# Location of gene *lum-3* in relation to *tl* and *gp*

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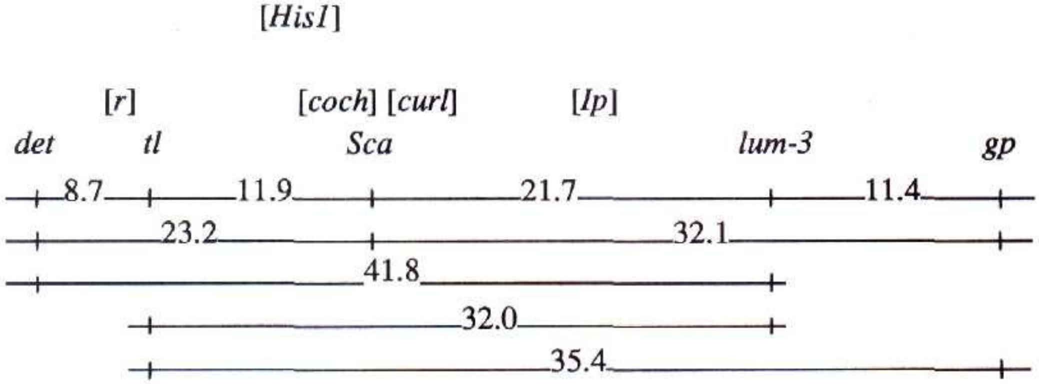
A *costata*-type mutant, *lum-3,* was isolated and localised in linkage group V about 10 cM from *gp* by Swiecicki (3). In the crosses analysed, Swiecicki did not find any linkage between *lum-3* and the *r–tl* segment of group V. As the relative linkage intensities among the markers examined *(lum-3, te, cp, gp)* were slightly contradictory (3), the precise position of *lum-3* could not be stated with certainty.

In my cross of testerline RT-2 *(det, Tl, Sca*$^{f}$*, Lum-3, Gp)* with the Wiatrowo type line for *lum-3,* WM5309 *(Det, tl*$^{w}$*, Sca*$^{s}$*, lum-3, gp),* I found a strong linkage between *lum-3* and gene *Sca,* known to be linked to *tl* (2), and *gp.* The dihybrid segregation data for this cross are shown in Table 1.

According to the data obtained in this cross and results given in the previous paper (1), the combined *r–tl–gp* chromosome segment may be drawn as follows:



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1. Rozov, S.M., Temnykh, S.V., Gorel, F.L. and Berdnikov, V.A. 1993. Pisum Genetics, 25:46-51.
2. Smirnova, O.G., Rozov, S.M. and Berdnikov, V.A. 1989. Pisum Newsl. 21:63-65.
3. Swiecicki, W.K. 1988. Pisum Newsl. 20:36-37.

Table 1. Joint segregation data obtained from the $F_2$ of cross RT-2 (*det, Tl, Sca*$^{f}$*, Lum-3, Gp*) x Wt-15309 (*Det, tl*$^{w}$*, Sca*$^{s}$*, lum-3, gp*).

| Genes | | Phase | Number of progeny with designated phenotype[1] | | | | | | | | | Joint | Recomb. | SE |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | A/B | A/h | A/b | h/B | h/h | h/b | a/B | a/h | a/b | seg. $\chi^2$ | frac. | |
| *det* | *tl* | C | 13 | 38 | 3 | -- | -- | -- | 1 | 3 | 23 | 52.4*** | 8.7 | 3.3 |
| *det* | *Sca* | C | 18 | 28 | 8 | -- | -- | -- | 2 | 8 | 17 | 20.4*** | 23.2 | 5.2 |
| *det* | *lum-3* | R | 38 | -- | 16 | -- | -- | -- | 22 | -- | 5 | 1.6 | 41.8 | 9.1 |
| *det* | *gp* | R | 36 | -- | 18 | -- | -- | -- | 23 | -- | 3 | 4.3* | 32.3 | 9.9 |
| *tl* | *Sca* | C | 20 | 6 | 1 | 5 | 43 | 7 | 0 | 4 | 21 | 98.7*** | 11.9 | 2.4 |
| *lum-3* | *tl* | C | 22 | 44 | 11 | -- | -- | -- | 5 | 11 | 14 | 12.7** | 32.0 | 5.3 |
| *gp* | *tl* | C | 22 | 37 | 11 | -- | -- | -- | 3 | 12 | 8 | 5.3 | 35.4 | 5.9 |
| *lum-3* | *Sca* | C | 23 | 44 | 10 | -- | -- | -- | 2 | 9 | 19 | 28.4*** | 21.7 | 4.4 |
| *gp* | *Sca* | C | 23 | 33 | 14 | -- | -- | -- | 2 | 10 | 11 | 8.8* | 32.2 | 5.7 |
| *lum-3* | *gp* | C | 65 | -- | 5 | -- | -- | -- | 5 | -- | 18 | 47.0*** | 11.5 | 3.5 |

[1] A,a - first gene; B,b - second gene; h - heterozygous. Where both genes are dominant, the capital letter stands for the dominant allele. Where the second gene is codominant, capital A stands for the dominant allele of the first gene and capital B for an allele of the second gene which is in coupling with A. Where both genes are codominant, the capital letter stands for an allele of the first parent.

*,**,*** $P < 0.05$,0.01 and 0.001, respectively. Data were analysed by the LINKAGE-1 program.