A NEW GENE CRISPOID (crd) ON CHROMOSOME 1

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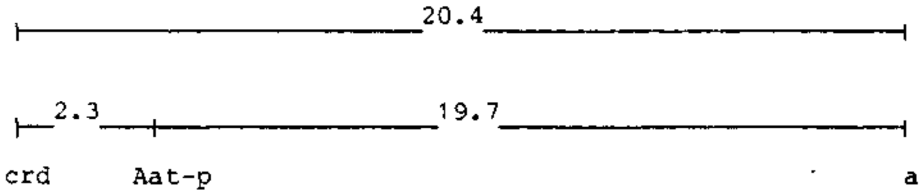
In experiments on induced mutations (1) a mutant of *crispoid* type was selected after seed treatment of line Wt 3527 by 0.014% NEU and included in the Wiatrowo pea gene bank in 1981 under catalogue number Wt 11300. *Crispoid* pea plants are characterized by a bigger and more waved leaf surface than normal and the stipules are toothed at the base (Fig. 1). Some connection with the *cerosa* and *wilty* phenotypes could also be seen. Locus identity tests for *crispoid* (Wt 11300) with *crispa* (Wt 11297, *cri*), *crispi folius fertilis* (Wt 16118, *crif*) and *curled* (Wt 15855, *curl*) showed that all of these phenotypes are controlled by different loci. A good monohybrid segregtion was obtained in the F2 population of cross Wt 3527 x Wt 11300 (153 normal: 48 mutant plants; $X^2 = 0.13$). Therefore the symbol *crd* for *crispoid* is suggested.

To locate the new gene, several crosses were made with tester lines. Monogenic recessive inheritance of *crd* was confirmed in these F2 populations (e.g. Table 1A). Linkage between *crd* and the a locus was found in the F2 of crosses Wt 11300 x Wt 11288 (recomb. fract. 21.2) and Wt 11300 x Wt 11238 (recomb. fract. 20.4, Table IB). The latter cross also revealed tight linkage between *crd* and the isozyme locus *Aat-p* (recomb. fract. 2.3) but the recombination fraction of 35.7 ± 8.7 for *crd* and the d locus does not differ significatnly from that expected with free recombination (Table IB). These results suggest that *crd* is located on chromosome 1 close to *Aat-p*, probably between *Aat-p* and *Est*-3 (2). The latter locus should be utilised in more detailed mapping studies. The following linkage map is tentatively suggested.



I acknowledge the help of Dr. Bogdan Wolko in separating genotypes or the *Aat-p* locus.

1. Swiecicki, W. K. 1984. PNL 16:84-86.
2. Weeden, N. F. 1985. In: The Pea Crop. A Basis for Improvement. Eds. P. D. Hebblethwaite, M. C. Heath, and T. C. K. Dawkins, Butterworths, London, pp. 55-66.

Table 1. Phenotypic distribution in an F2 population from a cross between Wt 11300 (crispoid) and Wt 11238 (tester line).

A. Monohybrid F2 segregation

Phenotype		Total	Chi-square (3:1)
A	a		
98	26	124	1.08
D	d		
71	27	98	0.34
Aat-p	aat-p		
92	32	124	0.04
Crd	crd		
91	33	124	0.17

B. Joint segregation of Crd with A, D and Aat-p

Phenotype				Total	Joint Chi-square	Recomb. fract.	S.E.	Phase
A Crd	A crd	a Crd	a crd					
88	15	8	18	124	30.0	20.4	4.1	C
A Aat-p	A aat-p	a Aat-p	a aat-p					
84	14	8	18	124	30.2	19.7	4.1	C
A D	A d	a D	a d					
71	27	1	1	98	1.0	63.1	6.4	R
D Crd	D crd	d Crd	d crd					
58	13	25	2	98	1.6	35.7	8.7	R
D Aat-p	D aat-p	d Aat-p	d aat-p					
59	12	25	2	98	1.6	37.0	8.6	R
Crd Aat-p	Crd aat-p	crd Aat-p	crd aat-p					
90	1	2	31	124	102.1	2.3	1.4	C

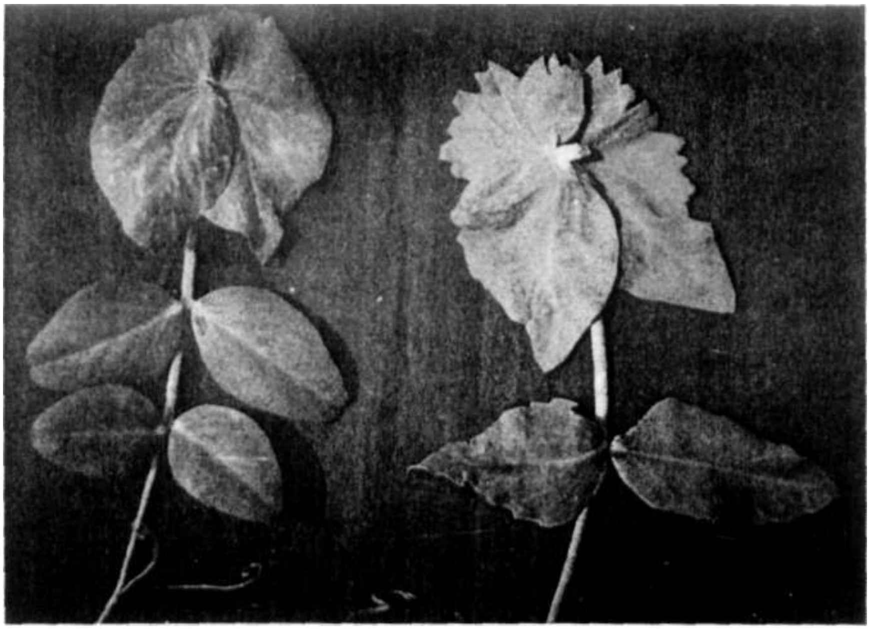


Fig. 1. The leaf of crispoid mutant Wt 11300 (left) and the initial line Wt 3527 (right).