The *chlorotica* mutation in line Wt11019 shows linkage with group 6 marker *Pl*

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'Chlorophyll' mutations are quite common in *Pisum.* In one of our earlier experiments, mutations in this general category amounted to some 45% of all mutations observed (1). While multiplying our pea collection, we found some plants showing clear chlorophyll abnormalities in a plot of line Wt6103. The *chlorotica* phenotype was visible from the 3-4 leaf stage up to the flowering stage. The plants became normal in phenotype during the reproductive phase and seed set was normal. Unfortunately, the mutation does not express in greenhouse conditions. We selected the accession Wt11019 from among the mutant plants and crossed this line with our usual set of tester lines. The mutation showed monogenic recessive inheritance and evidence of linkage with group 6 marker *Pl* (Table 1). No other *chlorotica* loci are known in linkage group 6 and the locus was tentatively symbolised *chi-33.* There was no evidence of linkage between *chi-33* and another group 6 marker, *wlo* (Table 1). We decided to present this preliminary data because *chi-33* could be a useful morphological marker for linkage group 6.

1. Swiecicki, W.K. 1983. Hod. Rosl. Aklim. Nas. 27:221-276.

Table 1. Monohybrid (a) and dihybrid (b) segregation in the F_2 of cross Wt11019 (*chi-33, Wlo, pl*) x Wt10345 (*Chi-33, wlo, Pl*).

(a)	Phenotype[1]			
Locus	D	R	Total	χ^2(3:1)
Chi-33	154	50	204	0.03
Wlo	163	44	207	1.55
Pl	130	63	193	6.01*

(b)		Phenotype[1]							
Loci	DD	DR	RD	RR	Total	Joint seg. χ^2	Recomb. frac.	SE	Phase
Chi-33/Wlo	119	35	41	9	204	0.5	45.9	5.5	R
Chi-33/Pl	111	33	19	29	192	23.2****	29.0	4.0	C
Wlo/Pl	91	59	39	4	193	13.7***	25.8	6.6	R

[1] D = homozygous dominant + heterozygous; R = homozygous recessive.
*,***,**** $P < 0.05$, 0.001 and 0.0001, respectively.