

The new gene *alts* determining stem chlorophyll deficiency in pea

Sidorova, K.K. and Mischenko, T.M.

Inst. of Cytology and Genetics, Novosibirsk, Russia

Seeds of pea variety Torsdag were treated with 0.15% ethylmethane-sulfonate for 12 h. In different experiments, two white-stem mutants, K186 and K468, were obtained. Chlorophyll deficiency was characteristic of the stem above the fifth or sixth internode, while the lower part of the stem remained green. In several plants slightly white regions were also observed in some leaves and stipules located above the fifth or sixth internode. Leaf veins were white, while the leaf lamina between them was green (Fig. 1). The mutant trait was expressed most efficiently during blooming. According to the character of expression, this mutation can be assigned to the *albina-terminalis* type. Contrary to the well-known mutations of this type, the new mutation induced pre-dominantly stem chlorophyll deficiency in K186 and K468. The leaves of these latter lines were green with only occasional whitish spots.



Fig. 1. Plant of the original Torsdag variety (left) and the

Expression of stem chlorophyll deficiency differed under different growth conditions. Observations were made in plants grown in the field and in a hydroponic greenhouse for several years. In the field, the stem and leaf segments varied in color from slight to bright white in different years. This was also observed in plants grown in the greenhouse from October to December and February to April. The expression was more pronounced in the field than in the greenhouse. The plant productivity was lower in mutants than in the original variety. Hybrid analysis showed that both K186 and K468 carry a monogenic recessive mutation. (Table 1).

Table 1. Segregation of F₂ hybrids from crosses of the mutants with the cv. Torsdag.

Hybrid	F ₂ segregation 3:1 (original variety : mutant)		χ^2	P
	observed	expected		
Mutant K186 x Torsdag	69 : 22	68.25 : 22.75	0.03	0.9-0.8
Mutant K468 x Torsdag	71 : 28	74.25 : 24.75	0.57	0.5-0.4

Crossing of K186 with K468 showed that these mutations are allelic.

The new mutant gene was designated *alts*. To study the chromosomal location of the gene, the K186 mutant was crossed with a tester line 1238. The *alts* gene was localized to linkage group II.

<i>k</i>	<i>wb</i>	<i>alts</i>
15.6	19.9	
39.7		

The article was published in *Genetika* (Russian), 1998.