Multiple steps control immunity during the intracellular accommodation of rhizobia
Fathi Berrabah, Pascal Ratet, Benjamin Gourion

To cite this version:
Fathi Berrabah, Pascal Ratet, Benjamin Gourion. Multiple steps control immunity during the intracellular accommodation of rhizobia. Journal of Experimental Botany, Oxford University Press (OUP), 2015, 66 (7), pp.1977-1985. 10.1093/jxb/eru545. hal-02410342

HAL Id: hal-02410342
https://hal-cnrs.archives-ouvertes.fr/hal-02410342
Submitted on 27 May 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L’archive ouverte pluridisciplinaire HAL, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d’enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Distributed under a Creative Commons Attribution 4.0 International License
RESEARCH PAPER

Multiple steps control immunity during the intracellular accommodation of rhizobia

Fathi Berrabah, Pascal Ratet* and Benjamin Gourion*
Institut des Sciences du Végétal, CNRS, Saclay Plant Sciences, Avenue de la Terrasse, 91198 Gif sur Yvette, France

* To whom correspondence should be addressed. E-mail: benjamin.gourion@isv.cnrs-gif.fr; ratet@isv.cnrs-gif.fr

Received 21 October 2014; Revised 15 December 2014; Accepted 16 December 2014

Abstract

Medicago truncatula belongs to the legume family and forms symbiotic associations with nitrogen fixing bacteria, the rhizobia. During these interactions, the plants develop root nodules in which bacteria invade the plant cells and fix nitrogen for the benefit of the plant. Despite massive infection, legume nodules do not develop visible defence reactions, suggesting a special immune status of these organs. Some factors influencing rhizobium maintenance within the plant cells have been previously identified, such as the M. truncatula NCR peptides whose toxic effects are reduced by the bacterial protein BacA. In addition, DNF2, SymCRK, and RSD are M. truncatula genes required to avoid rhizobial death within the symbiotic cells. DNF2 and SymCRK are essential to prevent defence-like reactions in nodules after bacteria internalization into the symbiotic cells. Herein, we used a combination of genetics, histology and molecular biology approaches to investigate the relationship between the factors preventing bacterial death in the nodule cells. We show that the RSD gene is also required to repress plant defences in nodules. Upon inoculation with the bacA mutant, defence responses are observed only in the dnf2 mutant and not in the symCRK and rsd mutants. In addition, our data suggest that lack of nitrogen fixation by the bacterial partner triggers bacterial death in nodule cells after bacteroid differentiation. Together our data indicate that, after internalization, at least four independent mechanisms prevent bacterial death in the plant cell. These mechanisms involve successively: DNF2, BacA, SymCRK/RSD and bacterial ability to fix nitrogen.

Key words: bacA, CRK, DNF2, innate immunity, nifA, nifH, nitrogen fixation.

Introduction

Legume plants can be cultivated without application of nitrogen fertilizers on soil poor in nitrogen. This capacity is the result of the associations with soil bacteria, referred to as rhizobia, that fix nitrogen for the benefit of the legume (for recent review, see Udvardi and Poole, 2013). These symbioses are efficient thanks to the spectacular bacterial density within the symbiotic organ, the nodule. Despite the massive and chronic colonization by bacteria, legume nodules do not develop defences. As an illustration of this, expression of defence-related genes is drastically reduced in nodule infected cells as compared to non-infected cells (Limpens et al., 2013). A growing body of recent publications indicates that (the control of) plant innate immunity plays a major role during the early steps of rhizobium/legume interactions (Jones et al., 2008; Yang et al., 2010; Gough and Jacquet, 2013; Liang et al., 2013; Lopez-Gomez et al., 2012; Okazaki et al., 2013).

However, the control of legume immunity is not only critical during the first steps of the symbiotic process but is also required once the nodule is formed when bacteria are released into the plant cells. In Medicago truncatula Gaertn., one of the favourite model legumes, two genes required to repress defence-like reactions into the nodules have been identified.
Recently, DNF2 and SymCRK (Bourcy et al., 2013; Berrabah et al., 2014a). These genes encode for a phosphatidylinositol specific phospholipase C-like protein and a cysteine-rich receptor-like kinase respectively. Mutants altered in these genes develop nodules in which transcription of defense-related genes is induced and phenolic compounds accumulate (Bourcy et al., 2013; Berrabah et al., 2014a). Rhizobia viability is drastically reduced in these mutants maybe as a consequence of the observed defense-like reactions.

Interestingly, defenses are not totally abolished in M. truncatula wild type (WT) nodules. Indeed, in indeterminate nodules (i.e. those harbouring a persistent meristem), legumes related genes is induced and phenolic compounds accumulate (Bourcy et al., 2013; Berrabah et al., 2014a). NCR peptides are specifically produced in infected cells and have a toxic effect on bacteria and prevent their division. As a consequence, in M. truncatula, intracellular rhizobia (called bacteroids) are elongated bacteria, up to 10 µm long, that contain multiple genome copies, up to 24C (Mergaert et al., 2006). NCR toxicity is partially countered by the bacterial BacA protein (Haag et al., 2011), which is believed to act as a peptide importer. The bacterial bacA mutants are more susceptible to NCR peptides in vitro as well as in planta (Van de Velde et al., 2010; Haag et al., 2011). Indeed, once released into the plant cells the bacA mutant does not elongate as the WT bacteria and is rapidly killed (Haag et al., 2011). Interestingly, the ability of the bacA mutant to survive within the plant cells is restored in the M. truncatula dnf1 mutant (Haag et al., 2011). DNF1 is required for bacteroid differentiation and encodes a nodule-specific subunit of a signal peptidase necessary to address plant proteins (including NCR peptides) to the cellular compartments containing the bacteroids (Wang et al., 2010). In addition to DNF1, three other genes (RSD, DNF2 and SymCRK) are also required for bacteroid elongation in M. truncatula (Bourcy et al., 2013; Sinharoy et al., 2013; Berrabah et al., 2014a). These three genes are specifically expressed in nodules and the symbiotic organs of the rsd, dnf2 and symCRK mutants accumulate brown material (Bourcy et al., 2013; Sinharoy et al., 2013; Berrabah et al., 2014a), reminiscent of defence reactions.

Defence-like reactions are not developed in bacA-triggered nodules indicating that the lack of bacteroid elongation and the lack of nitrogen fixation do not elicit dnf2- and symCRK-like defences (Berrabah et al., 2014b). However, the bacA mutant is unable to colonize massively the plant cells and the question remains as to whether the lack of nitrogen fixation associated with a massive bacterial intracellular colonization could elicit the plant defenses.

We aim to better understand the repression of defense-like reactions in nodules by identifying the factors involved in this process and by determining precisely the sequence of events that conduct defense development in the mutants. Herein we show that early bacterial death is associated with bacterial inability to fix nitrogen and that RSD is also required to prevent defense-like reactions in nodules. In addition, by combining the use of the dnf2, symCRK and rsd mutants together with various bacterial mutants, we define two steps in the symbiotic control of immunity after rhizobia internalization.

### Materials and methods

**Bacteria strains, plant lines, cultivation and inoculation methods**

Sinorhizobium meliloti strain 1021 (Galibert et al., 2001), bacA (Ferguson et al., 2002), nifH, nifA, Smn11, Rm41 (Kondorosi et al., 1984), strain AK631 (eps+) (Putnok et al., 1988), strain P711(kps+) (Becquéart-de Kozak et al., 1997) were cultivated in YEB medium (Krall et al., 2002) for 24h at 30°C. M. truncatula ecotype R108, also referred to as M. truncatula ssp. tricula, and its derived lines NF0737, i.e. symCRK, MS240, dnf2-4, NFI1265, rsl-1, NFI776 and NFI7452 (Tadege et al., 2009; Pilarriu et al., 2012; Bourcy et al., 2013; Sinharoy et al., 2013; Berrabah et al., 2014a, Cheng et al., 2014) as well as M. truncatula cv. Jemalong, line A17 and the dnf1 (Mitra and Long, 2004; Starer et al., 2006; Wang et al., 2010; Young et al., 2011) derived line were cultivated as previously described (Berrabah et al., 2014a). Briefly, seeds were scarified by incubation in sulphuric acid for 7 mins followed by 4 washing steps in sterile distilled water. After scarification, seeds were surface sterilized by incubation in 15 ml of 0.3% chlorine followed by four washing steps in 50 ml of sterile distilled water. Sterile seeds were then incubated at 4°C onto agar plates for 48 h at 4°C. Seeds were then transferred to non-agar medium for 24 to 48h. After germination, seedlings were transferred onto buffered nodulation medium (BNM) (Ehrhardt et al., 1992) supplemented with AVG 1 µM and immediately inoculated. Bacterial cells were washed with distilled sterile water before seedling inoculation. Optical densities of the bacterial cell suspension were adjusted to OD600=0.1 and 1 ml of this suspension was used per 12 x 12 cm plate containing eight seedlings. After 30 mins, liquid excess was removed by pipetting and the plates were sealed on three sides. Plants were cultivated in a growth chamber at 26°C at 60% humidity with a photoperiod of 16h/8h light/dark respectively.

**Molecular methods**

Nodules were collected on plants with forceps and histology and immediately frozen in liquid nitrogen. Samples were reduced to powder by grinding material with steel beads in 2 ml tubes using a Qiagen tissue lyser 2 x 30 s at 25 pulsations/second. RNAs were extracted using GeneJET Plant RNA Purification Mini kit (Thermo Scientific) as recommended by the manufacturer, RNA extracts were treated with Turbo DNAse ambiion (Life Technology) to remove DNA traces. RNAs were reverse transcribed using SuperScriptII (Life Technology) as recommended by the manufacturer. qPCR was then carried out on Light Cycler 480 using the LightCycler 480 SYBER Green I (Roche) device as previously described (Gonzalez-Rizzo et al., 2006). Samples were normalized using the constitutive MtACTIN2 as a reference gene (Limpens et al., 2005). Progeny of mutant lines altered in DNF1 was genotyped using primers listed in Supplementary Table S1 following the method described in Ratet et al. (2010). Primers used are listed in Supplementary Table S1.

**Imaging and histological analysis**

Entire nodules were imaged using Nikon microscope AZ100. To produce sections, nodules were embedded in 6% agarose (water) and 70 µm sections were produced using vibratome VT1200S from Leica. To observe necrosis, nodule sections were also imaged with a microscope AZ100. Sections mounted between slide and slipcover were bright light illuminated and observed with CIS illumination. For live and dead staining, we used the protocol previously described in Haag et al. (2011). Briefly, nodule sections were incubated in a 50 mM Tris-HCl buffer (pH 7.2) containing 30 µM propidium iodide and 5 µM Cyto9 (Life Technology) for 20 mins. Stained sections were then mounted between slide and slipcover with a few Tris-HCl buffer drops and observed using a Leica SP8 confocal microscope.

For phenolic staining, a protocol derived from (Vasse et al., 1993) was used. Briefly, nodule sections were fixed for 30 to 40 mins using potassium permanganate 0.02%. Sections were washed as necessary using PIPES 100 mM (pH 7.2) buffer to remove precipitate. Phenolics were
bacteroid differentiation does not elicit expression of defence genes or phenolics accumulation that are observed in the 
\( \text{dnf}2 \) and the \( \text{symCRK} \) nodules (Berrabah et al., 2014b). Nevertheless, the \( \text{bacA} \) mutant is hypersensitive to NCR peptides and this sensitivity does not allow massive colonization of the plant cells (Haag et al., 2011). In order to determine if a massive colonization by ineffective bacteria triggers defence reactions, \( M. \text{truncatula} \) WT plants were inoculated with the \( S. \text{melloti} \) \( nifA \) mutant. NifA is a key regulator of the nitrogenase synthesis and the corresponding mutant does not fix nitrogen (Zimmerman et al., 1983; Dixon and Kahn, 2004). Nodules induced by \( nifA \) are infected and bacteroids clearly undergo terminal differentiation (Fig. 1). However, in contrast to the WT, the mutant bacteria prematurely died as revealed by the live/dead assay that stains viable bacteria green and dead bacteria red (Fig. 1). The bacterial death occurs only after bacteroid elongation in the \( nifA \) mutant (Supplementary Fig. S1). Beyond genes responsible for nitrogenase synthesis, NifA regulates additional genes (Bobik et al., 2006) and the \( nifA \) mutant displays pleiotropic phenotypes (Gong et al., 2007). To determine whether \( nifA \) bacteroid death is caused by the lack of nitrogen fixation or to another \( nifA \)-regulated process, \( nifH \) bacteroid viability was also studied; \( nifH \) encodes a subunit of the nitrogenase. Like for the \( nifA \) mutant, bacteroid death was observed for elongated \( nifH \) bacteroids (Supplementary Fig. S1) suggesting that lack of nitrogen fixation is responsible for the death of \( nifA \) and \( nifH \) elongated bacteroids. In order to determine if defence reactions such as those observed in the nodules of the \( \text{symCRK} \) and the \( \text{dnf}2 \) mutants could be responsible for \( nifA \) bacterial death, the induction of these defences

**Results**

The \( nifA \) fix mutant undergoes bacterial death that is not associated with \( \text{symCRK}/\text{dnf}2 \)-like defence reactions

Using the bacterial \( \text{bacA} \) mutant that is unable to differentiate elongated bacteroids, we previously showed that lack of

**Fig. 1.** Mutation in \( nifA \) elicits early bacterial death that is not mediated by \( \text{symCRK}/\text{dnf}2 \)-dependant defence reactions. (A): a–d: On these sections of 26dpi nodules imaged using a confocal microscope after live/dead staining assay, the early death of the \( nifA \) mutant within the plant cell is observable. Green and red stain alive and dead bacteria respectively. a and b represent WT bacteria induced nodules, c and d: \( nifA \) induced nodules, note that like the WT bacteria, the \( nifA \) mutant undergoes terminal differentiation, scale bars correspond to, 20\( \mu \)m (a, c) and 10\( \mu \)m (b, d). (B): \( nifA \) mutant does not elicit the accumulation of phenolics in nodules. Sections of WT plant nodules induced by WT bacteria or by \( nifA \) mutant as well as \( \text{dnf}2 \) and \( \text{symCRK} \) nodules induced by WT bacteria were stained with methylene blue to reveal phenolics in blue. Scale bars correspond to 500\( \mu \)m. (C): PR10, VSP, BGL and \( \text{NDRI} \) defence-related genes are not induced in \( nifA \)-triggered nodules. In contrast these defence-related genes are induced in \( \text{dnf}2 \) and \( \text{symCRK} \) nodules as revealed by RT-qPCR analysis. Results are expressed as induction fold vs R108 nodules induced by WT bacteria after normalization using \( \text{Mtactin}2 \) constitutive gene as an internal standard.
was evaluated by RT-qPCR and histological approaches. In contrast to the *dnf2* and *symCRK* mutant nodules, the expression of the defence-related genes *PR10*, *VSP*, *BGL*, and *NDR1* was not induced in the *nifA*-triggered nodules, which also do not accumulate phenolics (Fig. 1). In agreement of a role of *nifA* after *DNF2* and *SymCRK*, mutation in the *nifA* gene does not prevent the development of defence-like reactions in *dnf2* and *symCRK* nodules (Supplementary Fig. S2). Together these results suggest that lack of nitrogen fixation induces early death of the bacteria. Furthermore this bacterial death is not associated with defence-like reactions observed in the *dnf2* and *symCRK* mutants (Fig. 1).

**DNF2, bacA and SymCRK act successively during the symbiotic process**

In order to get an insight into the development of the symbiotic process and the timing of immunity suppression during symbiosis, nodulation tests were conducted using *dnf2* and *symCRK* mutants in combination with bacterial mutants altered in surface components or in the symbiotic process. Defence-like reactions were evaluated 14 days after inoculation in the nodules induced by *S. meliloti* strain Rm41 eps and *kps* mutants (altered in exopolysaccharide and capsular polysaccharide respectively) as well as *S. meliloti* Sm1021 bacA, and *nifH* mutants. Defence reactions were monitored by following the expression of the *NDR1* and *PR10* genes using RT-qPCR. In addition, nodule sections were observed under bright field illumination to reveal the presence of necrotic zones accumulating phenolics. The *eps* and *kps* mutants elicit a moderate induction of the expression of *NDR1* and *PR10* genes in nodules of the WT plants (Fig. 2A). These inductions were not associated with the development of necrotic zones in the WT plant nodules (Fig. 2B). In contrast, the expression of defence-related genes was observed when these bacterial mutants were nodulating *dnf2* and *symCRK* plant mutants and this was associated to the presence of necrotic zones (Fig. 2B). In nodules developed on WT plants inoculated by Sm1021 or its *nifH* or *bacA* mutant derivatives, the *NDR1* and *PR10* genes are not induced (Fig. 2A) and these nodules do not accumulate phenolics. In contrast to the WT plants, *dnf2* and *symCRK* nodules display necrosis and induction of the defence markers with these strains, except for *symCRK* inoculated with the *bacA* mutant; in this plant/bacteria mutant combination the expression of defence-related genes and nodule necrosis were not observed (Fig. 2A, B). This absence of defence reactions in *symCRK/bacA* nodules was further confirmed in 21 and 27 day-old nodules (Fig. 2C, Supplementary Fig. S3). However, acetylene reduction assays indicate that nitrogen fixation was not restored in the *symCRK/bacA* nodules (Supplementary Fig. S4). Furthermore, despite the reduction in the expression of late *NCR* genes (Berrabah et al., 2014a) (Supplementary Fig. S5) and the absence of defence-like reactions in the *symCRK* mutant upon *bacA* infection, the *bacA* mutant viability was not restored in these *symCRK/bacA* nodules (Supplementary Fig. S6) contrasting with what was observed in *dnf2/bacA* nodules (Haag et al., 2011).

The double mutant *dnf2/symCRK* was analysed with respect to defence development in nodules elicited with WT bacteria or *bacA* mutant strain. We did not observe any additive effect of the mutation in the double mutant nodules upon inoculation with the WT bacteria (Fig. 2C, Supplementary Figs S3 and S6). When inoculated with the *bacA* mutant, defence reactions were observed in the *dnf2/symCRK* nodules but not on the *symCRK* mutant (Fig. 2C, Supplementary Fig. S3). These results thus indicate that the double mutant behaves as the *dnf2* mutant in terms of defence reactions and that *DNF2* is epistatic to *SymCRK* in the *M. truncatula* R108 background. Together, these results suggest that *DNF2, bacA* and *SymCRK* act successively during the symbiotic process.

**SymCRK correct expression requires initiation of bacteroids differentiation**

In order to improve our understanding of the *SymCRK* gene function, its expression pattern inside nodules was studied using in situ hybridization in WT nodules. This experiment (Fig. 3A) suggests that *SymCRK* is specifically expressed in infected cells in agreement with its timing of expression (Berrabah et al., 2014a; see also below). In order to define more precisely the role of *SymCRK* and *DNF2* during the symbiotic process, we investigated the expression of the two genes in *M. truncatula* nodules induced by the *S. meliloti* Sm1021 *nifA* and *nifH* mutants altered in the production of nitrogenase (for review, see Dixon and Kahn, 2004) as well as by the *bacA* mutant. In nodules induced by the *nifA* and *nifH* bacterial mutants (Fig. 3B), expression of the two symbiotic genes *SymCRK* and *DNF2* was not altered, indicating that nitrogen fixation is not necessary for their expression. *DNF2* transcript accumulation is not modified in nodules induced by the *bacA* mutant or in *symCRK* mutant nodules induced by WT bacteria placing *DNF2* upstream or in a parallel pathway to *BacA* and *SymCRK*. In contrast, the level of *SymCRK* transcripts was reduced in WT nodules induced by the *bacA* mutant or in *dnf2* mutant nodules induced by WT bacteria, in agreement with the data shown above, indicating that *SymCRK* act downstream of *DNF2* and *bacA* during the symbiotic process. As mentioned previously, bacteroids do not differentiate and are not maintained viable in both the *dnf2* and the *bacA* nodules. In contrast, in the *dnf1* *M. truncatula* mutant, bacteria do not undergo terminal differentiation but bacteroids remain viable during colonization (Haag et al., 2011). Thus, this mutant constitutes a good tool to discriminate whether the colonization defect and/or the differentiation defect is responsible for incorrect *symCRK* expression. We have used two *Tnt1* insertion mutant lines for *DNF1* (NF8776 and NF17452) in the *M. truncatula* R108 background (in which the *dnf2* and *symCRK* mutants used in this study were generated). In these lines the *Tnt1* retrotransposon is inserted in the first intron 131 bp and 324 bp after the predicted start codon. However, we could not observe any symbiotic phenotypes in the progeny, possibly as a result of the insertion in the intron or of the absence of homologous mutant (Supplementary Fig. S7). The expression of
SymCRK was thus studied in the only dnf1 available mutant (generated in the A17 background). This experiment shows that SymCRK expression was reduced in the dnf1 mutant, suggesting that not only bacterial colonization but also bacteroid differentiation is required for SymCRK expression (Fig. 3C).
RSD represses defence-like reactions and act downstream of bacA and DNF2

Like dnf2 and symCRK, rsd displays necrotic nodules in which bacteroids do not undergo terminal differentiation (Sinharoy et al., 2013). In order to determine if rsd also shares the defence-like reactions observed in the dnf2 and symCRK mutants, induction of defence-related genes was evaluated in rsd-1 nodules. Expression of the PR10 and NDR1 genes was evaluated by RT-qPCR and was found to be induced in rsd-1 as compared to WT nodules (Fig. 4). In addition, presence of phenolic compounds was detected in rsd-1 nodules (Fig. 4) indicating that rsd develops defence-like reactions similar to those of symCRK and dnf2. In order to position RSD with respect to SymCRK and DNF2 during the development of the symbiosis, we analysed the expression of RSD in the dnf2 and in the symCRK backgrounds. RSD expression is strongly reduced in both mutants (Fig. 4C) suggesting a role for RSD downstream of DNF2 and SymCRK.

In order to determine whether the development of defence-like reactions in the rsd-1 mutant is dependent on bacterial invasion and differentiation, we evaluated defences in this mutant upon nodulation with the bacA mutant. In contrast to dnf2 and similarly to symCRK, the rsd mutant does not accumulate phenolics upon infection with bacA (Fig. 4A). In agreement with these results, defence-related gene expression was strongly reduced in rsd/bacA nodules as compared to rsd nodules triggered by WT bacteria (Fig. 4B). Thus, similar to what is observed in the symCRK mutant, development of defence-like reactions in rsd relies on the presence of a functional bacA.

Discussion

Herein we have investigated the sequence leading to the symbiotic suppression of immunity in legume nodules after rhizobia internalization within the plant cells (chronic infection). We showed that the bacterial mutants nifA and nifH died prematurely within the plant cells despite that defence reactions similar to those observed in symCRK and dnf2 nodules were not detected in these nodules. In addition, we showed that DNF2 and SymCRK act successively during the symbiotic process and that bacA is required after DNF2 and before SymCRK. Furthermore, our data indicate that rsd-1 behave like the symCRK mutant and acts after bacA. These results are in agreement with the observation that SymCRK and RSD expression is reduced in WT plants nodulated with bacA, a condition in which expression of DNF2 is not modified (Fischer et al., 1986) reminiscent of symCRK/dnf2-like defences. Altogether our results indicate that multiple steps are required for the symbiotic suppression of immunity after bacterial internalization. Furthermore the present study indicates that at least two types of defence can be the cause of bacterial death in the plant cells, one associated with nodule necrosis and induction of PR10 and NDR1 defence genes and another observed upon nifA- or nifH-triggered nodulation.

Based on our results, we propose a model focused on the intracellular stage of symbiosis, which describes the actors preventing bacteroid death (Fig. 5). In this model, DNF2 is
Multiple steps in the symbiotic control of immunity

Immunity suppression is not only required for the intracellular stage of the symbiosis; various actors have been identified or proposed to be important to prevent plant defences during the infection process. For example the nodulation (Nod) factors might participate in the suppression of plant immunity triggered by microbial motifs (Liang et al., 2013). In agreement with this novel Nod factor's role, the type three secretion system (often used by phytopathogenic bacteria to suppress plant immunity) of *Bradyrhizobium elkanii* can bypass the requirement of Nod factors for the nodulation of soybean (Okazaki et al., 2013). Also, two soybean resistance genes modify the rhizobial host range of the plant (Yang et al., 2010) and exopolysaccharides were shown to be important to reduce the induction of defence-related genes at the early stages of the symbiosis (Jones et al., 2008). Finally, defence-related phytohormones also interfere with the nodulation process (Penmetsa and Cook, 1997; Stacey...
et al., 2006; Sun et al., 2006). These data indicate that suppression of immunity during the early steps of the symbiotic process is required for nodulation. In agreement with this, the expression of a PR10 gene is drastically reduced in bumps (young nodules) and mature nodules as compared to roots. We showed that DNF2 prevents defence-like reactions in nodules only after bacteria internalization (Bourcy et al., 2013) and that in bumps, the expression of the PR10 gene is similar in the dnf2 and WT nodules (Bourcy et al., 2013). These results indicate that a mechanism distinct from DNF2 and SymCRK suppresses immunity in early developing nodules and reinforce the hypothesis of the existence of multiple steps in the suppression of plant immunity during the symbiotic process. It is now a challenge to gather the identified actors of the symbiotic suppression of immunity within an integrated model.

Supplementary data

Supplementary data are available at JXB online.

Supplementary Fig. S1. Lack of nitrogen fixation triggers bacterial death after bacteroid elongation.

Supplementary Fig. S2. dnf2 and symCRK act before nifA.

Supplementary Fig. S3. Defence reactions are abolished in the symCRK bacA nodules.

Supplementary Fig. S4. Nitrogen fixation is not restored in symCRK/bacA nodules.

Supplementary Fig. S5. NCR99 expression is reduced in bacA-triggered nodules of the dnf2 and symCRK mutants.

Supplementary Fig. S6. bacA viability is not restored in the symCRK mutant.

Supplementary Fig. S7. DNF1 gene structure (based on MTR_3g027890 sequence) and position of the Tnt1 insertions present in mutant lines NF8776 and NF17452.

Supplementary Table S1. List of primers used during this study.

Acknowledgements

This work was supported by the Centre National de la Recherche Scientifique (CNRS) and the grant Agence Nationale de la Recherche (ANR) Blanc International SVSE 6.2010.1 (LEGUMICS) to PR. This work has benefited from a French State grant (reference ANR-10-LABX-0040-SPS) managed by the French National Research Agency under an Investments for the Future programme (reference ANR-11-IDEX-0003-02). This work has benefited from the facilities and expertise of the IMAGIF Cell Biology Unit (Général de l’Essonne). We are grateful to Michael Udvardi, Jiangqi Wen and Domonkos A, Horvath B, Marsh JF, Halasz G, Ayaydin F, Olldroyd GE, Kondorosi A, Banfalvi Z, Kondorosi E, 2007. Genomic organization and evolutionary insights on the composite genome of Sinorhizobium meliloti. Science 261, 668–672.

References


