The *Sym35* Gene Required for Root Nodule Development in Pea Is an Ortholog of *Nin* from *Lotus japonicus*[1]

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Comparative phenotypic analysis of pea (*Pisum sativum*) s*ym35* mutants and *Lotus japonicus nin* mutants suggested a similar function for the *PsSym35* and *LjNin* genes in early stages of root nodule formation. Both the pea and *L. japonicus* mutants are non-nodulating but normal in their arbuscular mycorrhizal association. Both are characterized by excessive root hair curling in response to the bacterial microsymbiont, lack of infection thread initiation, and absence of cortical cell divisions. To investigate the molecular basis for the similarity, we cloned and sequenced the *PsNin* gene, taking advantage of sequence information from the previously cloned *LjNin* gene. An RFLP analysis on recombinant inbred lines mapped *PsNin* to the same chromosome arm as the *PsSym35* locus and direct evidence demonstrating that *PsNin* is the *PsSym35* gene was subsequently obtained by cosegregation analysis and sequencing of three independent *Pssym35* mutant alleles. *L. japonicus* and pea root nodules develop through different organogenic pathways, so it was of interest to compare the expression of the two orthologous genes during nodule formation. Overall, a similar developmental regulation of the *PsNin* and *LjNin* genes was shown by the transcriptional activation in root nodules of *L. japonicus* and pea. In the indeterminate pea nodules, *PsNin* is highly expressed in the meristematic cells of zone I and in the cells of infection zone II, corroborating expression of *LjNin* in determinate nodule primordia. At the protein level, seven domains, including the putative DNA binding/dimerization RWP-RK motif and the PB1 heterodimerization domain, are conserved between the *Lj*NIN and *Ps*NIN proteins.

Legumes establish endosymbiosis with bacteria belonging to the genera *Azorhizobium*, *Bradyrhizobium*, *Mesorhizobium*, and *Sinorhizobium* a.o., collectively called rhizobia. The development of this symbiosis is a multistep process mediated by signal exchange between partners (Bladergroen and Spaink, 1998; Schultze and Kondorosi, 1998; Stougaard, 2000; Hirsch et al., 2001). *Rhizobium* spp. secretes lipochitin-oligosaccharide molecules triggering the compatible host to initiate development of specialized organs, root nodules, from already differentiated root cells (Downie and Walker, 1999). Afterward, the microsymbionts invade the nodule primordia, and intracellular compartments containing nitrogen-fixing endosymbionts, termed symbiosomes, are formed (Roth and Stacey, 1989). The infection process differs among legume species, and different legumes develop morphologically distinct nodule types. Two of these, the determinate and indeterminate nodules, have been described in detail. Determinate nodules are generally initiated by division of root cells in the outer cortex, but activity of the root nodule meristem will cease before the nodule becomes fully functional. Soybean (*Glycine max*), *Lotus japonicus*, and bean (*Phaseolus vulgaris*) follow this developmental pathway. Indeterminate nodules are founded by inner cortical cells, and the meristem remains active throughout the life time of the nodule giving rise to elongated root nodules, for example of pea (*Pisum sativum*), alfalfa (*Medicago sativa*), and clover. The meristem is located in the tip of indeterminate nodules, and the differentiation process is visible in nodule sections as a developmental zonation, with the youngest dividing cells in the nodule tip and the oldest senescent cells closest to the root.

Plant mutants incapable of forming nodules and mutants arrested during nodule development have been found in many legume species (Borisov et al., 2000; Harrison, 2000; Stougaard, 2001). Interestingly, some of the non-nodulating mutants were also un-

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able to interact with mycorrhizal fungi, demonstrating that a set of "common genes" is required for initiating both bacterial symbiosis and endosymbiosis with vesicular arbuscular mycorrhizal fungi (Duc et al., 1989; Wegel et al., 1998; Bonfante et al., 2000; Stougaard, 2001). One of the legume plants traditionally used for gene mapping and investigations of the genetic basis of plant-microbe interactions is pea. As a result of this worldwide effort, more than 200 independent symbiotic pea mutant lines are known to date (for review, see Borisov et al., 2000). Complementation analysis involving around 100 symbiotic mutants has defined more than 40 symbiotic (*Sym*) loci (Borisov et al., 2000), but efficient methods for cloning and characterization of genetically defined loci still need to be developed in pea. Like other agriculturally important legumes (soybean and alfalfa) that for decades have been used in genetic analysis of symbiotic systems, pea has a large and complex genome and is difficult to transform. Such disadvantages make these species less suitable for molecular genetics and genomics (Udvardi, 2001). For this reason, *L. japonicus* has been adopted as model legume (Handberg and Stougaard, 1992). One of the ideas behind the model legume concept was the exploitation of synteny and microsynteny between genomes of traditional and model legume species to accelerate the isolation and comparative characterization of genes in traditional legumes. A variant of this approach has recently been used successfully to clone and characterize the *PsSym19* gene (Endre et al., 2002; Stracke et al., 2002). An earlier illustration of the advantages of the model approach was the transposon tagging, cloning, and characterization of the *L. japonicus Nin* gene encoding a putative transcriptional regulator (Schauser et al., 1999). Using *Nin* as example, we have taken a direct approach to demonstrate how model legume knowledge can be effectively used for comparative studies on cultivated legumes. Focusing on a set of pea mutants with a phenotype comparable with *L. japonicus nin* mutants, we show that the pea *Sym35* gene is the ortholog of *LjNin*. The role of the two genes encoding the same type of developmental regulator is compared between pea and *L. japonicus*, which develop indeterminate and determinate root nodules, respectively.

RESULTS

Comparative Phenotypic Description of Pea Mutants and *L. japonicus nin* Mutants

L. japonicus nin mutants are characterized by their excessive root hair deformation in response to *Mesorhizobium loti*, lack of infection thread formation, and lack of cortical cell divisions. In contrast, *nin* mutants have normal mycorrhizal interaction, suggesting a function of the *Nin* gene downstream of the "common genes" required for both rhizobial and mycorrhizal invasion (Schauser et al., 1999; Stougaard, 2001). In the collection of well-characterized pea symbiotic mutants, similar nodulation and mycorrhization phenotypes were observed in *Pssym7*, *Pssym14*, and *Pssym35* mutants (Tsyganov et al., 1999; 2002). However, the excessive root hair curling response, as observed on *Ljnin* mutants, was only observed on *Pssym35* mutants but not on *Pssym7* or *Pssym14* mutants, and further characterization suggested that the phenotype of *Pssym35* mutants was identical to the *Ljnin* phenotype (Fig. 1). Three independent *sym35* mutants (lines SGENod$^-$-1, SGENod$^-$-3 (Tsyganov et al., 1994, 1999), and RisNod8 (Engvild, 1987) matched the phenotype of *Ljnin* mutants because they were all (a) blocked in infection thread initiation, (b) characterized by absence of cortical cell divisions, (c) displaying "excessive" root hair curling, and (d) colonized by arbuscular mycorrhiza (Tsyganov et al., 1999, 2002).

Cosegregation of *PsNin* and *Pssym35*

The phenotypic comparison suggested that the *PsSym35* locus could be identical to the *PsNin* gene, and this hypothesis was first tested by genetic mapping and cosegregation analysis. A 2.5-kb fragment of the *PsNin* gene was isolated using degenerate primers designed from alignment and identification of conserved nucleotide sequences between *LjNin* and an Arabidopsis *Nin*-like gene. RFLP analysis in the parent lines, JI281 and JI388, of a pea recombinant inbred mapping population identified an *Eco*RV RFLP polymorphism. Subsequent mapping in the population placed the *PsNin* RFLP on the top of the pea linkage group I about 1 cM from the marker C2/2^{++-} marker (Hall et al., 1997). In parallel, the linkage of *sym35* and several classical morphology

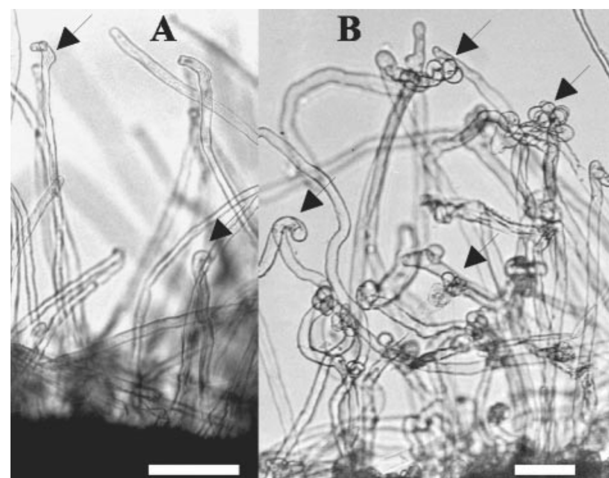

Figure 1. Root hair curling phenotype of wild-type SGE plant (A) and an SGENod$^-$-1 (*sym35*) mutant (B). Both were inoculated with *Rhizobium leguminosarum* bv *viciae*, and root hairs were photographed 23 d after inoculation. Arrows point at curled root hairs; bar = 0.1 mm.

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markers of the pea genetic map was tested in a *sym35* (SGENod^{-}-3) × NGB1238 mapping population. This analysis showed a weak linkage between *sym35* and the *d* marker from linkage group I locating *sym35* on the same chromosome arm as *PsNin* (*sym35-d*, linkage 37.5% ± 4.67%, $P_{(0.5)} < 0.05$). The other possible candidates *sym7* and *sym14* map to pea linkage groups III and II, respectively (Weeden et al., 1998). Hence, mapping confirmed *PsSym35* as the most likely candidate for *PsNin* and placed *PsNin* at the end of chromosome I reminiscent of the position of *LjNin* on the *L. japonicus* map (Hayashi et al., 2001; Pedrosa et al., 2002; Sandal et al., 2002).

To perform a cosegregation analysis between *PsNin* and *Pssym35*, a PCR strategy based on nucleotide polymorphisms within the *PsNin* gene of the parental lines NGB1238 and *sym35* (SGENod^{-}-3) was chosen. On the basis of the DNA sequence of the 2.5-kb *PsNin* fragment isolated from *sym35* and NGB1238, respectively, mapping primers specific for either one or the other parent were designed. DNA of individual wild-type and mutant F_3 plants of the *sym35* × NGB1238 mapping population was subjected to PCR amplification using the allele-specific primers described above. Analysis of 121 plants homozygous for the *Sym35* wild-type allele and 149 plants homozygous for the mutant *sym35* allele in F_3 showed 100% cosegregation of *Sym35* and *PsNin*. Absence of recombination in 540 meiotic events maps *sym35* less than 0.19 cM from *PsNin*. This result made it likely that *PsSym35* is *PsNin* and encouraged us to isolate and sequence the complete *PsNin* gene and to characterize the alleles of *PsNin* in the three *sym35* mutants.

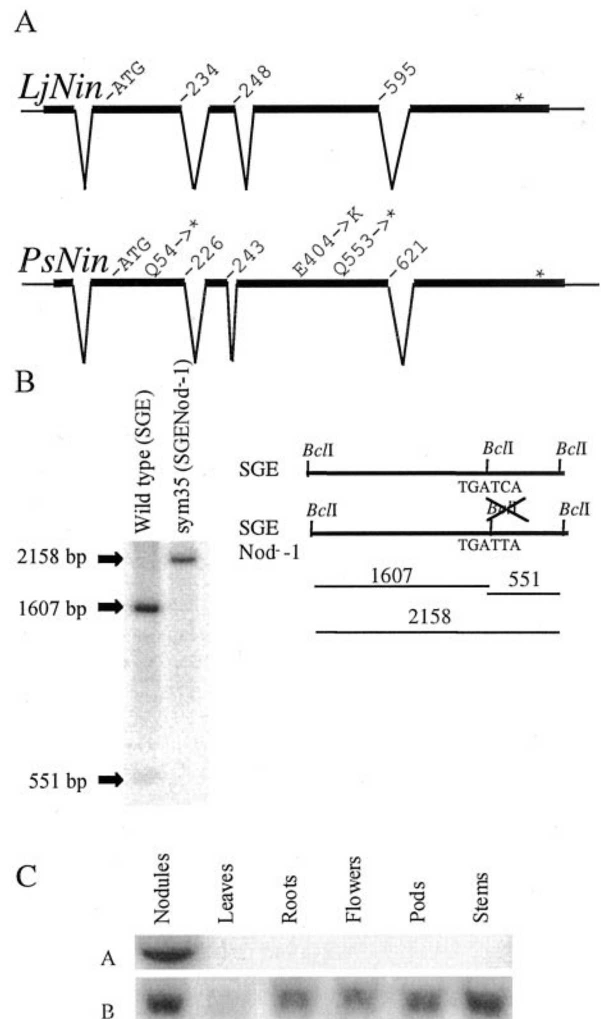

Figure 2. The intron-exon structure of *LjNin* and *PsNin* genes is conserved. A, The sequences of *Sym35* from pea cv Finale and *L. japonicus* were compared with their respective cDNAs and aligned. Apart from short stretches in the promoter regions (Fig. 5), the genomic sequences show little or no similarity outside of the exons. Amino acid positions at the exon-intron boundaries and the changes in *sym35* mutant alleles are indicated. B, Southern hybridization visualizing the RFLP generated by mutation of a *Bcl*I restriction site in the *sym35* SGENod^{-}-1 allele. Positions of the *Bcl*I sites in the mutant and wild-type alleles and the fragments generated by *Bcl*I digestion of genomic DNA are shown in the schematic drawing. The hybridization probe used covers 2 kb of the coding sequence. C, Northern analysis of *PsNin* expression in various pea organs. A visualizes the hybridization with the *Sym35*-specific probe. B shows the control hybridization with ubiquitin.

Primary Structure of the *PsNin* Gene

The *PsNin* gene was isolated from a genomic λ-library of the pea cv Alaska and an 8-kb region including approximately 3 kb of the promoter was sequenced. As a first step in the analysis of *sym35* mutant alleles present in pea cv SGE or pea cv Finale genetic backgrounds, the pea cv Alaska *PsNin* sequence information was used to identify PCR amplification primers, and the *PsNin* gene from the pea line SGE and Finale variety was sequenced from the obtained PCR products. As a result, the wild-type *PsNin* sequence was determined in three pea varieties. The corresponding cDNA was isolated from a root hair enriched library of pea cv Finale. Comparison with the *L. japonicus Nin* cDNA and the pea genomic sequence showed that the longest 2,033-bp cDNA was incomplete. The 5′ end of *PsNin* was therefore isolated by 5′-RACE, and a full-length cDNA of 3 kb was assembled. Comparison of the *PsNin* gene sequence and the full-length cDNA showed that the exon/intron structure is conserved between *L. japonicus* and pea *Nin* genes (Fig. 2A). Even the length of the introns is very similar. At the nucleotide level, there is an overall 60% identity between the coding regions of the *L. japonicus* and pea *Nin* genes, whereas large blocks of several hundred nucleotides are more than 80% identical. The *Lj*NIN and *Ps*NIN proteins have 55% identical amino acids.

Identification of Mutations in Three Independent *Psnin/sym35* Mutants

To verify that pea *Sym35* is *PsNin*, a region of approximately 4 kb covering all exons and introns of

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PsNin was amplified by PCR and sequenced from the three allelic *sym35* mutants of pea SGENod$^-$-1, SGENod$^-$-3 (Tsyganov et al., 1999), and RisNod8 (Engvild, 1987). In all three mutants, single-nucleotide substitutions were identified when compared with the *PsNin* gene sequence from the respective pea line SGE or cv Finale wild-type parents: SGENod$^-$-1 (*sym35*) has a C to T transition in position 1,657 of the predicted coding sequence. This creates a stop codon (CAG to TAG) after D552. In addition, this point mutation destroys a *Bcl*I restriction site creating an RFLP shown in Figure 2B. The mutant allele SGENod$^-$-3 (*sym35*) has a C to T transition in position 160 of the predicted coding sequence. This creates a stop codon (CAA to TAA) after P53, and finally RisNod8 (*sym35*) has a G to A change (GAG to AAG) in position 1,210 of the predicted coding sequence. This causes an amino acid substitution from E to K in position 404 of the protein. E404 is embedded in domain IV (Fig. 3) and is strictly conserved among all NIN-like proteins (NLPs; data not shown).

Domains of the PsNIN Protein

The open reading frame of the pea cDNA encodes a conceptual protein of 922 amino acids (101 kD) compared with the *Lj*NIN of 878 amino acids (Fig. 3). Conserved domains shared by all known NLPs were identified by aligning *Lj*NIN and *Ps*NIN to the nine NLPs identified in Arabidopsis (L. Schauser, W. Wieloch, and J. Stougaard, unpublished data). Six regions of high conservation were identified (domains I–VI). At present, no function can be suggested for domains I through III. Domain IV contains the hydrophobic stretches suggested to be either membrane-spanning regions or hydrophobic pockets (Schauser et al., 1999). Domain V is the most conserved region and makes up the previously identified RWP-RK region, suggested to serve in dimerization and DNA binding in this family of putative transcriptional regulators (Schauser et al., 1999). Domain VI has similarity to the PB1 domain, a motif conserved in animals, fungi, and plants (Ponting et al., 2002). The tertiary structure of the PB1 domain has been determined and was shown to belong to the ubiquitin-like β-grasp fold-containing proteins. This domain is present in many eukaryotic cytoplasmic signaling proteins for example Ras^{GTP}-binding proteins. The function of this domain is the selective formation of PB1 domain heterodimers (Ito et al., 2001) In addition to these widely conserved domains, another domain (L) is conserved among *Lj*NIN, *Ps*NIN, and the Arabidopsis NLP translated from At4g35270. Altogether, this uneven distribution of conserved amino acids suggests a modular domain structure of the NIN proteins.

Both the *Lj*NIN and *Ps*NIN proteins contain a hexa-Gln stretch, and although the position is not conserved, their occurrence in both is puzzling and may have functional significance. Additional accumula-

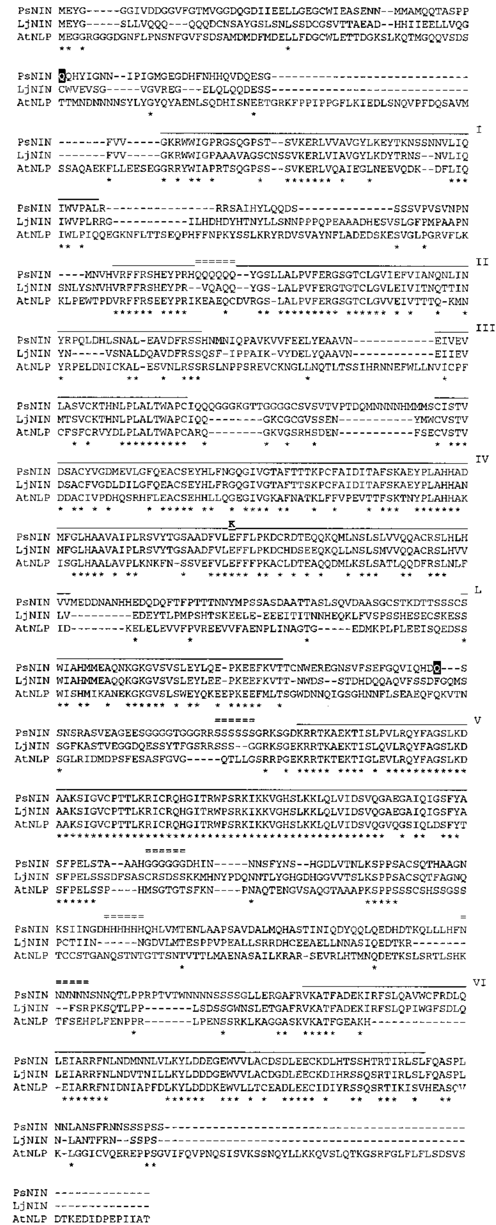

Figure 3. Identification of conserved domains in *Lj*NIN and *Ps*NIN. The translation products of *LjNin* and *PsNin* cDNAs are aligned with the most homologous NLP from Arabidopsis using ClustalX. For assignment of protein domains, an alignment including all nine NLPs from Arabidopsis was carried out, but only the sequence of the most homologous NLP from Arabidopsis is shown in the figure. Six regions of high conservation between all 11 proteins are shown (domains I–VI) together with one region (L) conserved between *Lj*NIN, *Ps*NIN, and the most homologous NLP from Arabidopsis. Region V is the most conserved region and surrounds the putative DNA binding and dimerization, RWP-RK, motif. Region VI has similarity to the PB1 heterodimerization domain conserved in animals, fungi, and plants. Domains I to VI and L are overlined and identical amino acids marked by asterisks. Positions of stop codons (aa in black shadow) or amino acid changes caused by the three *sym35* mutations are indicated in the *Ps*NIN sequence. The small tracts of repeated amino acids are marked by double lines.

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tion of short tracts of particular amino acids is a peculiar feature observed in the pea NIN protein. Among the small tracts of Gln, His, Gly, Asn, and Ser (Fig. 3), only the hexa-His and hexa-Asn tracts are encoded by a triplet repeat reminiscent of the genetic expansion of poly-Gln repeats associated with several neurodegenerative disorders (Richards et al., 1992). The functional significance, if any, of these repeats is unclear but none of them are conserved in *Lj*NIN or the other NLPs.

Analysis of Expression of *PsNin*

The similarity of the phenotype between *Pssym35* and *Ljnin* mutants suggests that the orthologous genes are active with a similar temporal and spatial expression pattern. To determine the expression of the *PsNin* gene in various organs, a northern analysis was performed on RNA extracted from roots, leaves, nodules, flowers, pods, and stems. As seen in Figure 2C, expression was detected only in nodules. This expression pattern is comparable with the previously determined expression pattern of the *LjNin* gene where steady-state mRNA was only detected in nodules in northern hybridizations (Schauser et al., 1999).

L. japonicus and pea develop determinate and indeterminate root nodules, respectively. It was therefore of interest to investigate if there were major differences in the cellular accumulation of *PsNin* transcripts in the pea nodules. In *L. japonicus*, *Nin* is expressed early in the nodule primordium (Schauser et al., 1999), and to determine the cellular expression pattern in pea, in situ hybridization was performed on sections of nodules harvested 4 weeks after inoculation with *R. leguminosarum* bv *viciae*. Figure 4, A and D, shows that *PsNin* is expressed in the meristematic cells (zone I) and cells of the infection zone (zone II). Cells of interzone (II–III) mark the boundary where transcripts were detectable, and in the nitrogen fixation zone (III), transcripts were not detected. These cells are either not expressing *PsNin*, or expression is below the level of detection for the in situ hybridization technique. Expression of the bacterial subunit of nitrogenase *nif*H (Fig. 4, B and E) is a diagnostic feature of cells in interzone (II–III; Yang et al., 1991; Kawashima et al., 2001). The *PsNin* expression in zone I and II was comparable with the expression of *LjNin* detected in the dividing cells and the later stages of nodule primordia in the determinate *L. japonicus* nodules (Schauser et al., 1999). The apparent down-regulation of expression in interzone II to III and zone III differed from the continued presence of *LjNin* transcripts in cells of the central zone of fully developed determinate nodules.

The expression pattern for the two genes predicts that distinct DNA regulatory elements could be present in both the *PsNin* and *LjNin* promoter regions. A ClustalX alignment identifies several blocks of conserved sequence (Fig. 5). Assignment of functional

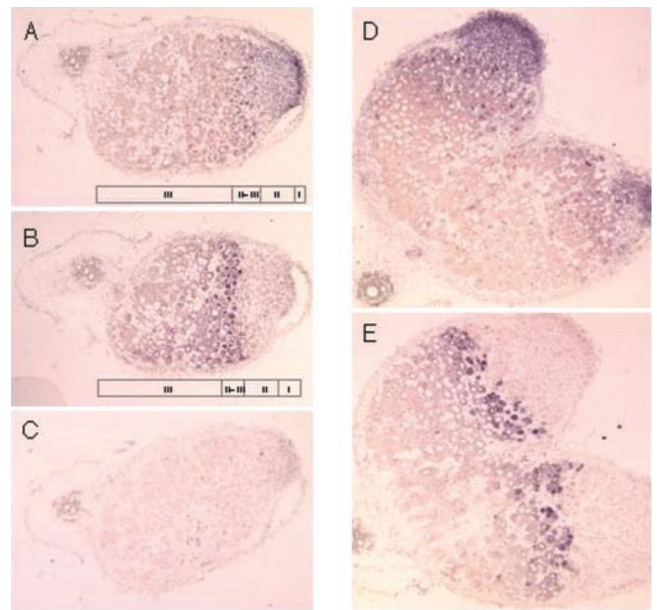

Figure 4. In situ localization of *PsNin* transcripts in longitudinal sections of pea nodules. Nodules were harvested 4 weeks after inoculation with *R. leguminosarum* bv *viciae*, sectioned, and hybridized with digoxigenin-labeled RNA probes. Hybridizing transcripts are visualized as purple color. A, *PsNin* antisense probe. B, Bacterial *nif*H antisense probe. C, *PsNin* sense probe. D, *PsNin* antisense probe on bifurcated nodule. E, Bacterial *nif*H antisense on bifurcated nodule. *nif*H was used to define interzone II to III and nitrogen fixation zone (III) in the nodules.

significance to these sequences would require detailed deletion analysis and site-specific mutagenesis. However, the sequence content of two adjacent 14- and 12-nucleotide blocks located between position −384 and −352 of the *LjNin* promoter and between −385 and −352 of the *PsNin* promoter attracts attention. The proximal 14-nucleotide-long conserved sequence is a perfect match to the 3′ half (TTGTCTCTT) of the extended organ-specific element (AAAGATNNTT-GTCTCTT) first identified in the soybean and *Sesbania rostrata* leghemoglobin promoters and subsequently found in other nodule expressed genes (Stougaard et al., 1987; Ramlov et al., 1993; Szczyglowski et al., 1994). Interestingly, the same sequence encompasses a TGTCTC sequence shown in Arabidopsis to be an auxin-responsive element binding the ARF1 transcription factor (Ulmasov et al., 1997). The 12-nucleotide conserved sequence is AT rich, and although the sequence itself is different, the position is reminiscent of the AT-rich binding sites for the NAT2 trans-factor located immediately 5′ to the organ-specific element of the soybean and *S. rostrata* leghemoglobin promoters (Laursen et al., 1994).

DISCUSSION

We have identified and characterized the *PsNin* gene and shown that the *PsSym35* locus is *PsNin*. A simple sequence alignment between the *L. japonicus*

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                                              -384________________
LjNin --CATTTTGTACCCTTCAATCCTATAATAA----------CAGGAATAATATACCATT-C
PsNin CTAAATTTGTACCCTGCGAAGTATTAATAAAATTCAACGGCAAGAATAATATACCCATCC
         * ********** * *     ******          ** ************  * *
      _____________                           -385
LjNin TTGTCTCTTTCTGAATTTACTCCCTTATTAATATTCTTTCCTCAAGTCATGAGTAGTTAA
PsNin TTGTCTCTTTCTGTCTCTCATCTCATGGATTGAGTTCATAGTATATATATCTTTTTTTGA
      *************  * *  ** * *      * *   *  *  *   **   *  ** *

LjNin GTTTTAGAAGCTTGTTGTTTTGCTGTGTTGTTTCTTACTCGAGAGG------CAGCAAGC
PsNin TAATAGAGTACTTGATAGTATACTATATATGTTTATATGCATGTGTTACTCTCAACACGA
        *      **** *  * * ** * *   **  **  *  * *       ** ** *

LjNin ATATACTGAATACTACATTTATTTATAGAATATAATAATAATTTACAGCTGATAACTATG
PsNin GTGTATGTTCTACAAGAAGCAGCAAACACATAACATATTATATACAACAAGATCATCATC
       * **     *** * *   *   *    ***  *** *   *   *   *** *  **

LjNin AAAG---AATATTTATTTATATG-TTATATGTATTGTATATACCTGCCACGGTGAGGGGG
PsNin ATCATCCTATGATAATAAATAAATAAATAATTTACAGCGCTGCTACTTTGTGAAAG
      *       **  * **  ***   * * *  **   ** *   **** **  ** *   *

LjNin GATTAGGGATATAAAAACTGG-AGACCACTCTTTGATTTTGCTTACACTTGTGGGTCCTA
PsNin AGATTAATATTTTATAGATGATACACCAGTAGCTTCTTTTGCTTACCA--GTGGGTCCAA
         *    ** * * *  **  * **** *   *  **********    ******** *
        o
LjNin GCAAGATACAATTAAAGAAATTT-------TGGGTTTTAAATAAGAGACTTGTTGATCGC
PsNin CTCAATTATAATAAACTGAAATTGCGTTTTTGGTCATTAAATAGGAGACCTGTTTATTGC
         *  ** *** **   ** **       ***   ******* ***** **** ** **
                              •
LjNin ATGTTGAGGCAAGGCAATCATTTTC
              •
PsNin ATATGTTCA
      ** *
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Figure 5. Identification of putative conserved regulatory sequences in promoter regions of *LjNin* and *PsNin*. A region of 472 nucleotides upstream of the transcript start of *LjNin* was compared with the 486 nucleotides upstream of the transcript start of *PsNin*. A conserved block, indicated with a line, contains the 3′ half of the two-motif nodulin consensus AAAGAT-TTGTCTCTT (Stougaard et al., 1987; Ramlov et al., 1993; Szczyglowski et al., 1994) overlapping a sequence identical to auxin-responsive element TGTCTC (Ulmasov et al., 1997). ●, Transcription start site for *LjNin* and *PsNin*; ○, a minor transcription start in *LjNin*.

Nin gene and an Arabidopsis *Nin*-like gene present in the databases allowed primer design and PCR amplification of the pea *Nin* ortholog. The *PsNin* gene structure and the position of mutations in the three available *sym35* alleles were subsequently determined. This exemplifies how comparative phenotypic analysis and mapping makes it possible to transfer the achievements of molecular genetics from model legumes into agriculturally important crop species such as pea. Ongoing experiments are taking this one step further using the *L. japonicus* transformation system. Detailed characterization of the *PsSym35* gene and functional analysis of conserved protein domains is approached by complementation of *Ljnin* mutants. With the rapidly accumulating expressed sequence tag and genome sequences from members of the legume family, this approach will be even simpler in the future. Candidate genes can be isolated, and exploiting the recently released *L. japonicus* genome sequences mapping approximately 1,300 genes along the chromosomes (Nakamuro et al., 2002), new gene-specific legume markers can be developed to start saturating the crop legume maps. Such markers can also be used to determine the level of synteny in the legume family. Marker-assisted breeding in legumes is bound to benefit from this development of markers, genome, and map information achieved from model legumes.

In the course of characterizing the *PsNin* gene and identifying the sequence differences in the three *Pssym35* mutant alleles, the wild-type *PsNin* gene was sequenced from three varieties of pea. Alignment of the sequences demonstrates a low level of sequence polymorphism between the varieties. Pea cvs Alaska and Finale are very similar with only 18 single-nucleotide polymorphisms and four triplet indels in 3.9 kb, whereas the pea SGE line appears to be more distant with 33 single-nucleotide polymorphisms and three triplet indels of three, six, and 15 nucleotides, respectively, toward pea cv Alaska. This presents a small glimpse of the genetic variation in the European breeding stocks.

This comparative study between *L. japonicus* and pea led to the cloning of a symbiotic gene first identified after chemical mutagenesis and description of three mutant alleles. All three mutants of *Pssym35* have the same phenotype, although the mutations are quite different. The allele in SGENod$^-$-3 creates a stop codon and predicts that only a short protein of 53 amino acids without the RWP-RK domain and the PB1 dimerization domain is synthesized. This would most likely be a null mutation. SGENod$^-$-1 has a stop codon after D552 resulting in a protein without the RWP-RK domain. The amino acid change in RisNod8 exchanges an acidic E for a basic K residue in an 8-amino acid motif conserved between all NLPs presently in the databases. This motif lies embedded in domain IV (Fig. 3). Apart from characterizing the allele, such missense mutations will eventually contribute to the understanding of NIN protein function. Five domains were found to be conserved between *Ps*NIN and *Lj*NIN. Four of the domains (I, II, III and IV) appear to be family "specific," present only in NLPs, whereas the RWP-RK (V) and PB1 (VI) domains are conserved in other proteins (L. Schauser, W. Wieloch, and J. Stougaard, unpublished data). Interestingly, one additional domain (L) was found to be shared between *Lj*NIN, *Ps*NIN, and the most closely related Arabidopsis protein.

In *L. japonicus*, *Nin* expression was detectable only in nodules by northern hybridization, whereas more sensitive RNase protection assays were necessary to detect expression in other organs. Analyzed by northern hybridization, the expression pattern of *PsNin* appears to be comparable. Interestingly, the *PsNin* cDNA was found in a root hair-enriched library, indicating that *PsNin* is already expressed in the root hairs of pea. In 4-week-old pea nodules, the expression of *PsNin* was detected in cells of the meristem (zone I) and the infection zone (II). Across the interzone (II–III) and in the nitrogen fixation zone (III), transcripts were no longer detected. This expression pattern is in accordance with the mutant phenotype that suggests a function for *PsNin* in nodule inception and infection thread formation down-

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stream of lipochitin-oligosaccharide signal perception. Continued expression in the nodule meristem and the infection zone of indeterminate nodules indicate that *Ps*NIN is necessary for these developmental stages also after the onset of the organogenic process. In determinate *L. japonicus* nodules, expression of *Nin* was detected in the nodule primordia, central tissues, parenchyma, and vascular tissues in the mature nodules (Schauser et al., 1999). In the indeterminate pea nodule, expression was not detected in the more differentiated cell types, and although there might be differences in the sensitivity of the *in situ* hybridization techniques used, this appears to be a difference between determinate and indeterminate nodules. The overlapping expression pattern of the *LjNin* and *PsNin* genes is to some extent reflected in the sequences of their promoter regions. A promoter sequence identical to the 3′ half of the organ-specific element of the late nodulin leghemoglobin is conserved in both *PsNin* and *LjNin*. This may constitute a DNA regulatory element mediating *Nin* gene expression during nodulation. In addition, an auxin regulatory element appears to be embedded in this sequence. The involvement of auxin in initiating root nodule organogenesis (Mathesius et al., 1998) has been a long-standing hypothesis, and interestingly, the *LjNin* gene-promoter appears to respond to auxin addition in certain cell types (Y. Umehara and J. Stougaard, unpublished data). Together, these results demonstrate a comparable function for the *Ps*NIN and *Lj*NIN regulatory proteins and constitute another example of conservation of components in the development of determinate and indeterminate root nodules. Following this line of investigation in future comparative genomics, the numerous classical pea mutants and the well-established pea physiology will complement the functional analysis of model legume genes.

MATERIALS AND METHODS

Plant Material

The following pea (*Pisum sativum*) lines were used in the study: three allelic but independently obtained non-nodulating pea mutants SGENod$^-$-1 (*sym35*) and SGENod$^-$-3 (*sym35*; Tsyganov et al., 1994, 1999) and RisNod8 (*sym35*; Engvild, 1987; gene symbol was assigned according to Drs. G. Duc and M. Sagan [personal communication]) as well as the initial wild-type lines pea SGE line (Kosterin and Rozov, 1993) and pea cv Finale (Engvild, 1987). Also, the multiply marked genetic line NGB1238 (catalog no. of Nordic GenBank) or JI73 (catalog no. of *Pisum* Genetic Stocks Collection, John Innes Centre) was used in the experiments. Recombinant inbred lines from a cross between the lines JI281 and JI399 were used for mapping (Hall et al., 1997).

Bacterial Strains

For nodulation tests, the commercial, symbiotically effective strain CIAM 1026 (Collection of All-Russia Research Institute for Agricultural Microbiology) of *Rhizobium leguminosarum* bv *viciae* was used as the inoculant. For expression analysis, *R. leguminosarum* bv *viciae* R418 strain (kindly provided by Herman Spaink) was used as the inoculant.

Isolation of PsNin

A number of Arabidopsis homologs of *LjNin* can be found in the databases. Alignment between *LjNin* and an Arabidopsis homolog (F23E12.170; accession no. T06130) was used to design degenerate primers based on conserved regions. Combinations of the forward primers 5′-GCCCTTCC-TGTYTTCGAAAGAGG-3′ and the two reverse primers 5′-GGCAAKCTTTT-GGAATGAAAAACTCC-3′ and 5′-AGGCTTCCTGCAAAGTAYTG-TC-3′ gave PCR products in the expected size ranges from the pea lines JI399 and JI281. The PCR products were cloned with the Topo TA cloning kit (Invitrogen, Carlsbad, CA) and sequenced. The overlapping sequences representing a pea ortholog showed high similarity to *LjNin*.

Mapping Experiments and Cosegregation Analysis

To carry out the initial mapping of the *Sym35* gene, the mutant SGENod$^-$-3 (*sym35*) was crossed to the line NGB1238 (*wb*, *b*, *k*, *s*, *r*, *tl*, *gp*, *d*, *le*, *Fs*, and U^{st}) and F_1 plants were grown under greenhouse conditions with full mineral nutrition to obtain the seeds for F_2 progeny. The F_2 generation was analyzed for the segregating morphological markers, and the seeds for the F_3 generation were collected from individual F_2 plants. The symbiotic phenotype (presence/absence of nodules and signs of nitrogen starvation) of the plants in the F_3 generation (grown in sand without combined nitrogen [Borisov et al., 1997]) was analyzed to reveal homozygous (*Sym35/Sym35* or *sym35/sym35*), and heterozygous (*Sym35/sym35*) plants in the F_2. Data on segregation were processed to position *PsNin* on the pea genetic map with the use of computer programs “Plant” and “Cross” developed by Serge M. Rozov (Institute of Cytology and Genetics, Siberian Branch of Russian Academy of Sciences, Novosibirsk, Russia).

For cosegregation analysis, the pea mutant SGENod$^-$-3 (*sym35*) was crossed with the line NGB1238, and F_2 plants were obtained. Homozygous *Sym35/Sym35* and *sym35/sym35* F_2 plants were identified by phenotypic analysis of the F_3 offspring. In the F_3, only wild-type plants descending from homozygous F_2 plants were used for cosegregation analysis together with *sym35/sym35* mutant plants. Plants of the F_3 population were grown under greenhouse conditions with full mineral nutrition. Two leaves from each plant were collected for DNA isolation, and the genotype of individual plants was determined using the parent-specific primers: NGB1238fw, 5′-GAAAGAGGAAGCGGACTTGT-3′; NGB1238rev, 5′-TGGTCTTCTCCGC-CTTGG-3′; SN-3fw, 5′-GTGTCATTGATGTTGTTATCGCA-3′; and SN-3rev, 5′-GATGATGACCTGCGTCCACCA-3′.

Gene Libraries

Three pea gene libraries were used in the experiments: a nodule cDNA library (λ gt11 vector, pea cv Finale), a cDNA library enriched for root hairs (λ Zap II vector, pea cv Finale), and a genomic library (λ Dash II vector, pea cv Alaska).

Using a probe covering an approximately 2-kb fragment of the pea *Nin* gene, one million clones of each library were screened and processed according to the Stratagene (La Jolla, CA) protocols for λ-phage custom libraries.

DNA and RNA Techniques and Conditions of PCR

Pea genomic DNA was prepared essentially according to Saghai-Maroof et al. (1984). Total RNAs from different pea tissues were prepared using Trizol (Invitrogen) followed by LiCl precipitation or CsCl centrifugation and used for northern analysis and 5′-RACE. Isolation of phage λ-DNA and subcloning of the insert into plasmid vector (pBluescript SK±) were carried out using standard procedures. DNA sequences were produced using the Thermo Sequenase Dye Terminator Cycle Sequencing kit (Amersham Biosciences AB, Uppsala) and analyzed on an ABI prism 310 Genetic analyzer (Applied Biosystems, Foster City, CA). To get full-length cDNA, a combination of RT-PCR and 5′-RACE was performed with nodule RNA (cv Finale) using the SMART RACE kit according to supplier’s instructions (BD Biosciences Clontech, Palo Alto, CA). Primers for RT-PCR: reverse primer, 5′-GAATGCTG-TAATGTCGATTGCG-3′; forward primer, 5′-GCGGTGTATTTGGGAC-CATGG-3′. Primer for DNA synthesis for RT-PCR: 5′-CAGCTG-

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CAGAGCCAGTGTAG-3′. Primers for 5′-RACE: 5′-ACCACTTTCTTGATCAACTTG-3′ and 5′-GTTGGATTGAAGCTAGTGAGAA-3′. Southern blot, northern blot, and hybridization was performed as described (Sambrook et al., 1989) using a 2-kb probe produced by PCR amplification using the primers 5′-CTAAGGAGGAGATCGGCAATTCA-3′ and 5′-GAACAGAATCTATCACCAGTTG-3′ and final washing at 0.3 × SSC and 0.1% (w/v) SDS at 65°C. The probe covers the coding sequence between positions 503 and 2,084.

In Situ Hybridization and Microscopic Analysis

In situ hybridization was performed as described by Kouchi and Hata (1993). RNA probes covering approximately 1 kb of *PsNin* (between positions 213 and 1,662 of the cDNA) were prepared with digoxigenin-11-UTP (Roche Diagnostics, Basel). Hybridization signals were detected by antidigoxigenin-alkaline phosphatase conjugate with nitroblue tetrazolium salt and 5-bromo-4-chloro-3-indolyl phosphate toluidinium salt (Roche Diagnostics). Longitudinal sections (8 μm) of the nodules were hybridized. *nif*H of *R. leguminosarum* bv *vicea* (kindly provided by Dr. H. Kouchi) was used for reference (Yang et al., 1991).

ACCESSION NUMBERS

The accession numbers from this study are as follows: *PsNin* cv Alaska, AJ493063; *PsNin* cv Finale, AJ493064; *PsNin* line SGE, AJ493065; *PsNin* mRNA cv Finale, AJ493066; and *LjNin* promoter region, AJ493067.

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