Dominant alleles of the locus *Tl* may differ in their strength

Bogdanova, V.S., Kosterin O.E. and
Berdnikov, V.A.

Institute of Cytology and Genetics of Russian Academy of Sciences
Acad. Lavrentiev ave. 10, Novosibirsk 630090, Russia

The *Tendril-less* (*Tl*) gene of *Pisum sativum* participates in controlling development of the compound leaf and is located in the linkage group V. A number of recessive alleles have been described. Homozygotes tl^w, tl^{pet} condition formation of leaflets in place of tendrils (2). Heterozygotes exhibit an intermediate structure that can be called 'flat tendril', that is tendril with a very narrow leaf blade. Another recessive allele tl^x is supposed to be a small deletion (3), and only was observed in hemizygote which appears quite similar to the heterozygote Tl/tl^w. However, little is known of variants of dominant alleles. Here we show that probably there exist at least two *Tl* alleles that differ in their strength, that is, visible expression in heterozygote against tl^w.

In 1997 we performed a cross of the lines Delta and Sprint-Vologda as a part of investigation of the line Delta. The lines are described in (1), an important point for the present study is that Delta is heterozygous ($r\ Tl/R\ tl^x$) and Sprint-Vologda is homozygous (*R Tl/R Tl*), the genes *R* and *Tl* being closely linked (4). For convenience, we will designate the *Tl* allele originating from the line Delta as Tl^D and that from the Sprint-Vologda line as Tl^{SV}. Thus, in the F_1 from the cross Delta x Sprint-Vologda there appear plants with flat tendrils heterozygous for *Tl* ($R\ tl^x/R\ Tl^{SV}$) and plants with round tendrils homozygous for *Tl* ($r\ Tl^D\ /R\ Tl^{SV}$). Plants of the latter class were test-crossed as a pollen parent with the line WL1018 ($r\ tl^w$). We obtained 16 wrinkled ($r\ tl^w/r\ Tl^D$) and 49 round ($r\ tl^w/R\ Tl^{SV}$) seeds. The ratio of *r* to *R* seeds differed significantly from the expected 1:1, perhaps due to peculiarities of the line Delta (1). All plants resulting from this test-cross expressed flat tendrils. Visual comparison of flat tendril width in these two classes suggested a significant difference. We therefore measured length and width of flat tendrils in the leaves at node 8 in individual plants. The results are presented in Table 1.

Table 1. Mean values with standard errors and standard deviations of parameters of flat tendrils of the terminal position and of the ultimate pair in *r* and *R* phenotypic classes.

Parameters	**Plants grown from *r* seeds**	**Plants grown from *R* seeds**	**Tst**
Terminal tendril	**n = 16**	**n = 28**	**–**
length (l, mm)	**48.19 ± 3.99**	**58.96 ± 3.99**	**–1.77**
	σ = 15.96	**σ = 21.13**	*****
width (w, mm)	**1.56 ± 0.24**	**0.55 ± 0.02**	**5.51**
	σ = 0.97	**σ = 0.10**	********
w/l x 100	**3.09 ± 0.33**	**1.10 ± 0.12**	**6.68**
	σ = 1.33	**σ = 0.65**	********
ln(w/l x 100)	**1.03 ± 0.12**	**-0.02 ± 0.08**	**7.53**
	σ = 0.47	**σ = 0.43**	********
Tendrils of the ultimate pair	**n = 14**	**n = 31**	**–**
length (l, mm)	**29.71 ± 2.70**	**43.90 ± 2.21**	**–3.77**
	σ = 10.09	**σ = 12.30**	*******
width (w, mm)	**2.28 ± 0.50**	**0.48 ± 0.02**	**5.44**
	σ = 1.86	**σ = 0.11**	********
w/l x 100	**8.87 ± 2.04**	**1.19 ± 0.09**	**5.64**
	σ = 7.65	**σ = 0.50**	********
ln(w/l x 100)	**1.78 ± 0.26**	**0.12 ± 0.06**	**8.64**
	σ = 0.97	**σ = 0.32**	********

n – number of plants; Tst – student's coefficient; * – probability (p) less than 0.05; *** p < 0.001; **** p < 0.0001

The dimensions of the flat tendrils, particularly their width:length ratio, in two phenotypic classes, differ significantly. As one of the phenotypic classes has a much higher variance for this character, it is reasonable to perform logarithmic transformation. After this procedure, the difference between plants carrying Tl^D and Tl^{SV} alleles (more precisely, grown from *r* and *R* seeds) becomes more evident. Distributions of the logarithm of the value (*width/length* x 100) for the tendrils of the ultimate pair are shown in Fig.1. The difference observed indicates that a factor controlling the width of flat tendrils co-segregates with the alleles of *R* locus. It could be some modifier closely linked to *R* and, therefore, to *Tl*. However, we believe the effect is more likely due to the *Tl* gene itself. The distributions overlap to some extent, probably due to high values of the variance or, possibly, misclassification of *Tl*-classes due to rare crossing-over between *r* and *Tl* (or between *r* and the hypothetic modifer). These results allow us to propose that the two wild-type *Tl* alleles studied in this work differ in their strength manifested in the width of flat tendrils of the heterozygote Tl/tl^{w}. The Tl^{D} allele originating from the line Delta may be termed “weak”, and the Tl^{SV} allele that comes from the line Sprint-Vologda may be regarded as “strong”.

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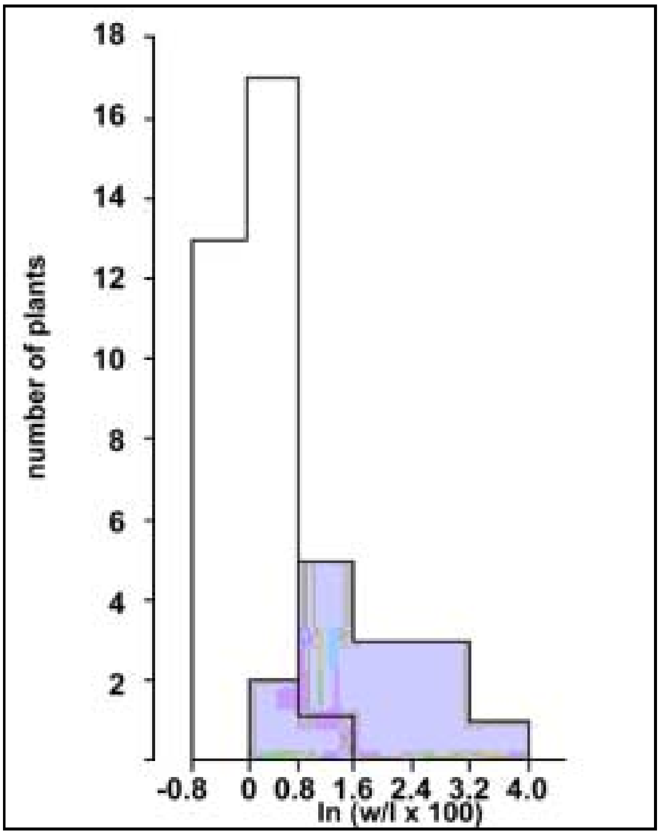

Fig. 1. Distributions of the logarithm of the value (width/length x 100) of the tendrils of the ultimate pair. White histogram - plants grown from round seeds, grey histogram - plants grown from

1. Berdnikov, V.A., Gorel’, F.L., Bogdanova, V.S., Kosterin, O.E., Trusov, Y.A., Rozov, S.M. 1999. Genet. Res. 73: 93-109.
2. Blixt, S. 1972. Agri Hortique Genet. 30: 1-293.
3. Gorel’, F.L., Berdnikov, V.A., Temnykh, S.V. 1994. Pisum Genet.. 26: 16-17.
4. Weeden, N.F., Ellis, T.H.N., Timmerman-Vaughan, G.M., Swiecicki, W.K., Rozov, S.M., Berdnikov, V.A. 1998. Pisum Genet. 30: 1-4.