

Confirmation on location of *Dsc* on linkage group VI

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Dull seed coat (gene *Dsc*) was reported as a Mendelian trait in pea by Marx (1). The character was reported to be linked to *Pl* (where genotypes with *Pl* also had darker seed coat than *pl* lines) but segregates independently as a dominant factor. The character was scored in *a* (anthocyanin inhibitor) backgrounds by Marx (1988) to ensure that the blackish pigment in the seed coat was not related to anthocyanin synthesis. Variable expression in glasshouse and field screening, as well as other problems such as interaction with the *r* (wrinkled seed) phenotype has been reported (M. Ambrose, personal communication). *Dsc* was mapped by Marx (1) near *Pl* in linkage group VI (2). The gene symbol *Dsc* was however dropped from the 1993 genetic map of pea (3) because of insufficient confirmation of its existence and chromosomal location. It remains to be confirmed whether this trait is really controlled by a separate specific gene or appears only as pleiotropic effect

Table 1. Joint segregation analysis of dull seed coat (*Dsc*) with black hilum (*Pl*) in pea

Cross	Gene pair	F ₂ segregation				Chi-square			RF %	SE %
		DD	DR	RD	RR	Locus 1 (3:1)	Locus 2 (3:1)	Joint		
P 1597 x P 1563	<i>Pl-Dsc</i>	163	5	3	46	0.94	0.43	178***	3.8	1.3
P 1563 x P 1597	<i>Pl-Dsc</i>	111	2	3	32	0.14	0.32	121***	3.5	1.5
Pooled over two crosses	<i>Pl-Dsc</i>	274	7	6	78	0.77	0.57	296***	3.7	1
Heterogeneity								3.57		1

Both crosses had dominant alleles in the coupling phase.

***Significant at 0.0001 level

of other gene(s). In the former case, the location of gene needs to be confirmed.

To investigate the inheritance and determine the map position of the gene causing dull seed coat the line P 1597 (*Pl*, dull seed coat) was crossed with P 1563 (*pl*, bright seed coat) in both (direct and reciprocal) directions. To nullify the effect of environmental fluctuations, the F₁ seeds were grown in the phytotron. Table 1 presents data obtained from joint segregation analysis of F₂ populations of the two crosses (direct and reciprocal). In both crosses monogenic segregation for dull seed coat was in good fit to the ratio of 3 dull : 1 bright seed coat, confirming the dominant nature of dull seed coat trait. Joint segregation analysis for *Dsc* and *Pl* in the F₂ of the cross in both directions showed a significant linkage between these two genes. Based on the pooled analysis of data of the cross the gene *Dsc* maps 3.7 ± 1 crossover units away from the gene *Pl* on linkage group VI. The precise location of the gene *Dsc* in relation to the other markers on linkage group VI is under investigation.

1. Marx, G.A. 1988. PNL 20: 25-26.
2. Weeden, N.F., Ambrose, M., and Świącicki, W.K. 1991. Pisum Genetics 23: cover.
3. Weeden, N.F., Świącicki, W.K., Ambrose, M. and Timmerman, G.M. 1993. Pisum Genetics 25: 4 and cover.