

LOCUS AND ALLELISM TESTS FOR THE pet AND apu MUTANTS

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In 1960 Blixt included into the Weibullsholm pea gene bank, the mutant petiolulatus, induced in cv Witham Wonder by EI treatment (catalogue no. WL5478 - Wt15871 in the computer data bases). Petiolulatus is characterized by leaflets sitting on short petiolules. In 1979 Harvey (1) described the spontaneous mutant apulvinic in cv Dark Skinned Perfection (catalogue no. in John Innes Institute - JI1349 = Wt15868 = WL2806). According to the description, apulvinic plants bear leaves in which all foliar pulvini are replaced with rigid petioles. Marx investigations (2), which included the apulvinic line, revealed that the gene, with provisional symbol apu, is localized in chromosome 3 with the gene order St - Apu - Tac. Further studies by Weeden and Wolko (3) have provided additional linkage information for the St - Apu - Acp-3 region.

Field as well as greenhouse observations at Wiatrowo showed phenotypic identity of both mutants. Locus and allelism tests were therefore made in order to determine whether the mutants belonged to the same or different loci. Accordingly, the cross Wt15871 (petiolulatus) x Wt15868 (apulvinic) was done at Wiatrowo in 1989. The F<sub>1</sub> generation was tested in the greenhouse in 1990. All F<sub>1</sub> plants were of the mutant type showing that the traits are controlled by the same locus. Line Wt15871 was also crossed with the testerline Wt11288 (st) and the F<sub>2</sub> data (Table 1) show linkage of pet with st, which supports the previous conclusion. According to the base of priority we should accept the older name petiolulatus for the character and my suggestion is that the symbol pet should be used for the gene.

1. Harvey, D.M. 1979. Seventieth Ann. Rpt. John Innes Inst.: 34.
2. Marx, G.A. 1984. PNL 16:46-48.
3. Weeden, N.F. and B. Wolko. 1990. In Genetic Maps, Ed. S. O'Brien, Cold Spring Harbor, pp 6106-6112.

Table 1. Distribution of phenotypes in the F<sub>2</sub> population of cross Wt15871 (pet) x Wt11288 (st)

<u>Monohybrid segregation</u>				Total	Chi-square (3:1)		
Phenotype (number)							
<u>St</u>	(288)	<u>st</u>	(77)	305	0.01		
<u>Pet</u>	(243)	<u>pet</u>	(62)	305	3.55		
<u>Dihybrid segregation (repulsion)</u>				Total	Joint chi-sq.	Recomb fract.	SE
<u>St Pet</u>	<u>St pet</u>	<u>st Pet</u>	<u>st pet</u>				
166	62	77	1	305	23.87***	12.9	5.6

\*\*\* P < 0.001