Supplemental mapping of the gene *Chi-32* on chromosome 3

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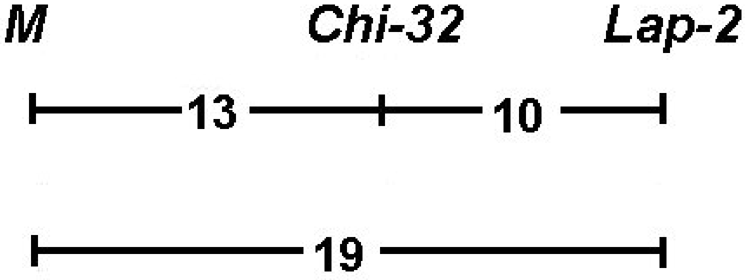
The chlorotica mutant *chi-32* was induced in the line Wt3519 by using fast neutrons for the radiation treatment of dry seeds. The F$_9$ generation analysis of the two point cross Wt11288 (testerline) x WT15325 (mutant) showed linkage between *chi-32* and gene *M* in chromosome 3 (CrO% = 8.5 ± 1.7) (1). A recombinant line with genotype *chi-32 M* was selected from fhis test and included in our *Pisum* gene bank as the line Wt15327.

We chose a second marker, the gene *Lap-2,* for mapping of the *chi-32* locus. According to Weeden and Marx (2) the recombination fraction for *M* - *Lap-2* equals 9.0 ± 4.9. Line Wt15327 (*chi-32 M Lap-2*^{S}) was crossed with line Wt8905 (*Chi-32 m Lap-2*^{f}) and single locus segregation data are shown in Table 1 A. All polymorphisms displayed segregation ratios close to those expected for single gene traits. Joint segregation analysis of *chi-32* and markers on chromosome 3 revealed a non random assortment with *M* (CrO% = 13.7 ± 7.1) and with *Lap-2* (CrO% = 10.2 ± 2.3). The recombination fraction for the pair *M* - *Lap-2* was 18.8 ± 7.0 (Table 1 B) This three-point linkage analysis on chromosome 3 indicates the following ranking of the loci:



Our results indicate that the gene *Chi-32,* which controls a chlorophyll mutation, is placed between *M and Lap-2* on chromosome 3. Previous results of Weeden and Marx (2) reveal a smaller distance between *M* and *Lap-2.* The cause of this inconsistency is not presently known.

Table 1. Phenotypic distribution in an F_2 population derived from cross Wt8905 (*Chi-32 m Lap-2*^{f}) xWt15327 (*chi-32 M Lap-2*^{S})

A. Monohybrid segregation

Locus	X	x	Total	Chi-square (3:1)
Chi-32	144	49	193	0.01
M	136	51	187	0.51
Lap-2	140	51[1]	191	0.29

B. Joint segregation of chlorotica *chi-32* with *M* and *Lap-2:*

Gene pair	XY	Xy	xY	xy	Total	Joint Chi-sq.	Rec. fract.	S.E.
Chi-32 : M	91	51	45	1	187	19.77***	13.74	7.14
Chi-32 : Lap-2	132	11[1]	8	40[1]	191	105.06***	10.23	2.33
M : Lap-2	88	46[1]	49	2[1]	185	17.77***	18.88	7.03

***P< 0.001

[1] Homozygous slow *Lap-2*^{S} *Lap-2*^{S}.

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1. Czerwinska, St. 1988. PNL 20:9-10.
2. Weeden, N.F. and Marx, G.A. 1984. J. Heredity 75:365-370.