prob.	Recomb. Fraction	SE
		DD	DR	RD	RR	Locus 1	Locus 2		Joint					
		DD	DR	RD	RR									
<i>Lv Wlo</i>	1	99	2	3	24		128	1.04	1.50	99.41	<0.0001	4.2	1.8	
<i>Lv Arg</i>	1	87	14	13	14		128	1.04	0.67	17.99	<0.0001	26.2	4.7	
<i>Lv Pl</i>	1	87	14	13	14		128	1.04	0.67	17.99	<0.0001	26.2	4.7	
<i>Wlo Arg</i>	1	86	16	14	12		128	1.50	0.67	11.25	<0.001	30.2	5.0	
<i>Arg Pl</i>	1	99	1	1	27		128	0.67	0.67	116.56	<0.0001	1.7	1.1	
<i>Wlo Pl</i>	1	86	16	14	12		128	1.50	0.67	11.25	<0.001	30.2	5.0	
<i>Lv Wlo</i>	2	45	30	24	0		99	0.03	1.48	13.77	<0.001			
<i>Lv Na</i>	3	130	3	2	46		181	0.22	0.41	156.44	<0.0001	2.7	1.2	
		DF	DH	DS	RF	RH	RS							
<i>Lv Prx3</i>	2	3	32	25	19	3	0	82	0.15	1.98	54.83	<0.0001	7.6	3.0
<i>Wlo Prx3</i>	2	22	32	6	0	3	19	82	0.15	1.98	44.80	<0.0001	11.0	3.6

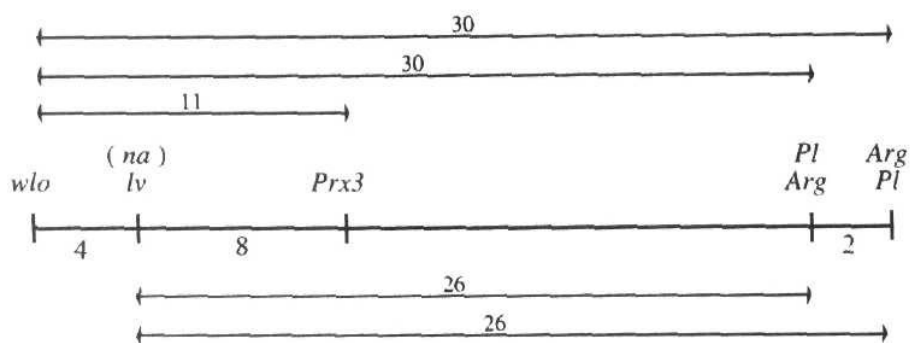
^aCross: 1) line 80m (*lv wlo arg pl*) x line 224 (*Lv Wlo Arg Pl*)

2) line 232⁻ (*lv Wlo Prx3^F*) x line 111 (*Lv wlo Prx3^S*)

3) line 107 (*Lv Na*) x *lv na* segregate from cross NEU3 (*lv Na*) x L81 (*Lv na*)

^bD = dominant, R = recessive, F = homozygous fast, H = heterozygous, and S = homozygous slow. The first named locus is shown first.

The data in Table 1 generate the following map:



In summary, these results obtained from three different crosses and using two different *lv* alleles are consistent and they provide convincing evidence that *lv* is located in linkage group VI between *wlo* and *Prx3* and close to *na*. We have planned a 5-point coupling phase cross involving standard line JI1794 and markers *wlo*, *lv*, *Gty*, *Prx3* and *Pl* to further examine distances in this section of group VI and other crosses to determine the position of *na*.

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