Review

The NMN Module Conducts Nodule Number Orchestra

Zhijuan Wang,1 Lixiang Wang,1,2 Yongliang Wang,1 and Xia Li1,*

Legumes control nodule number through nodulation and autoregulation of nodulation (AON) pathways. Nodule Inception (NIN) is essential for rhizobial infection and nodule organogenesis in legumes. The GmNINa-miR172c-NNC1 (NMN) module, which consists of two positive regulators, GmNINa and miR172c, and a suppressor, NNC1, integrates both pathways. GmNINa activates miR172c to downregulate NNC1, leading to nodulation, while NNC1 inhibits miR172c expression, forming a negative feedback loop. GmNINa and NNC1 interact with each other and antagonistically fine-tune GmRIC1/RIC2 expression, turning AON on and off. Conversely, activation of AON inhibits GmNINa and miR172c expression, thereby reducing their inhibitory effects on NNC1 to attenuate both nodulation signaling and AON. The NMN module functions not only as an “accelerator” of the nodulation signal to promote nodulation but also as a “brake” on the signal by activating AON to orchestrate nodule number.

The nodule is a unique root organ of legumes and several nonlegume plants that hosts soil-borne rhizobia or Frankia bacteria to construct mutually beneficial relations. Nodule formation is initiated by the molecular communication between rhizobia and the host plant through the nodulation signaling pathway. Because nodulation and symbiotic nitrogen fixation are highly energy-demanding processes that are tightly linked to photoassimilate consumption of the host, nodule number is also dynamically and precisely controlled by a long-distance feedback loop, named autoregulation of nodulation (AON). Coordination of nodule formation and systemic nodulation inhibition underpins the growth of the host plant. To achieve maximum gains, plants have evolved a molecular machinery that integrates nodulation and AON signaling pathways to coordinate downstream cellular responses. In soybean, the NMN regulatory module, which consists of soybean Nodule Inception (GmNINa), MicroRNA172c (miR172c) and Nodule number control 1 (NNC1), has been shown to control nodule number by orchestrating dynamic cross talk between nodulation and long-distance feedback signaling in soybean. In this study, we provide a review of the NMN module control of nodule number and discuss how it functions and whether its function is conserved, thereby helping to elucidate the mechanistic control of nodule number.

NIN IS A CENTRAL REGULATOR OF NF SIGNALING IN LEGUMES

Nodule formation is initiated by the host plant. Under low nitrogen conditions, the plant exudes flavonoid signals from its roots, which are perceived by compatible nitrogen-fixing bacteria rhizobia to induce the production of Nod factor, specialized lipochitooligosaccharide signals (Dakora, 2003; Downie, 2014). Perception of the Nod factor molecules (NFs) by the LysM-type receptor kinases (NF receptors) of the host plant triggers a signaling cascade resulting in cell responses of the root to NFs, rhizobial infection and the formation of root nodules (Limpens and Bisseling, 2003; Limpens et al., 2003; Madsen et al., 2003; Radutoiu et al., 2003; Arrighi et al., 2006; Indrasumunar and Gresshoff, 2010; Downie, 2014).

Regulation of rhizobial infection and nodule organogenesis relies on the action of nodulation-promoting regulators. *Nodule Inception (NIN)* in *Lotus japonicus* is an essential component of symbiotic nodulation and is the founder gene for the NIN-like protein (NLP) transcription factor family in plants, which contains conserved Phox and Bem1 (PB1) and RWP-RK domains (Schauser et al., 1999; Konishi and Yanagisawa, 2013; Griesmann et al., 2018; van Velzen et al., 2018). There is extensive evidence showing that NIN in legumes regulates nearly all the processes of rhizobial infection and nodule organogenesis (Marsh et al., 2007; Heckmann et al., 2011; Kosuta et al., 2011; Popp and Ott, 2011; Yoro et al., 2014). For example, NIN plays a key role in rhizobial infection by activating expression of infection-specific genes, such as *ENOD11* encoding a putative repetitive proline-rich cell wall protein in *Medicago truncatula* (Andriankaja et al., 2007; Journet et al., 2001; Vernié et al., 2015), *NODULATION PECTATE LYASE (NPL)* involved in pectate degradation in the cell wall (Xie et al., 2012), SCAR-Nodulation (SCARN) responsible for actin

---

1State Key Laboratory of Agricultural Microbiology, College of Plant Science and Technology, Huazhong Agricultural University, Wuhan, Hubei 430070, P.R. China
2Key Laboratory of Plant Stress Biology, School of Life Sciences, Henan University, Kaifeng, China
*Correspondence: xli@mail.hzau.edu.cn

https://doi.org/10.1016/j.isci.2020.100825

iScience 23, 100825, February 21, 2020 © 2020 The Author(s). This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).
NMN MODULE CONTROLS NODULATION IN SOYBEAN

Comparative sequencing analysis results reveal that NIN is one of the genes that are essential for symbiotic root nodulation in legumes and non-legume plants (Griesmann et al., 2018; van Velzen et al., 2018). In soybean, GmNINa is a functional ortholog of NIN in L. japonicus and M. truncatula (Wang et al., 2019). GmNINa has a typical NLP protein structure and is highly similar to NIN in Lotus and Medicago. Most importantly, GmNINa has the same role as NIN in Lotus and Medicago during soybean nodulation (Wang et al., 2019). Knockdown or overexpression of GmNINa results in developmental defect in rhizobial infection and nodule organogenesis of soybean. Similarly, GmNINa promotes the transcription of the putative homologues of NIN target genes (e.g., GmNF-YA1a) during rhizobial infection. Thus, GmNINa may exert its function in rhizobial infection and symbiotic root nodule organogenesis through a conserved regulatory mechanism.

Interestingly, GmNINa has been shown to transcriptionally activate a noncoding small RNA miR172c (Wang et al., 2019). MiR172c is specifically induced by rhizobia in an NF receptor-dependent manner to promote soybean nodulation by mainly cleaving the mRNA of its target gene NNC1 (Nodule Number Control1), which encodes an AP2 transcriptional repressor. Downregulation of NNC1 reduces NNC1-mediated transcriptional repression of the early nodulin genes ENOD40-1 and ENOD40-2, leading to nodule formation (Wang et al., 2014). NNC1 can also directly target miR172c to repress its transcription in a short feedback loop, and interestingly, NNC1 can interact with GmNINa to repress the transcriptional activation of GmNINa on miR172c with an unknown molecular mechanism. NNC1-mediated transcriptional feedback and antagonistic repression of GmNINa on miR172c may maintain the proper level of miR172c, which is crucial for optimal nodulation (Wang et al., 2019). Taken together, these findings indicate that GmNINa and miR172c, two components of the NMN module, act as key activators of nodule formation during nodulation through downregulating the third component NNC1, a nodulation suppressor in soybean. Reduced expression of NNC1 by GmNINa-miR172c promotes nodule formation, and conversely, NNC1 represses miR172c expression to inhibit nodulation. Beyond its functional role in nodulation regulation, the NMN module forms a central signal integrator that allows dynamic cross talk of nodulation and AON signaling to define the optimal nodule number.

NMN MODULE CONTROLS AON IN SOYBEAN

AON is a long-distance negative feedback loop that prevents the host plant from excessive nodulation. It has been known that the AON signaling pathway is initiated at the nodule primordia formation stage by root production of nodulation-specific CLAVATA/EAR-related (CLE) peptides (Fletcher et al., 1999; Brand et al., 2000; Penmetsa et al., 2003). These highly conserved nodulation-specific CLE peptides (e.g., MtCLE12 and MtCLE13 in M. truncatula, LjCLE-RS1 and LjCLE-RS2 in L. japonicus, and GmRIC2 and GmRIC2 in G. max) are transported from root to shoot, where they are perceived by their receptors, leucine-rich-repeat receptor-like kinases (e.g., MsSUNN in M. truncatula, LjHAR1 in L. japonicus, and...
GmNARK in *G. max* located in the parenchyma cell membrane of phloem in leaves to induce SDIs that can be transported to root to inhibit further nodulation (Krusell et al., 2002; Nishimura et al., 2002; Lim et al., 2011; Reid et al., 2011; Mortier et al., 2012). Recently, research found that miR2111 is involved in AON by repressing its target gene Too much love (TML) to keep the plant susceptible to nodulation (Tsikou et al., 2018). Autoregulation is a manifestation of systemic nodulation regulation and is the intrinsic ability of plants to maintain a constant nodule number for optimal growth under low nitrogen conditions.

The first step for turning on AON signaling is to activate these nodule-specific CLE genes; thus, the timing and expression levels of these CLE genes are crucial to the autoregulation of nodulation. Most recently, the NMN module has been shown to mediate the on-off switch for autoregulation of nodulation. For example, GmNINa has been shown to directly target GmRIC1 and GmRIC2 to activate the transcription of two genes (Wang et al., 2019; Suzaki and Nishida, 2019). These findings reveal a conserved mechanism of NIN-mediated transcriptional activation of these nodulation-specific CLE genes in nodule number regulation. In addition to direct transcriptional activation of GmRIC1 and GmRIC2, GmNINa can also activate GmRIC1 and GmRIC2 by activating miR172c, which reduces the repression of NNC1 on GmRIC1 and GmRIC2. It has been shown that miR172c acts as a positive regulator of GmRIC1 and GmRIC2, whereas NNC1 functions as a repressor of these two genes. The double tuning system of GmRIC1 and GmRIC2 may be essential for the precise production of specific CLE peptides. Interestingly, NNC1 has stronger binding activity to the cis element of GmRIC1 and GmRIC2 than GmNINa to outcompete GmNINa from binding the same sequence, reducing the transcriptional activation of GmRIC1 and GmRIC2. Moreover, NNC1 physically interacts with GmNINa, although the function of the NNC1-GmNINa interaction in antagonistically regulating GmNINa transcriptional activity on the expression of GmRIC1 and GmRIC2 has not been determined. It is apparent that NNC1 and GmNINa antagonistically regulate GmRIC1 and GmRIC2 transcription, leading to CLE production and switching on AON. Thus, the NMN module plays a central role in the activation and attenuation of AON signaling and responses that control nodule number (Figure 1).

REFINING NODULATION SIGNALS

Early developmental patterning and organ number usually involve a master transcriptional response to morphogenetic signals followed by refinement of this expression domain. One crucial mechanism that can initiate refinement is autoregulation, which can maintain a certain threshold for transcriptional activation. The NMN module is a central transcriptional activator for both nodulation and autoregulation. During rhizobial infection and nodule organogenesis, gene expression of NIN is induced (Schauer et al., 1999). NIN activates rhizobial infection and nodule formation, and it can also activate LjCLE-RS1 and LjCLE-RS2 and subsequent activation of AON that, in turn, suppresses expression of NIN through a long-distance negative feedback loop (Soyano et al., 2014). This autoregulatory circuit is able to refine the expression of NIN and maintain a well-defined optimal level for nodulation. The most recent data have shown that GmNINa is a downstream gene and that the expression of GmNINa is negatively regulated by the Glycine max nodule autoregulation receptor kinase (GmNARK) and AON signaling (Wang et al., 2019), indicating that the autoregulatory circuit for refining transcriptional activation of nodulation is conserved in legumes.

During nodulation, the level and activity of NIN determine the function of the NMN module in soybean. Thus, repression of GmNINa by AON would lead to downregulation of miR172c and upregulation of NNC1. Indeed, miR172c acts downstream of GmNARK, and the level of miR172c transcription is negatively regulated by GmNARK (Wang et al., 2014, 2019). In the loss-of-function mutant of GmNARK, the expression of miR172c was strongly increased; downregulation or overexpression of miR172c in the mutant of gmnark restored or exacerbated the hypernodulation phenotype of the mutant, respectively. Consequently, NNC1 expression is also regulated by GmNARK and AON (Wang et al., 2014, 2019). Thus, the activation of AON by the NMN module can maintain the activity of the master regulatory module of NMN below a potentially harmful level to control nodulation and nodule number. The molecular mechanism of AON-mediated transcription maintenance of NIN transcription factors has not been determined.

REPROGRAMMING NODULE NUMBER UNDER HIGH NITRATE

The ability of legumes to reprogram nodulation in response to changing environment cues underpins the adaptation of legumes. Nitrogen availability is a primary environmental factor determining rhizobia-legume symbiosis of legumes. Nodule number is a characteristic feature of nitrogen-affected nodulation. With increasing levels of nitrogen, nodule number is gradually reduced and even completely abolished in the presence of sufficient nitrate (Mortier et al., 2011). It has been shown that AON positively regulates

---

*References*

- Krusell et al., 2002
- Nishimura et al., 2002
- Lim et al., 2011
- Reid et al., 2011
- Mortier et al., 2012
- Soyano et al., 2014
- Wang et al., 2014, 2019
- Tsikou et al., 2018
- Schauer et al., 1999
- Mortier et al., 2011
- Mortier et al., 2012
- Krusell et al., 2002; Nishimura et al., 2002; Lim et al., 2011; Reid et al., 2011; Mortier et al., 2012.
nitrate-induced nodulation inhibition because loss of function mutations in L. japonicus HAR1, M. truncatula SUNN, and glycine max GmNARK reduce the sensitivity of nodulation to high nitrate (Carroll et al., 1985a; Carroll et al., 1985b; Magori and Kawaguchi, 2009; Wopereis et al., 2000; Mortier et al., 2011).

As common components in nodulation and AON, the NMN module has recently been shown to mediate nitrate-induced nodulation inhibition. The nitrate signaling pathway seems to converge toward the NMN module to regulate nodulation. NIN-like protein 1 (NLP1) in M. truncatula can translocate into the nucleus under high nitrate to suppress the transcriptional activity of NIN on downstream target genes by directly interacting with NIN during nodulation (Lin et al., 2018). In addition, NITRATE UNRESPONSIVE SYMBIOSIS 1 (NRSYM1), an NLP family transcription factor in L. japonicus, enters the nucleus in response to high nitrate to directly activate CLE-RS2 expression and production of CLE-RS2, resulting in activation of AON (Nishida et al., 2018). This finding, together with the antagonistic function of GmNINa and NNC1 in the expression and production of nodule-specific CLEs, supports the hypothesis that, during nodulation,
NRSYM1 interacts with NIN and/or NNC1 or their counterparts in legumes to regulate ON and OFF of AON in response to environmental nitrate change and to control nodule number for optimal growth of plants, whereas in uninoculated root, nitrate triggers NRSYM1 to activate CLE gene expression and inhibits nodulation independently of NIN (Nishida et al., 2018). Thus, the NMN module may also be a central integrator of environmentally modulated nodulation and nodule number regulation in legumes.

CONCLUDING REMARKS
In light of these recently discovered evidence, it is immediately apparent that the NMN module is a master integrator of nodulation and autoregulatory signaling pathways that determine the ultimate nodule number. The NMN module is a shared regulatory unit between nodulation and AON signaling pathways that connect two pathways together to act as one regulatory system. This arrangement may enable plants to systemically monitor incoming signals (e.g., hormones, nutrients, cellular energy levels) from nodulation and energy sensors to activate a cellular machinery that regulates nodulation and autoregulation of nodulation. The various interactions between its components and between the NMN module and other regulators enable the integration of different developmental and environmental pathways to provide a coordinated regulation of nodule formation. Ultimately, the functioning of this molecular regulatory hub ensures that nodule number is precisely and dynamically controlled under certain soil conditions, enabling adaptive growth.

These works have established a fundamental role for the NMN module in nodule number control in soybean. The apparent conservation of the components of the NMN module or the NMN module suggests that leguminous plants may have evolved this unique module to master-switch the nodule number during evolution of rhizobia-legume symbiosis. Thus, the presence of the NMN module as a master switch for nodule number control might be shared by a large number of legumes. The common thread that links the NMN module to various aspects of nodule number control is its transcriptional regulation of numerous genes during nodulation and autoregulation. It is important to determine how the NMN module interacts with other transcription factors through various cis elements, particularly how the NMN-mediated nodule number regulation is integrated spatially and temporally. Many outstanding questions in this research direction await to be answered. These include: what are the cellular cues that controls this master integrator? How does this master switch integrate with other regulators in the control of nodule number? The precise mechanisms by which the NMN module controls these biological processes are likely to vary among different leguminous plants. Thus, understanding the regulatory circuit of the NMN module in nodule formation and development in these species will help decipher the genetic basis and evolution of nodule number regulation and will facilitate genetic improvement of the symbiotic nitrogen fixation efficiency of leguminous crops.

In conclusion, unveiling how this NMN master switch spatially and temporally orchestrates the nodule number of legumes may help to elucidate the molecular mechanism of nodule number control. The integration of these intrinsic and extrinsic signaling pathways at the NMN module may help to elucidate how the number of symbiotic nodules is continuously optimized to respond to the changing environment.

ACKNOWLEDGMENTS
This work was supported by grants from the National Key Research and Development Program of China (2016YFA0500503), the National Natural Science Foundation of China (31730066), the Huazhong Agricultural University Scientific and Technological Self-Innovation Foundation (2015RC014) and the Fundamental Research Funds for Central Universities (2662018PY075).

AUTHOR CONTRIBUTIONS
X.L. outlined the manuscript. All authors wrote the manuscript and prepared the figures. X.L. and Z.W. edited and provided feedback on the manuscript.

REFERENCES
Andriankaja, A., Boisson-Dernier, A., Frances, L., Sauviac, L., Jauneau, A., Barker, D.G., and de Carvalho-Niebel, F. (2007). AP2-ERF transcription factors mediate Nod factor dependent MtENOD11 activation in root hairs via a novel cis-regulatory motif. Plant Cell 19, 2866–2885.
Arrighi, J.F., Barre, A., Ben Amor, B., Bersoult, A., Soriano, L.C., Mirabella, R., de Carvalho-Niebel, F., Journet, E.P., Gherardi, M., Huguet, T., et al. (2006). The Medicago truncatula lysis motif-receptor-like kinase gene family includes NFP and new nodule-expressed genes. Plant Physiol. 142, 265–279.
Brand, U., Fletcher, J.C., Hobe, M., Meyerowitz, E.M., and Simon, R. (2000). Simon Dependence of stem cell fate in Arabidopsis on a feedback loop regulated by CLV3 activity. Science 289, 617–619.
Kressel, L., Madsen, L.H., Sato, S., Aubert, G., Genua, A., Szczegowsli, K., Duc, G., Kaneko, T., Tabata, S., de Bruijn, F., et al. (2002). Shoot control of root development and nodulation is mediated by a receptor-like kinase. Nature 420, 422–426.

Lim, C.W., Lee, Y.W., and Hvang, C.H. (2011). Soybean nodule-enhanced CLE peptides in roots act as signals in GmNARK-mediated nodulation suppression. Plant Cell Physiol. 52, 1613–1627.

Limpens, E., and Bisseling, T. (2003). Signaling in symbiosis. Curr. Opin. Plant Biol. 6, 343–350.

Limpens, E., Franken, C., Smit, P., Willemsje, J., Bisseling, T., and Geurts, R. (2003). LysM domain receptor kinases regulate rhizobial Nod factor-induced infection. Science 302, 630–633.

Lin, J.S., Li, X., Luo, Z.L., Mysore, K.S., Wen, J., and Xie, F. (2018). NIN interacts with NLPS to mediate nitrate inhibition of nodulation in Medicago truncatula. Nat. Plants 4, 942–952.

Liu, C.W., Breakspear, A., Guan, D., Cerri, M.R., Lin, J.S., Li, X., Luo, Z.L., Mysore, K.S., Wen, J., and Xie, F. (2018). NIN interacts with NLPS to mediate nitrate inhibition of nodulation in Medicago truncatula. Nat. Plants 4, 942–952.

Madsen, E.B., Madsen, L.H., Radutoiu, S., Olbryt, M., Rakwalska, M., Szczegowsli, K., Sato, S., Kaneko, T., Tabata, S., Sandal, N., et al. (2003). A receptor kinase gene of the LysM type is involved in legume perception of rhizobial signals. Nature 425, 637–640.

Magori, S., and Kawaguchi, M. (2009). Long-distance control of nodulation: molecules and models. Mol. Cells 27, 129–134.

Marsh, J.F., Rakosevic, A., Mitra, R.M., Brocard, L., Sun, J., Escherth, A., Long, S.R., Schultz, M., rates, P., and Oldroyd, G.E. (2000). Medicago truncatula NIN is essential for rhizobial-independent nodule organogenesis induced by autoactive calcium/calmodulin-dependent protein kinase. Plant Physiol. 144, 324–335.

Mortier, V., De Wever, E., Vuytskeste, M., Holsters, M., and Goormachtig, S. (2012). Nodules are governed by interaction between CLE peptides and cytokinin signaling. Plant J. 70, 367–376.

Mortier, V., Fenta, B.A., Martens, C., Rombauts, S., L.S.R., Cook Dual genetic pathways controlling nodule number in Medicago truncatula. Plant Physiol. 131, 998–1008.

Popp, C., and Ott, T. (2011). Regulation of signal transduction and bacterial infection during root nodule symbiosis. Curr. Opin. Plant Biol. 14, 458–467.

Qiu, L., Lin, J.S., Xu, J., Sato, S., Parmiske, M., Wang, T.L., Downie, J.A., and Xie, F. (2015). SCARN is a novel class of SCAR protein that is required for root-hair infection during legume nodulation. PLoS Genet. 11, e1005623.

Radutoiu, S., Madsen, L.H., Madsen, E.B., Felle, H.H., Umehara, Y., Gronlund, M., Sato, S., Nakamura, Y., Tabata, S., Sandal, N., et al. (2003). Plant recognition of symbiotic bacteria requires two LysM receptor-like kinases. Nature 425, 585–592.

Reid, D.E., Ferguson, B.J., and Gresshoff, P.M. (2011). Inoculation-and-nitrate-induced CLE peptides of soybean control NARK-dependent nodule formation. Mol. Plant Interact. 24, 605–618.

Schauer, L., Roussis, A., Stiller, J., and Stougaard, J. (1999). A plant receptor controlling development of symbiotic root nodules. Nature 402, 191–195.

Schless, K., Lilley, J.L.S., Lee, T., Tamvakis, I., Kohler, W., Bailey, P.C., Thomine, S., Lupeik, J., Ramakrishnan, K., Carpenter, M.D., et al. (2019). NODULE INCEPTION recruits the lateral root developmental program for symbiotic nodule organogenesis in Medicago truncatula. Curr. Biol. 29, 3657–3668.

Soyano, T., Hirakawa, H., Sato, S., Hayashi, M., and Kawaguchi, M. (2014). NODULE INCEPTION creates a long-distance regulatory feed-back loop involved in homeostatic regulation of nodule organ production. Proc. Natl. Acad. Sci. U S A 111, 14607–14612.

Soyano, T., Kouchi, H., Hirota, A., and Hayashi, M. (2013). Nodule inception directly targets NF-Y subunit genes to regulate essential processes of root nodule development in Lotus japonicus. PLoS Genet. 9, e1003352.

Soyano, T., Shimoda, Y., Kawaguchi, M., and Hayashi, M. (2019). A shared gene drives lateral root development and root nodule symbiosis pathways in Lotus. Science 366, 1021–1023.

Suzuki, T., and Nishida, H. (2019). Autoregulation of legume nodulation by sophisticated transcriptional regulatory networks. Mol. Plant 12, 1179–1181.

Tsikokou, D., Yan, Z., Holt, D.B., Abel, N.B., Reid, D.E., Madsen, L.H., Bhasin, H., Sexauer, M., Stougaard, J., and Markmann, K. (2018). Systemic control of legume susceptibility to rhizobial infection by a mobile microRNA. Science 362, eaat6907.

van Velzen, R., Holmer, R., Bu, F., Rutten, L., van Zeijl, A., Liu, S., Santuari, L., Cao, Q., Sharma, T., Shen, D., et al. (2018). Comparative genomics of the nonlegume Parasponia reveals insights into evolution of nitrogen-fixing rhizobium symbioses. Proc. Natl. Acad. Sci. U S A 115, E4700–E4709.

Vernié, T., Kim, J., Frances, L., Ding, Y., Sun, J., Guan, D., Niebel, A., Gifford, M.L., Carvalhaloneb, F.D., and Oldroyd, G.E.D. (2015).
The NIN transcription factor coordinates diverse nodulation programs in different tissues of the Medicago truncatula root. Plant Cell 27, 3410–3424.

Wang, Y.N., Wang, L.X., Zou, Y.M., Chen, L., Cai, Z.M., Zhang, S.L., Zhao, F., Tian, Y.P., Jiang, Q., Ferguson, B.J., et al. (2014). Soybean miR172c targets the repressive AP2 transcription factor NNC1 to activate ENOD40 expression and regulate nodule initiation. Plant Cell 26, 4782–4801.

Wang, L., Sun, Z., Su, C., Wang, Y., Yan, Q., Chen, J., Ott, T., and Li, X. (2019). A GmNIN-miR172c-NNC1 regulatory network coordinates the nodulation and autoregulation of nodulation pathways in soybean. Mol. Plant 12, 1211–1226.

Wopereis, J., Pajuelo, E., Dazzo, F.B., Jiang, Q., Gresshoff, P.M., Bruijn, F.J.D., Stougaard, J., and Szczyglowski, K. (2000). Short root mutant of Lotus japonicus with a dramatically altered symbiotic phenotype. Plant J. 23, 97–114.

Xie, F., Murray, J.D., Kim, J., Heckmann, A.B., Edwards, A., Oldroyd, G.E., and Downie, J.A. (2012). Legume pectate lyase required for root infection by rhizobia. Proc. Natl. Acad. Sci. U S A 109, 633–638.

Yoro, E., Suzaki, T., Toyokura, K., Miyazawa, H., Fukaki, H., and Kawaguchi, M. (2014). A positive regulator of nodule organogenesis, NODULE INCEPTION, acts as a negative regulator of rhizobial infection in Lotus japonicus. Plant Physiol. 165, 747–758.