<u>LINKAGE RELATIONS OF GENES</u> af-i <u>ON CHROMOSOME 1 AND</u> curl-tl ON CHROMOSOME 7 IN PEAS (Pisum sativum L.)

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The gene $\underline{\mathrm{af}}$ which converts the leaflets into tendrils is largely used in breeding programs for improving standing ability of pea. Its location on chromosome 1, first reported by Khangildin (2), subsequently has been confirmed by others (1,3,4,5,6,9) but the values of linkage intensity between $\underline{\mathrm{af}}$ and $\underline{\mathrm{i}}$ obtained by different authors has varied widely: 45.8% (2), 5.36% (3), 14.5% (9), 7.47% (1), 8.3% (4), 3.7% (5), 3.72% in the greenhouse, and 5.69% in the field (6). The factors leading to such great variation of recombination fraction values are still unknown.

Genetic analysis of the F2 population resulting from the cross F81-1261 (af af i i) x cv. 'Auralia' ($\underline{Af\ Af\ I\ I}$) confirmed the linkage af-i on chromosome 1. The recombination fraction value was 7.20+1.27 (Table 1).

Table 1. Analysis of joint segregation in F, for genes af and i.

Gene		Xy				Chi-sq	Recomb.		
pair	XY	XY		xy	X	Y	Linkage	fract.	S.E.
Af i	314	16	16	450	0.67	0.67	328.8***	7.20	1.27

*** Significant at 0.001

The mutant $\underline{\text{curl}}$ was obtained by Sidorova and Uzhintzeva (8) by treating 'Torsdag' seeds with EMS. The same mutant was obtained also at I.C.C.P.T.-Fundulea by gamma irradiation of seeds of line F70-413. The line possessing the mutant gene was designated MF-13 $\underline{\text{curl}}$. Marx (7) has located the gene $\underline{\text{curl}}$ on chromosome 7.

Analysis of F2 populations of crosses of MF-13 <u>curl</u>, line with several lines possessing marker genes for different chromosomes confirmed the location of <u>curl</u> gene on chromosome 7 (Table 2). The recombination fraction value between the genes <u>curl</u> and tl was 26.95 + 3.79.

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Table 2. Analysis of joint segregation in F2 for curl and different gene markers.

Gene							Chi-s	Recomb.		
pair	XY	Хy	xΥ	ху	Total	X	Y	Linkage	fract.	S.E.
Curl Af	258	91	77	29	455	0.70	0.46	0.06 ns		
Curl St	155	42	48	20	265	0.06	0.36	1.77 ns		
Curl Le	196	61	80	19	356	1.50	1.21	0.98 ns		
Curl Gp	99	39	36	12	186	0.06	0.58	0.19 ns		
Curl Pl	164	50	54	20	288	0.07	0.07	0.40 ns		
Curl -Tl	288	123-	108	8	527	2.51	0.01	30.60 **	26.95	3.79

^{**} Significant at 0.01
