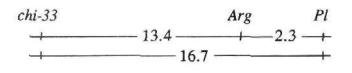
Linkage of gene chi-33 on linkage group VI

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The spontaneous *chlorotica* mutation *chi-33* (Wt11019) shows clear expression at the seedling stage except under greenhouse conditions (1). A preliminary linkage test (1) indicated significant linkage between *chi-33* and linkage group VI marker *Pl* (29 cM) but linkage with *wlo* on this chromosome was not significant.

To locate *chi-33* more precisely, we crossed Wt11019 with tester line Wt11777 which carries four group VI markers *Pl*, *Arg*, *wlo* and *art-1*. In the F_2 , *chi-33* and the four markers all showed normal monohybrid segregation (Table 1). Dihybrid segregation analyses (Table 1) provided strong evidence of linkage between *chi-33* and markers *Arg* (P<0.0001, 13.6 cM) and *Pl* (P<0.0001, 16.7 cM) but only weak evidence of linkage between *chi-33* and markers *wlo* (P<0.01, cM 25.4) and *art-1* (P<0.05, 29.7 cM). Together with the previous data (1), these results indicate *chi-33* is located in the linkage group VI and closer to *Pl* than *wlo*. The data in Table 1 suggest the following arrangement of loci:



(a)			Phenotype*						
Locus	D		R		Total	Chi-sq. (3:1)			
Chi-33	100)	30		130	0.26			
Arg	98		32		130	0.01			
Pl	96		31		127	0.02			
Art-1	102	102 27			129	1.14			
Wlo	96		34		130	0.09			
(b)		Phenotype*				Joint	Recomb		
Loci	DD	DR	RD	RR	Total	Chi-sq.	fract.	SE	
Chi-33/Arg	91	9	7	23	130	56.9	13.6	3.2	
Chi-33/Pl	88	11	8	20	127	43.0	16.7	3.7	
Arg/Pl	95	2	1	29	127	111.1	2.3	1.3	
Chi-33/Art-1	75	25	27	2	129	4.4	29.7	7.9	
Chi-33/Wlo	68	32	28	2	130	7.7	25.4	8.1	

Table 1. Monohybrid (a) and dihybrid (b) segregation in the F₂ population of the cross K. 1317 = Wt 11019 (*chi-33, arg, pl, Art-1, Wlo*) x Wt 11777 (*Chi-33, Arg, Pl, art-1, wlo*).

*D = homozygous dominant + heterozygous; R = homozygous recessive

1. Apisitwanich, S. and Swiecicki, W.K. 1993. Pisum Genetics 25:17.