EMS-induced lethal in the vicinity of the locus *lf*

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In a communication by Gorel et al. (1) in this issue we described an experiment performed to obtain EMS-induced mutations linked to the breakpoint of the Hammarlund translocation. We report here another mutation from that experiment and characterize the mutation as a sporophytic lethal near the locus *lf*.

Among the M_3 families (for experimental design see ref. 1) we found a family of 16 individuals, none of which had the phenotype *cri gp a*. This observation suggests the presence of a lethal located near the breakpoint on the normal chromosome set. Thirteen of the plants were tested for the *His(2-6)* phenotype. Six appeared to be heterozygous for this locus and, hence, for the translocation; seven were homozygous for *His(2-6)*, and these should be homozygous for the translocated karyotype. The progeny from the selfing of three heterozygous plants were sown and produced 85 *Cri* plants (44 structural heterozygotes and 41 homozygotes for the translocation) and two *cri* plants (structural homozygotes for normal karyotype). No crossover events between the breakpoint and the markers *a*, *cri*, and *gp* were observed. The progeny of 11 structural heterozygotes were again planted and produced 76 *Cri* plants (50 structural heterozygotes and 26 homozygotes for the translocation) and 2 *cri* plants. One of the structural heterozygotes had phenotype *gp*, indicating that a crossover event had taken place between this marker and the breakpoint.

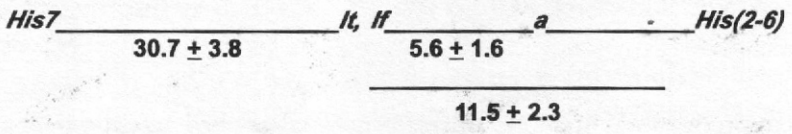
Combining all data from the M_3 to the M_5 generation gives a total of 100 structural heterozygotes, 74 homozygotes for the translocation, and 4 homozygotes for normal karyotype (with phenotype *cri*). We conclude that the line with the normal karyotype bears a sporophytic lethal closely linked to the Hammarlund translocation breakpoint. This lethal seems to reduce competing ability of the male gametophytes for fertilization, because the observed ratio (100:74) deviates significantly from the expected 2:1 (Chi-square=6.62; P<0.025). The crossovers observed suggest that the lethal may be either on linkage group II or on linkage group V distal to *cri* but not on linkage group V proximal to this gene. To test the first option we crossed a structural heterozygote with the testerline WL1238 and obtained four F_1 plants. One of them had semi-sterile pollen phenotype and presumably was heterozygous for the translocation. Three had fully fertile pollen and were assumed to have normal karyotype. The F_2 populations derived from these three plants (110 individuals in total) were grown and analyzed for deviations from the expected segregation ratios of markers *cri*, *His(2-6)*, *a*, *lf*, and *His7*. The normal karyotype of the hybrid Tau-2 has a genotype *His7*^{2} *lf a His(2-6)*^{1123} *cri*; the line WL1238 has *His7*^{3}; *Lf A His(2-6)*^{1221} *Cri*.

The following phenotype ratios were observed:

for the gene *cri*:	88 Cri : 22 cri
for haplotypes of *His(2-6)*:	36 1221 : 66 1221/1123 : 8 1123
for the gene *a*:	106 A : 4 a
for the gene *lf*:	110 Lf : 0 lf
for alleles of the gene *His7*:	32 3/3 : 59 3/2 : 19 2/2

Although deviation of the segregation for the gene *cri* from the expected 3:1 is not significant (χ^2=1.47 P>20%), segregation for the other markers, belonging to the linkage group II, is greatly disturbed. No crossovers were registered between the lethal and the gene *lf*. All the plants started flowering at a node not lower than 14, while the plants with a normal karyotype segregating from the hybrid Tau-2 always started flowering at node 8 or 9. The number of crossovers between the lethal and other markers of linkage group II correspond to their distance from *lf*. We derived equations for a maximum likelihood estimation of the crossover distances between

a lethal and a dominant or co-dominant marker, based on segregation deviations of a single gene segregation in F_2 from 3:1 and 1:2:1 models, respectively (2). Such calculations gave the following linkage relationships:



These distances correspond closely to the average map of this segment (3), with only the distance *lf*—*a* somewhat reduced:

This mutation appears to be the first mapped lethal in pea that stops sporophyte development at an early stage (before the seed is formed) and thus exhibits no visible phenotype. A question arises what nomenclature would be best for mutations of this kind. We propose to adopt, with modification, the system accepted for *Drosophila* and to symbolize such lethals as *l(x)y*, where x is the linkage group number and y is the order number of the lethal. Hence, the lethal described is to be named *l(2)1*.

This lethal can be useful for constructing some balancer systems in the pea, and we already have used it in some of our stocks.

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1. Gorel, F.L., Kosterin, O.E. and Berdnikov, V.A. 1999. Pisum Genetics 31:5-8.
2. Kosterin, O.E., Berdnikov, V.A. and Gorel, F.L. 1999. Pisum Genetics 31:33.
3. Kosterin, O.E., Bogdanova, V.S., Gorel, F.L., Rozov, S.M., Trusov, Y.A. and Berdnikov, V.A. 1994. Plant Science 101:189-202.