DETERMINATE GROWTH HABIT (det) IN PEAS: ISOLATION, SYMBOLIZATION, AND LINKAGE

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More than 26 genes are known to control stem characters in peas, a considerable number of which have implications for breeding. A mutant conferring a true determinate growth habit was isolated after chemical mutagenesis and described in 1975 by Popova (2). Popova's mutant regularly developed two reproductive nodes, each with a maximum of two flowers and pods, at the top of the stem.

Segregating populations indicated that the determinate habit has recessive monogenic inheritance (Table 1), and the gene controlling this character was previously designated as det (3).

An analysis to determine the localization of the new gene was performed on data from four crosses. Evidence of linkage between Tl and Det is shown in Table 2.

Estimates of linkage (Rf) intensity were calculated using the formula:

$$\frac{(2+\theta)\,\theta}{(1-\theta)^2} = \frac{n_1 \cdot n_4}{n_2 \cdot n_3}$$

where $rq...\hat{}$ are the observed frequencies of the XY, Xy, xY, and xy classes. Linkage in repulsion is shown by $\theta = rf2$ and in coupling by $\theta = (1-rf)^2$. Error estimate was calculated by the formula:

$$S_{rf} = \pm \sqrt{\frac{rf\,(2-rf)\,(3+2rf+rf^2)}{2\,N\,(3-4rf+rf^2)}}$$

Estimates of linkage intensity in four crosses (Table 2) were: 0.12, 0.07, 0.14, and 0.18, with an average of 11.1 + 1.1%.

Our results reveal that gene Det-det is located in linkage group 7 at a distance of 11.1% from Tl tl.

Offspring from separate crosses segregating for smooth (R) and wrinkled (r_) seeds confirmed the existence of strong linkage between _r and det alleles reported by Marx (1); we found no plants with determinate growth habit among the *R* offspring.

1. Marx, G. A. 1986. PNL 18:45-48.
2. Popova, I. A. 1975. Trudy po seleccii i semenowodstwu owoshchnykh cultur VNIISSOC 3:66-72.
3. Volchkov, Yu. A. 1986. Sbornic nauchnykh trudov po pricladnoj botanike, genetike i selectii 101:46-48.

Table 1.   Segregation for determinate stem growth (<u>det</u>) in
          populations derived from two crosses in peas (5).

Cross number	Generation	Det :det Observed	Expected	Expected ratio	X^2
544	F2	332 :119	338:113	3:1	0.42
544	F3	310 :215	328:197	5:3	2.63
542	F2	363: 99	347 :115	3:1	2.96

Table 2.   Joint segregation between Tl_ and <u>Det</u> in progenies
          from four crosses (3).

Cross no./ phenotypes	Mathematical model 1/	Segregation ratio Observed	Expected	X^2
584				
Tl - Det	0.64 84	976	1033.5	3.13
Tl - det det	0.1177	245	187.6	17.56
tl tl - Det	0.1979	373	315.5	10.47
tl tl - det det	0.0359	0	57.2	56.90
601				
Tl - Det	0.5808	355	390.9	3.30
Tl - det det	0.1694	150	114.0	11.37
tl tl - Det	0.1932	166	130.0	9.97
tl tl - det det	0.0564	2	37.9	34.01
586				
Tl - Det	0.7395	556	581.0	1.16
Tl - det det	0.1105	116	86.0	10.50
tl tl - Det	0.1305	114	102.0	1.40
tl tl - det det	0.0195	0	16.0	16.00
602				
Tl - Det	0.7080	375	385.2	0.27
Tl - det det	0.0638	45	34.7	3.06
tl tl - Det	0.2090	124	113.7	0.93
tl tl - det det	0.0188	0	10.2	10.20

1/ Mathematical model is determined taking into account low
   survival of recessive homozygotes in both genes.

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