

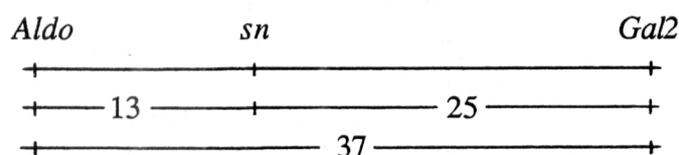
### Confirmation that the *sn* locus is between *Aldo* and *Gal2* in linkage group VII of pea

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*Sn* is one of three complementary dominant genes *Sn*, *Dne* and *Ppd* which together confer the ability to respond to photoperiod and a late flowering habit in pea (1-4). The recessive mutant allele *sn* causes a loss of the photoperiod response, and common early flowering, day neutral cultivars such as Sparkle, Massey, Alaska and Progress #9 are homozygous for this allele (2, 5, 7). Weeden et al. (7) reported very close linkage between *sn* and the amylase locus *Amyl* leading to placement of the *sn* locus between isozyme loci *Aldo* and *Gal2* in the lower section of linkage group VII in recent maps (e.g. 8).

We have recently obtained data from cross HL249 (*Aldo*<sup>S</sup> *Sn* *Gal2*<sup>S</sup>) x Sparkle (*Aldo*<sup>F</sup> *sn* *Gal2*<sup>F</sup>) which confirm that location. Monohybrid segregation for *Aldo* and *sn* was in good accordance with expectation ( $P > 0.5$ ), but segregation for *Gal2* was mildly disturbed ( $P < 0.01$ ). The dihybrid segregation data (Table 1) indicate linkage between all markers and generate the following map:



These results are in reasonable accordance with, and thus support, the 1993 (8) and current (9) maps for this section of the pea genome. Whether *sn* is located above or below *Amyl* remains undetermined.

Table 1. Dihybrid segregation data from the F<sub>2</sub> of the cross HL249 (*Aldo*<sup>S</sup> *Sn* *Gal2*<sup>S</sup>) x Sparkle (*Aldo*<sup>F</sup> *sn* *Gal2*<sup>F</sup>). The plants were grown under an 8-h photoperiod to allow unequivocal recognition of *Sn* and *sn* segregants. The data were analysed using the program LINKAGE1 (6).

Gene pair	Phenotype <sup>1</sup>						Total	Linkage Chi-square	Recomb Fract.	SE			
	DF	DH	DS	RF	RH	RS							
<i>Sn - Aldo</i>	6	33	17	16	4	0	76	35.10**	13	4			
<i>Sn - Gal2</i>	3	24	29	8	10	2	76	18.70**	25	6			
	FF	FH	FS	HF	HH	HS	SF	SH	SS				
<i>Aldo - Gal2</i>	5	13	4	6	15	16	0	6	11	76	10.27*	37	3

<sup>1</sup>D = dominant, R = recessive, F = homozygous fast, H = heterozygous, and S = homozygous slow. The first named locus is shown first.

\*, \*\*  $P < 0.05$  and  $0.0001$ , respectively.

1. Arumingtyas, E.L. and Murfet, I.C. 1994. J. Hered. 85:12-17.
2. Barber, H.N. 1959. Heredity 13:33-60.
3. King, W.M. and Murfet, I.C. 1985. Ann. Bot. 56:835-846.

4. Murfet, I.C. 1971. Heredity 27:93-110.
5. Murfet, I.C. 1990. Pisum Genetics 22:78-86.
6. Suiter, K.A., Wendel, J.F. and Case, J.S. 1983. J. Hered. 74:203-204.
7. Weeden, N.F., Kneen, B.E. and Murfet, I.C. 1988. Pisum Newsletter 20:49-51.
8. Weeden, N.F., Swiecicki, W.K., Ambrose, M. and Timmerman, G.M. 1993. Pisum Genetics 25: cover.
9. Weeden, N.F., Swiecicki, W.K., Timmerman-Vaughan, G.M., Ellis, T.H.N, and Ambrose, M. 1996. Pisum Genetics 28: cover.