The early nodulin gene *Enod12A* is in linkage group 3

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Enod12 was identified as a nodulin gene which is involved in an infection process during the pea-rhizobium interaction (3). There are two copies of the *Enod12* gene in the pea genome with known primary structure, i.e *Enod12A* and *Enod12B* (1). We have shown previously by the PCR method that there was a polymorphism in the promotor region of *Enod12A* (2). In order to follow segregation of the *Enod12A* gene by PCR, a pair of primers was chosen such that the PCR with DNA of line NGB1238 resulted in misamplification of *Enod12A* whereas both genes were amplified in case of the laboratory line Sprint-2 (Fig. 1). The sequences of the PCR primers used are as follows:

5' -AAGTGGTCACACATGATAAGA-3' - 5' -end of the promoter region
5' -GCTTTAGATATGGATGTTATGTTC - 3' -end of the coding region

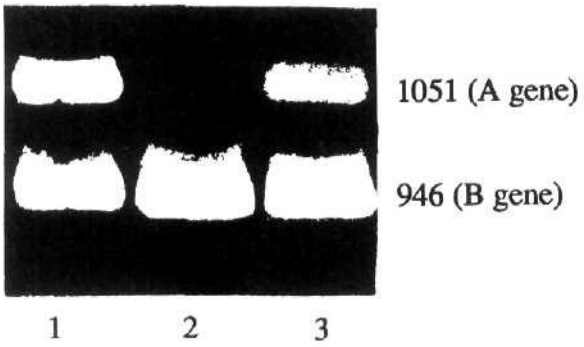

Fig. 1. Electrophoresis of the PCR products of genes *Enod12A* (upper band) and *Enod12B* (lower band) in 1.5% agarose gel. Molecular weights are indicated on the right side. 1. Parent line Sprint-2. 2. Parent line NGB1238. 3. F_1 hybrid NGB1238 x Sprint-2.

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Table 1. Segregation data for genes *B* and *Enod12A* obtained from the F_2 of cross NGB1238 x Sprint-2.

Number of plants with phenotype				Chi-squared			Recomb.
B Enod12A	*B enod12A*	*b Enod12A*	*b enod12A*	*B*	*Enod12A*	Joint	fract. ± SE
34	4	4	8	0.03	0.03	15.76*	17.9±6.1%

* P = 0.00007

The results of segregation in F_2 after crossing NGB1238 and Sprint-2 showed linkage between *Enod12A* and the linkage group 3 marker *b* (Table 1). Our results also indicate the location of gene *Enod12B* as preliminary data of A.V. Kozik (pers. comm.) show an absence of recombination between *Enod12A* and *Enod12B*.

A combination of the classic genetic and molecular-biological methods may also be useful for studying other pea genes affecting different stages of the symbiotic process.

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