IS THE LOCUS FOR THE GENE HET ON CHROMOSOME 7 or 5? A NEW LOOK AT LAMPRECHT'S LINKAGE GROUPS

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Previous results (2) analyzing the F_2 generation of cross Wt11291 (het) x Wt11744 (tl r wsp) indicated linkage for mutant gene het on chromosome 7. More recent results from crosses between the type line for het and several testerlines are given in Tables 1 and 2. The results from cross Wt11291 (het) x Wt11238 (A d k wb s b cp te gp tl r) confirmed linkage between het and markers tl and r but the linkage was somewhat weaker than previously reported (2). In addition, linkage of het with markers gp, te and cp from chromosome 5 was found in the same cross (recombination values 21-28%). These results indicate that one gene is in two chromosomes according to the Lamprecht linkage map (1). It is possible that the heterophylus character is controlled by two genes but there is a low probability for the double recessive of one character to occur in mutant induction and the segregation for Het-het is fairly close to a 3:1 ratio (Table 1). Alternatively, all markers linked with het (from chromosomes 5 and 7) are in fact in one chromosome.

The latter explanation seems quite credible, even after 40 years of accepting Lamprecht's version of the map, and is in accord with the recent results of Weeden and Wolko (3) who suggest some major rearrangements to the previous *Pisum* gene map. For example, according to their results, the segment det curl r tl from chromosome 7 is linked with the gp teu lum-3 region of chromosome 5.

The present results fit the more recent map and indicate that het is on chromosome 5, probably between r and gp.

Table 1. Monohybrid segregation data for the F_2 of cross Wt11291 (het) x Wt11238 (testerline)

Phenotype/Number		Total	Chi-square (3:1)
Tl 298	tl 91	389	0.54
Cp 233	cp 62	295	2.50
R 251	r 65	316	3.31
Te 214	te 81	295	0.95
Gp 303	gp 72	375	6.73**
Het 296	het 76	372	4.14*

*,**Probability less than 0.05 and 0.01, respectively.

Table 2. Dihybrid F_2 segregation data for *het* and several gene markers in the F_2 of cross Wt11291 x Wt11238

Phenotype/Number				Total	Joint chi-sq.	Rec. frac.	SE	Phase
Tl Het 218	Tl het 68	tl Het 78	tl het 8	372	8.53**	34.6	4.5	R
R Het 190	R het 60	r Het 60	r het 4	314	9.89**	29.1	5.1	R
Cp Het 175	Cp het 57	cp Het 58	cp het 3	293	11.45***	25.9	5.4	R
Te Het 156	Te het 57	te Het 77	te het 3	293	18.78***	21.7	5.5	R
Gp Het 224	Gp het 71	gp Het 65	gp het 4	364	11.41***	28.1	4.8	R
Tl Cp 188	Tl cp 40	tl Cp 45	tl cp 22	295	7.29**	38.7	3.8	C
Tl Te 174	Tl te 54	tl Te 40	tl te 27	295	7.18**	39.4	3.8	C
Tl Gp 248	Tl gp 42	tl Gp 55	tl gp 30	375	18.35***	34.4	3.1	C
Cp R 186	Cp r 43	cp R 40	cp r 17	286	3.36	41.6	4.0	C
Te R 172	Te r 38	te R 54	te r 22	286	3.96*	41.6	4.0	C
Gp R 211	Gp r 46	gp R 40	gp r 19	316	6.01*	39.4	3.7	C
Tl R 239	Tl r 6	tl R 12	tl r 59	316	219.14***	5.9	1.4	C

*,**,*** Probability less than 0.05, 0.01 and 0.001, respectively.

1. Blixt, S. 1972. Agri Hort. Genet. 30:1-293.
2. Swiecicki, W.K. 1989. PNL 21:75-76.
3. Weeden, N.F. and B. Wolko. 1990. *In* Genetic Maps, Ed. S. O'Brien, Cold Spring Harbor, pp 6106-6112.