

NEW CHLOROTICA GENE (chi 32) IN CHROMOSOME 3

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Physical mutagens were compared in investigations on the influence of genotype x mutagen combinations on the mutation spectrum in pea. Seeds of line Wt 3519 (cv. 'Porta') were treated with three doses of fast neutrons from a cyclotron (200r, 350r, 500r) and from a reactor (170r, 290r, 400r) and with gamma rays from a ⁶⁰Co source (4000r, 7000r, 10000r). In the M2 generation containing about 21,000 plants, 720 mutation cases were selected. Among them about 30 percent were chlorophyll mutations. Most numerous was the chlorotica type (72 mutation cases). Some of them were phenotypically similar to those described by Blixt (1), but mutant Wt 15325, induced by 350r Nf, was distinguishable. Plants were characterized by a yellow-green color affecting the whole plant (leaves, stem, tendrils, and sepals) being more visible in later stages of plant development.

The segregation in M2 family as well as the results of the original test cross showed Mendelian, recessive inheritance: [Wt 15325 (mutant) x Wt 3519 (initial line)]=91:34 observed (Chi-square=0.32); [Wt 3519 x Wt 15325]=130:40 observed (Chi-square=0.20).

There are 30 recessive genes of the chlorotica type described earlier. So to prove novelty of a new isolate a locus identity test cross should be performed. To shorten the process, we conducted linkage tests with the hope that the results would show the presence of a new gene. The mutant Wt 15325 was crossed with tester lines for the seven chromosomes. In F2, undisturbed monohybrid inheritance for most of gene markers was found; the populations also confirmed the recessive nature of the chlorotica mutant (Table 1A).

Table 1. Phenotypic distribution in an F2 population segregating for chlorotica from WL 1288 (testerline) x Wt 15325 (mutant).

A. Monohybrid F. segregation

Locus	X	X	Total	Chi-square (3:1)
Chi	296	104	400	0.21
B	185	67	252	0.34
St	302	94	396	0.34
M	230	50	280	7.62*
A	301	88	389	1.17

1. Joint segregation of chlorotica with b st M

Gene pair	XY	xy	xY	xy	Total	Joint Chi-square	Recomb. fract.	S.E.
Chi-B	153	54	32	13	252	0.14ns		
Chi-St	219	76	83	18	396	2.64ns		
Chi-M	217	9	11	41	278	168.10**	8.5	1.8
B-St	163	22	30	37	252	49.57**	23.1	3.1
B-M	141	26	55	10	232	0.00ns		

There was no evidence of linkage with markers on chromosomes 1,2,4,5,6,7. But deviations from independent dihybrid segregation of the gene pair Chi-M were found with a CrO value of 8.5 (Table IB). According to the present Pisum map there are no known chlorotica genes in the M-segment of chromosome 3, although chi-6 and chi-16 are known to reside elsewhere on the same chromosome. On these grounds I propose the symbol chi-32 for the new gene of chlorotica type. For final mapping we plan to confirm the above results in comparison to two loci - using uni or preferably isozymic loci Lap-2, Acp-3.

1. Blixt, S. 1972. Agri Hort. Genet. 30.

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