Linkage of *Td* with markers on linkage group III of peas

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A gene responsible for leaflet dentation in peas, *Td*, was reported by Lamprecht (1, 2) to be located on linkage group IV, about 40 map units from *Le*. More recently, Marx (3) studied *Td* in a cross that concurrently segregated for *b* on linkage group III and for *was* and *z* on linkage group IV. He found that *Td* was linked to *b* by about 15 recombination units and was independent of *was* and *z* on linkage group IV. In view of these results, he postulated that *Td* might be located on linkage group III. Marx data appear to be as conclusive in determining that *Td* is located on linkage group III as Lamprecht's data were in placing *Td* on linkage group IV.

In view of these contrasting results, we decided to carry out an experiment to clarify the location of *Td* in the pea genome. We analysed two different F_2 progenies that segregated for *Td* and several other morphological and isozymic markers (Table 1). The map of reference for the location of the different markers used in this study was developed by Weeden and Wolko (5).

Both F_2 families segregated as expected for the genetic markers. The segregation for *Td* and *Lap-1* (most anodal isozyme of leucine aminopeptidase) is shown in Table 2. The joint segregation data were analysed using the computer program Linkage-1 that uses the method of maximum likelihood to calculate recombination frequencies (4). In one of the crosses (A778-26-6 x WA788), *Td* was estimated to be about 20 map units from *Lap-1*, while in the other cross (84C-1063-4 x William Massey), *Td* and *Lap-1* were independent at the confidence level $\alpha = 0.05$; however, a recombination frequency of around 30% with *Lap-1* was found when $\alpha = 0.056$ (Table 3). The analysis of the progeny of the latter cross supports the probability that *Td* is located on linkage group III. When the data from the two crosses were combined and analysed, the recombination fraction was 23% between *Td* and *Lap-1*. Since *Lap-1* and *b* are closely linked (5) the recombination value of 23% between *Lap-1* and *Td* is clearly in accordance with the 15% found by Marx (3) between *b* and *Td*. Due to the small population size these results need to be taken with some caution.

There are two possible explanations for these results. It is possible that there are some genomic rearrangements in some pea lines involving *Td*. Thus, in some lines, *Td* is located on linkage group III while in others, such as those used by Lamprecht (1, 2), the gene is found on linkage group IV. The other possible explanation is that there are two different genes with a similar phenotypic expression of leaflet dentation. One of the genes may be situated on linkage group III and the other on linkage group IV. Our sources of *Td* were obtained from G.A. Marx who described the gene as expressing the classic *Td* phenotype (3).

Table 1. Genetic markers scored in two crosses.

84C-1063-4 x W. Massey	*Td, Dw, a, Pl, Bt, Pgd-c, Aldo-p, Acp-2, Aat-m, Aat-c, Skdh, Lap-1*
A778-26-6 x WA788	*Fw, Dw, Td, rups, a, Pl, r, Bt, Aldo-p, Pgd-p, Pgd-c, Skdh, Lap-1, Aat-m*

Table 2. Single locus goodness of fit tests[1].

84C-1063-4 x W. Massey									
Locus		Offspring genotype					Exp. ratio	χ^2	df	P
Td	*Td-:*	35	*tdtd:*	10			3:1	0.19	1	0.67
Lap-1	FF:	11	FS:	18	SS:	15	1:2:1	2.19	2	0.34
A778-26-6 x WA788										
Locus		Offspring genotype					Exp. ratio	χ^2	df	P
Td	*Td-:*	65	*tdtd:*	20			3:1	0.10	1	0.75
Lap-1	FF:	21	FS:	45	SS:	19	1:2:1	0.39	2	0.82

[1] Nomenclature: *Td-* = dominant phenotype, *tdtd* = recessive phenotype, FF = homozygous fast, FS = heterozygous and SS = homozygous slow.

Table 3. Joint segregation of *Td* with *Lap-1*[1].

Cross	*Td-*			*tdtd*			P	Recomb. ftact.	SE
	FF	FS	SS	FF	FS	SS			
84C-1063-4 x W. Massey	11	14	9	0	4	6	0.06	0.30	0.08
A778-26-6 x WA788	19	40	6	2	5	13	0.00	0.20	0.04
Combined	30	54	15	2	9	19	0.00	0.23	0.04

[1]Nomenclature: as for Table 2.

1. Lamprecht, H. 1945. Hereditas 31:347-382.
2. Lamprecht, H. 1948. Agri Hort. Genet. 10:51-74.
3. Marx, G.A. 1987. Pisum Newsl. 19:38-39.
4. Suiter, K.A., Wendel, J.F., and Case, J.S. 1983. J. Hered. 74:203-204.
5. Weeden, N.F., and Wolko, B. 1990. *In* Genetic Maps, Ed. S.J. O'Brien, Cold Spring Harbor Laboratory Psess, Cold Spring Harbor, New York, pp. 6106-6112.