

Additional information on the linkage of genes *apu* and *uni* of *Pisum sativum* L.

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There are only a few reports about the location of the *apu* (*apulvinic*) and *uni* (*unifoliata*) genes. Marx (1) reported linkage of *apu* and *tac* (tendrilled acacia) with gene *st* of linkage group III and a gene order of *tac-apu-st* while Marx *et al* (3) proved that *apu* and *uni* lie on the *M* side of *st*. Subsequently, Marx (2) showed *tac* was allelic with *uni* and Swiecicki (4) showed the *apulvinic* and *petiolulatus* mutants were allelic (4)^f. The purpose of our study was to obtain additional information on the linkage of *apu* and *uni*.

In 1989-92, linkage of genes *apu* and *uni*^{*tac*} with gene *st* was studied in four crosses. Results were analysed using the joint segregation Chi-square to detect linkage and the product ratio method to calculate the recombination fraction.

The joint segregation analysis (Table 1) indicated that gene *apu* is located between *st* and *uni* in linkage group III with the map distances as follows:

$$\begin{array}{ccccccc} uni & - & 20 & - & apu & - & 15 & - & st \\ & & \longleftarrow & & \longrightarrow & & & & \\ & & & & & & 30 & & \end{array}$$

These results are in agreement with those of Marx (1), who used the *apulvinic* line, and with the arrangement shown in the recent map of *Pisum* (5). Our calculated distance between *apu* and *st* is slightly larger than that shown on the latter map (15 versus 9 cM) but this difference is not statistically significant.

Table 1. F₂ joint segregation data and recombination fractions for genes *st*, *apu* and *uni*^{*tac*}.

Loci	Phase	Cross	Phenotype				Total	Joint χ^2	Recomb fract	SE
			XY	Xy	xY	xy				
<i>Apu St</i>	Repul	P 1297-2 x P 1426-2	64	27	28	1	120	8.45**	19.6	8.7
		P 1297-9 x P 1426-2	11	9	9	0	29	5.87*	<24.2	-
		P 1297-11 x P 1426-2	17	7	11	0	35	4.01*	<29.7	-
		Pooled data	92	43	48	1	184	17.56***	14.5	7.2
		Heterogeneity χ^2						0.77		
<i>Uni St</i>	Repul	P 1297-2 x P 1426-2	66	27	25	2	120	5.34*	28.2	8.3
		P 1426-2 x P 1297-1-21	519	188	194	16	917	33.69***	30.0	3.0
		Pooled data	585	215	219	18	1037	39.01***	29.8	2.8
		Heterogeneity χ^2						0.02		
<i>Uni Apu</i>	Coupl	P 1297-2 x P 1426-2	82	11	10	17	120	30.59***	20.2	4.2

*, **, ***P<0.05, 0.01 and 0.0001, respectively

1. Marx, G.A. 1984. *Pisum* Newsl. 16:46-48.
2. Marx, G.A. 1986. *Pisum* Newsl. 18:49-52.
3. Marx, G.A., Weeden, N.F. and Provvidenti, R. 1985. *Pisum* Newsl. 17:57-60.
4. Swiecicki, W.K. 1990. *Pisum* Newsl. 22:66.
5. Weeden, N.F., Swiecicki, W.K., Ambrose, M. and Timmerman, G.M. 1993. *Pisum* Genetics 25:4 and cover.

^f Some confusion exists over the use of symbols *uni/tac* and *apu/pet*. The valid gene symbols are *uni* and *apu*. See Ambrose (*Pisum* Genetics 26:44,1994). Editor