A new gene for supernodulation in pea: *nod6*

Sidorova, K.K., Shumny, V.K., Mischenko, T.M. and Vlasova, E.Yu
Inst. of Cytology and Gen., Russian Acad. of Sci. Novosibirsk, Russia

Five supernodulating mutants, K10a, K11a, K12a, K21a and K22a, have been induced from Rondo by treatment of seeds with EMS. The morphological and symbiotic properties were described previously [1]. K10a, K11a, and K12a are allelic to one another and to the *nod3* mutant. K21a and K22a are monogenic recessive mutations eliciting pleiotropic effects. Additionally, they have a short stem and short lateral roots. Monohybrid segregation was observed following crosses with the original variety (Table 1). K21a and K22a are allelic to each other, but not to the *nod3* mutant or the supernodulating K301a *(nod4)* mutant induced from Ramonsky 77 [2].

Table 1. Segregation in hybrid progenies.

Table 1. Segregation in F_2 hybrid progenies.

Hybrid	Segregation in F_2 at 3:1 (original : mutant) Observed	Predicted	χ^2	P
K21a x Rondo	91:29	90:30	0.04	0.7–0.8
K22a x Rondo	96:22	88.5:29.5	2.5	0.1–0.2

Reciprocal grafting of *nod6* shoots on original Rondo stocks and vice versa suggests that nodulation in K21a and K22a is controlled by the stem, whereas in KlOa, K11a, and K12a nodulation is determined by the root. It has been concluded that K21a and K22a are mutations at a different locus, which is associated with supernodulation. We designated this mutation *nod6.*

Chromosomal localization of the *nod6* gene was performed using tester lines 851 and 1238, and the *sym11* mutant *(sym11* seeds were courtesy of Prof. N.F. Weeden). No linkage was found between *nod6* and any of the marker genes by crossing K22a to 1238 plants. Linkage was detected between *nod6* and *oh* and *sym11,* both located on chromosome 4 (linkage group VII), by crossing K22a to 851 and *sym11* plants [3].

Monohybrid segregation for the *nod6* gene and the marker oh and *sym11* genes was observed in populations F_2 *nod6* X 851 and F_2 *nod6* X *sym11* (Table 2).

Table 2. Segregation for the *nod6* gene and the marker oh and *sym11* genes in populations F_2 *nod6* X 851 and F_2 *nod6* x syml l.

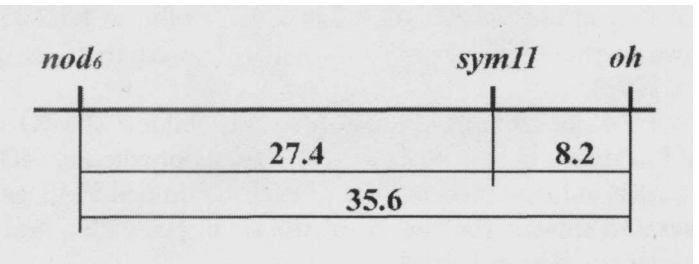
Hybrid	Gene	Plants assayed	Segregation in F_2 observed	predicted	χ^2 (3:1)	P
nod6 x 851	*Nod6 : nod6*	141	101:40	105.75:35.25	0.85	0.40–0.30
	Oh : oh	141	107:34	105.75:35.25	0.06	0.90–0.80
nod6 x sym11	*Nod6 : nod6*	154	115:39	115.50:38.50	0.01	0.95–0.90
	Sym11: sym11	154	115:39	115.50:38.50	0.01	0.95–0.90

It has been established that the new gene, *nod6,* which controls supernodulation in pea, is located on chromosome 4 (linkage group VII) 35.6 cM away from the oh gene and 27.4 cM away from the *sym11* gene. Gene mapping of *nod6* is consistent with chromosome mapping [3].

Recombination frequencies between *nod6* and the *oh* and sym11 genes are presented in Table 3.

Table 3. Joint segregation data for the loci *nod6*, *oh* and *syml1* on linkage group VII obtained in F_2 of the cross K22a X L851 and K22a X syml1.

Variants	AB	Ab	aB	ab	N	χ^2	P	Recombination frequency (%)	Mean square error
A – *Nod6-*, a – *nod6 nod6* B – *Sym11-*, b – *sym11 sym11*	79	36	36	3	154	8.75	0.003	27.4	7.3
A – *Nod6-*, a – *nod6 nod6* B – *Oh-*, b – *oh oh*	72	29	35	5	141	5.34	0.148	35.6	7.2



1. Sidorova, K.K., Vlasova, E.Yu., Mischenko, T.M., Glianenko, M.N. and Shumny, V.K. 1999. Pisum Genetics 31: 34.
2. Sidorova, K.K. and Uzhintseva L.P. 1995. Pisum Genetics 27: 21.
3. Weeden, N.F., Ellis, T.H.N., Timmerman-Vaughan, G.M., Swiecicki, W.K., Rozov, S.M. and Berdnikov, V.A. 1998. Pisum Genetics 30: 1-4.