Mapping of *nod-4,* a new hypernodulating mutant in pea*

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Recently we have described a new hypernodulating mutant in pea, obtained after the treatment of seeds of cv. 'Ramonsky 77' with N-nitroso-N-ethylurea (3). The mutant line K301 is characterized by excessive nodule number (more than 1000 per plant), by high nitrogenase activity even in the presence of nitrate, and by a different (fasciated) stem morphology. The phenotype is inherited as a recessive. The gene symbol *nod-4* is proposed (3).

The location of *nod-4* on the pea genetic map was investigated by conventional segregation analysis of several crosses involving tester lines WL1238, WL1132 and WL741 from the Nordic Gene Bank (4). Linkage was found between *nod-4* and two morphological markers *gp* (yellow pod) and *cp* (curved pod), suggesting that *nod-4* is located on linkage group V. The data are given in Table 1.

Table 1. Results of joint segregation analysis for genes *nod-4, cp* and g*p.*

Cross	Gene pair	Phase	Phenotype				Joint seg. $\chi 2$	Recomb. freq. ± SE
			AB	Ab	aB	ab		
K301xWL1238	*nod-4-gp*	R	173	92	81	3	31.2	18.0 ± 5.1
	nod-4 -cp	R	188	77	82	2	25.9	16.6 ± 5.2
	gp-cp	C	244	11	26	68	181.5	10.4 ± 1.7
K301xWL1132	*nod-4 - gp*	R	161	88	62	5	19.8	25.0 ± 5.2
K301xWL741	*nod-4 - gp*	R	103	53	51	5	13.0	27.9 ± 6.2

The mapping data indicate that *nod-4* is distinct from *nod-3,* a previously described gene conditioning hypernodulation, which has been localized near *D* on linkage group IB (2, 5). The interactions between these two hypernodulating mutants *(nod-3, nod-4),* as well as with four other mutants (190F, 191F, P77, P79) with excessive nodule number described by Duc et al. (1), remain to be investigated.

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