Additional mapping data for *lum-2* on chromosome 3

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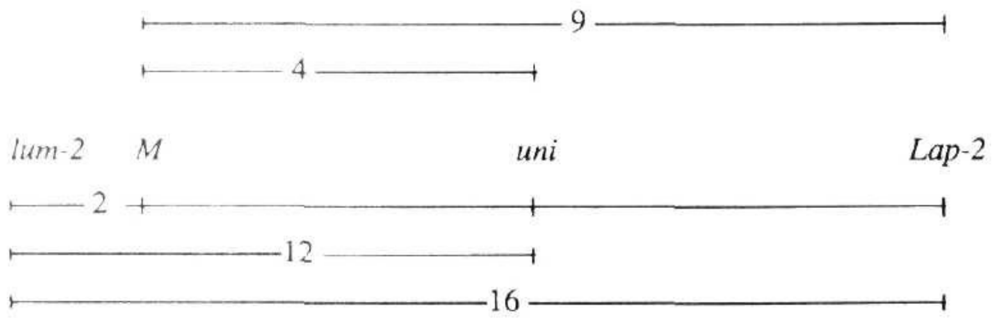
Swiecicki (2) described mutation cases of the *costata* type obtained at Wiatrowo. One of them was subsequently found (3) to be controlled by a gene, *lum-2,* which was strongly linked with *M* on chromosome 3 (Cr-0% = 2). Further linkage data are now available for *lum-2* with two genes close to *M*: *uni* (Cr-0% = 4; Blixt 1977) and *Lap-2* (Cr-0% = 9; Weeden 1985). Unfortunately, there was no suitable tester line available for multipoint analysis and additional difficulty was caused by the sterility of *uni* flowers (the mutant is maintained through heterozygous lines). In the first F$_2$ population raised from the cross Wt15299 (*lum-2 Lap-2*^{s} *Uni*) x Wt10187 (*Lum-2 Lap-2*^{f} *Uni/uni*) segregation data were obtained only for alleles at the *Lum-2* and *Lap-2* loci. No *uni* segregates occurred (presumably no *uni* gametes were provided by the Wt10187 parent). The Cr-0 value for *Lum-2* and *Lap-2* was 17% in this cross and 15% in the F$_2$ of cross Wt15299 (*lum-2 Lap-2*^{s}) x Wt8905 (*Lum-2 Lap-2*^{f}) (Table 1). In a second F$_2$ population from cross Wt15299 x Wt10187 some families did segregate for *uni.* Small disturbances occurred in the monohybrid segregation but a strong deviation from independent assortment occurred for *lum-2* and *uni* (Cr-0% = 12; Table 1). The following map is suggested based on our data and other results in the literature.



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1. Blixt, S. 1977. PNL 9 Suppl.
2. Swiecicki, W.K. 1983. Hod. Rosl., Akl., Nas. 27(4): 221-276.
3. Swiecicki, W.K. 1987. PNL 19:70-71.
4. Weeden, N.F. 1985. *In:* The Pea Crop: A Basis for Improvement, Eds P.D. Hebblethwaite, M.C. Heath and T.C.K. Dawkins, Butterworths, Lond. pp 55-66.

Table 1. Phenotypic distribution in an F_2 population from crosses:

1) Wt15299 (*lum-2 Lap-2*^{s}) x Wt10187 (*Lum-2 Lap-2*^{f})
2) Wt15299 (*lum-2 Uni*) x Wt10187 (*Lum-2 Uni/uni*)
3) Wt15299 (*lum-2 Lap-2*^{s}) x Wt8905 (*Lum-2 Lap-2*^{f})

A. Monohybrid segregation

Phenotype		Total	Chi-sq. (3:1)
1) *Lum-2*	*lum-2*		
81	25	106	0.11
Lap-2^f	*Lap-2*^{s}		
72	24	96	0.00
2) *Lum-2*	*lum-2*		
244	53	297	8.11**
Uni	*uni*		
202	95	297	7.73**
3) *Lum-2*	*lum-2*		
110	21	131	5.62*
Lap-2^f	*Lap-2*^{s}		
102	28	130	0.83

B. Joint segregation of *lum-2* with *Lap-2* and *Uni*

Phenotype				Total	Joint chi-sq.	Recomb. fract.	SE	Phase
1)*Lum-2 Lap-2*^{f}	*Lum-2 Lap-2*^{s}	*lum-2 Lap-2*^{f}	*lum-2 lap-2*^{s}					
67	10	5	14	96	29.94***	17.1	4.3	C
2)*Lum-2 Uni*	*Lum-2 uni*	*lum-2 Uni*	*lum-2 uni*					
149	95	53	1	297	27.84***	11.9	5.7	R
3)*Lum-2 Lap-2*^{f}	*Lum-2 Lap-2*^{s}	*lum-2 Lap-2*^{f}	*lum-2 Lap-2*^{s}					
97	12	5	16	130	44.26***	14.9	3.4	C

*,**,*** $P < 0.05$, 0.01 and 0.001, respectively.
In segregating progenies, the phenotype designated *Lap-2*^{f} includes both *Lap-2*^{f}*/Lap2*^{f} and *Lap-2*^{f}*/Lap-2*^{s} plants.