



Symbiosis genes for immunity and vice versa

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Basic molecular knowledge on plant–pathogen interactions has largely been gained from reverse and forward genetics in *Arabidopsis thaliana*. However, as this model plant is unable to establish endosymbiosis with mycorrhizal fungi or rhizobia, plant responses to mutualistic symbionts have been studied in parallel in other plant species, mainly legumes. The resulting analyses led to the identification of gene networks involved in various functions, from microbe recognition to signalling and plant responses, thereafter assigned to either mutualistic symbiosis or immunity, according to the nature of the initially inoculated microbe. The increasing development of new pathosystems and genetic resources in model legumes and the implementation of reverse genetics in plants such as rice and tomato that interact with both mycorrhizal fungi and pathogens, have highlighted the dual role of plant genes previously thought to be specific to mutualistic or pathogenic interactions. The next challenges will be to determine whether such genes have similar functions in both types of interaction and if not, whether the perception of microbial compounds or the involvement of specific plant signalling components is responsible for the appropriate plant responses to the encountered microorganisms.

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Plants have to cope with a plethora of microorganisms in their natural environment. Legumes that establish mutualistic interactions with nitrogen-fixing rhizobacteria and arbuscular mycorrhizal (AM) fungi [1] also deal with various pathogenic microbes, including oomycetes [2], fungi [3] and bacteria [4]. Legume plants must therefore adapt constantly to engage compatible interactions with mutualistic symbionts and fight to control pathogens [1]. This Ying and Yang response has been uncovered at

multiple steps of molecular and cellular plant cell reprogramming. The N-acetylglucosamine (NAG)-based signals produced by microbes and their perception by host plants hold a central role in this process (see [Box 1](#)). Similar chemical structures of microbial molecules suggest the existence of common actors used by plants, and notably legumes, to perceive and respond to pathogens and beneficial microbes. Identifying such commonalities can help us understand how plants deal simultaneously with multiple microbes, identify other specific actors explaining how plants distinguish friends and foes, and assess whether microbes can exploit plant molecular actors to hijack plant defences and colonise their host successfully. In addition, this could facilitate genetic improvement of plant resistance to pathogens without affecting beneficial symbioses.

Arabidopsis thaliana was instrumental for deciphering the molecular dialog between plants and pathogens [5] but its inability to establish endosymbioses was a major limitation to compare immune and mutualistic molecular processes. In parallel, research on model legumes initially focused on endosymbiotic associations. To assess putative connections between symbiosis and immunity, research groups developed several strategies. These included the inoculation of *Medicago truncatula* symbiotic mutants with root pathogens [3,6,7,8,9], the use of hosts such as rice, tomato and maize able to interact with both arbuscular mycorrhizal (AM) fungi and pathogens [10–12] and the treatment of various plants (including *Arabidopsis*) with symbiotic or pathogenic microbe-derived molecules [13,14,15]. This review summarizes recent results obtained in this frame but focuses only on genes for which a dual function in response to both symbiont and pathogen inoculations has been demonstrated. Hence, we excluded from the scope of this article symbiotic genes such as DNF22, SymCRK [16] or the recently described NAD1 [17] which intervene during late stages of rhizobial symbiosis following nodule formation. Despite the fact that their characterisation clearly points to roles in the regulation of nodule immunity, assessment of these genes in plant–pathogen interactions has not been performed yet. The list of genes with dual functions in plant–microbe interactions is dominated by genes from the model legume *Medicago truncatula* for which pathosystems were established earlier than in *Lotus japonicus*. Subtle discrepancies often exist in the functioning of symbiosis genes between these two plants, therefore we draw parallels between the two plants only when experimental validation exists in both plants. The development of a novel *L. japonicus* pathosystem with *Phytophthora palmivora* will help to bridge this gap of

Box 1 Roles of microbial N-acetylglucosamine signals in the equilibrium of plant symbiosis and defence responses.

Among the chemically diverse signals released by microbes, N-acetylglucosamine (NAG) based oligomers hold a central role in the recognition steps of both mutualistic symbionts and pathogens [1,71]. Arbuscular endomycorrhizal fungi have evolved a set of NAG-derived signals ranging from monomeric NAG [72], to short chito-saccharides (chitotetramers, CO4) [10,73] as well as tailored CO4/CO5: the so-called lipochitooligosaccharides (LCOs) [12,15]. Chitooctamers (CO8) [19,29**], LCOs and CO4 signal at the plasma-membrane through specific pathways triggering immunity and the common symbiotic signalling pathway (CSSP) in the case of the other signals [74]. The specificity of CSSP is likely achieved by activation of nuclear calcium oscillations [1]. Simultaneously, LCOs can suppress typical defence responses [13**,75]. Parallels occur on the pathogen side, since fungi can also produce CO4 and oomycete cell walls can release signals triggering nuclear calcium oscillations [15,71]. Perplexingly, CO4 was recently shown to trigger defence responses in *Lotus japonicus* roots suggesting that specificities in plant responses to these signals might exist at the species and/or the tissue level [39*,73]. Altogether, these data illustrate that control or activation of plant immunity by similar microbial components are very subtle and not completely understood.

knowledge in the future [18]. All the genes described in this review, along with their positive or negative impact on microbial colonisation are presented in Figure 1.

Haste makes waste: a not so obvious classification of plant LysM receptors among immune or symbiotic components

Numerous microbial signals rely on NAG-derived molecules (see Box 1) and so far, all their identified or putative receptors in plants contain extracellular Lysin Motif (LysM) domains associated to an active or inactive intracellular kinase domain (LysM-RLKs) or just anchored to the plasmalemma [19]. These LysM receptor proteins were classified as either immunity-related or symbiosis-related, based on the initial process in which they were identified. Recent results indicate that this initial function may only constitute one among many biological functions they fulfil, as exemplified thereafter by the Chitin Elicitor Receptor Kinase 1 (CERK1) and the Nod Factor Perception (NFP) receptor proteins.

CERK1 is the best-characterised LysM-RLK. It was identified first in *Arabidopsis* and then in rice, as an RLK essential for chitin signalling that triggers plant defences against fungi [19]. Although CERK1 shows no or low chitin binding activity, it acts as a co-receptor associated in complex with either CEBiP in rice or LYK5 in *Arabidopsis* [20]. The role of CERK1 in immunity was strengthened in *Arabidopsis* by its additional functions in bacterial perception through peptidoglycan (PGN) sensing, in association with AtLYM1 and AtLYM3; and in rice, since OsCERK1 also plays a critical role in the perception of Lipopolysaccharide (LPS) [21]. Hence, parallels can be drawn between the immune functions of CERK1 and those of the BRI1-ASSOCIATED

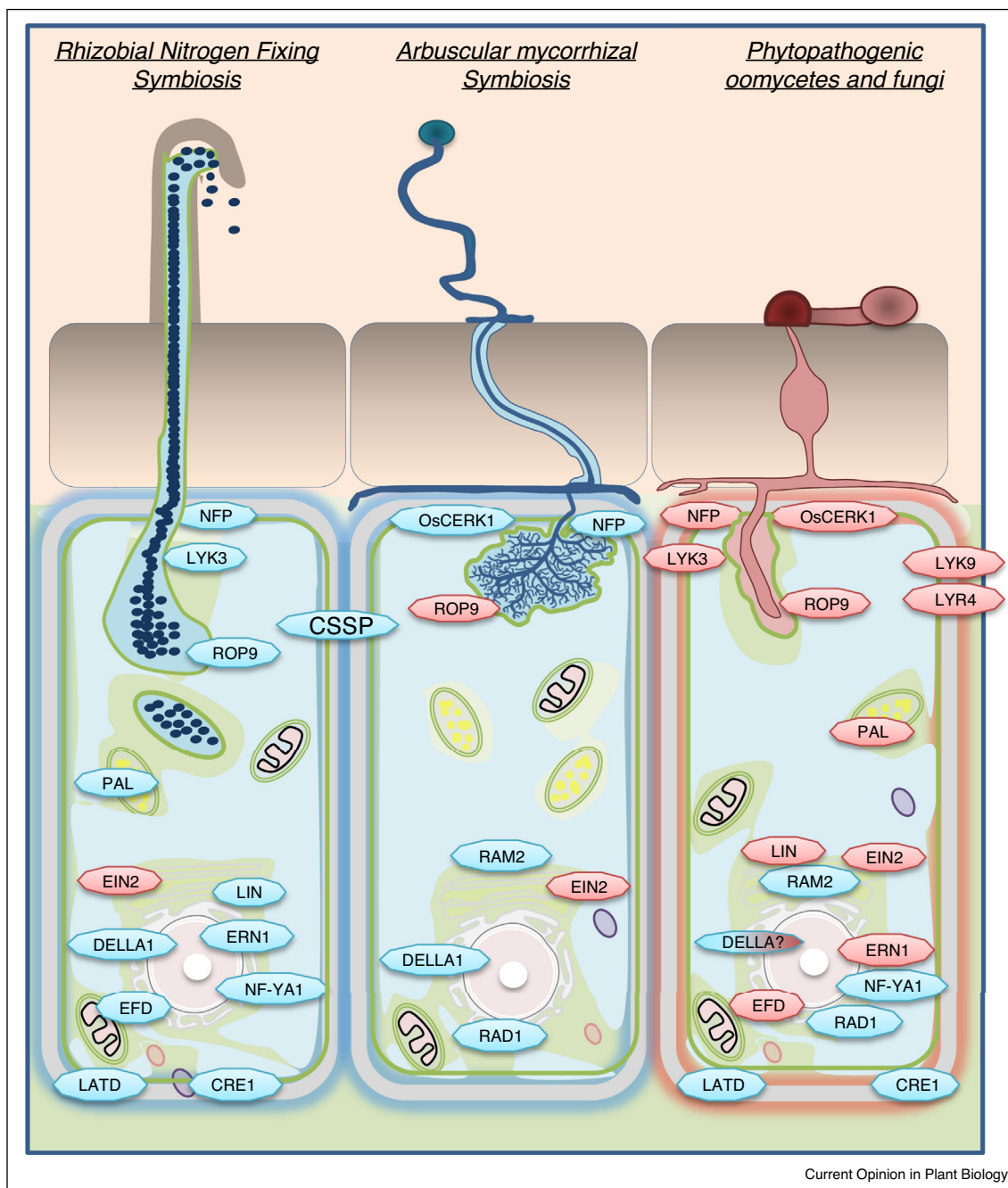
RECEPTOR KINASE (BAK1) receptor, which are both co-receptors of other LysM-RLKs or LRR-RLKs, respectively.

Despite these well-described functions leading to the activation of PAMP-triggered immunity, recent reports have also revealed the key involvement of OsCERK1 in the AM symbiosis [10,22**,23]. These versatile functions of OsCERK1 are associated either with perception of octameric chitooligosaccharides (CO8) in the frame of immunity or of shorter molecules (CO4) to facilitate the AM symbiosis [14**]. In order to prevent or attenuate pathogen CO8-triggered immunity signalling, it has been proposed that CO4 released by mycorrhiza may hinder OsCERK1 homodimerisation or heteromerization with other LysM CO receptors [24]. Alternatively, it can be anticipated that specific signalling involving CERK1 and leading either to immunity or symbiosis may be achieved by the recruitment of alternative co-receptors [23,25,26] and other downstream signalling components [27,28]. The recent discovery of CERK1 involvement in *Arabidopsis* salt stress response through its interaction with ANNEXIN1 (ANN1), is a supplementary example showing that CERK1 cannot be restrained to immunity signalling anymore and plays a much broader role in the adaptation of plants to their biotic and abiotic environment [29**].

NFP (Nod Factor Perception) is a LysM receptor kinase protein initially assigned in *M. truncatula* to specific functions in the nitrogen fixing symbiosis (NFS) [30]. However MtNFP also plays a role in the AM-endosymbiosis by sensing mycorrhizal LCOs, leading in turn to modifications of root architecture and differential gene expression [31]. In non-legumes, the NFP ortholog in tomato (SILYK10) is required for the formation of mycorrhiza [32] and in *Parasponia*, PaNFP is directly involved in both bacterial and mycorrhizal endosymbioses [33]. In the NFS, *Medicago truncatula* NFP and *Lotus japonicus* Nod Factor Receptor 5 (NFR5) function jointly with the LysM-RLKs MtLYK3 and LjNFR1 respectively [34]. The higher susceptibility of *nfp* and *lyk3* mutants to root oomycetes [6*,7**] and to fungi for *nfp* [6*,8] showed that these genes are also positively involved in plant disease resistance. This additional immunity-related function is also supported by the observation of defense-like responses (including induced cell death) when *NFP* and *LYK3* or *L. japonicus* NFR1 and NFR5 are co-overexpressed in *Nicotiana benthamiana* leaves [35,36]. Further transcriptomic data showed that NFP interplays with ethylene to balance signalling events from symbiosis to immunity [37*,38]. Again, formation of heteromers with other receptors, is a plausible explanation for these multiple functions [33].

While CERK1 and NFP represent members of the LysM receptor protein family involved in plant responses to

Figure 1



Commonalities and differences in the genetic framework underpinning root symbiotic interactions with mutualistic and pathogenic microbes. Pioneering genetic work in legumes revealed that nodulation defective mutants were often also unable to establish a mycorrhizal symbiosis. The concept of 'common symbiotic signalling pathway (CSSP)' arose from this point, suggesting that rhizobial symbionts co-opted early signalling events evolved in the frame of mycorrhiza. With the advent of root legume pathosystems, symbiotic mutant collections were assessed to detect putative molecular overlaps between colonisation mechanisms enabling ingress of pathogens and mutualistic microbes. Here the genes promoting interaction of rhizobial symbionts, endomycorrhizal fungi or filamentous pathogens are displayed in blue, while genes playing a negative role in the plant-microbe interactions are displayed in red. *Abbreviations:* NFP, Nod Factor Perception; LYK3, LysM-Receptor like Kinase 3; LYK9, LysM-receptor like Kinase 9; LYR4, LysM-Receptor like Kinase Related 4; ROP9, RHO-Related Protein from Plants 9; CERK1, Chitin Elicitor Receptor Kinase 1; PAL, phenyl ammonia lyase; EIN2, Ethylene Insensitive 2; LIN, Lumpy Infection; RAM2, Required for Arbuscular Mycorrhization 2; ERN1, ERF Required for Nodulation 1; EFD, ERF required for nodule differentiation; NF-YA1, Nuclear Factor Y Subunit A1; LATD, Lateral Deficiency; CRE1, Cytokinin Receptor 1; RAD1, Required for Arbuscule Development 1.

multiple microbes, a recent report indicates that LysM receptors might nevertheless be key components for the plant to distinguish mutualistic microbes from pathogens. *Mtlyr4* and *Mtlyk9/Ljlys6* mutants are thus impaired in the induction of plant defences and are more susceptible to fungal or bacterial leaf pathogens while no significant change was observed in the phenotype of these mutants following inoculation with rhizobia or AM fungus [39^{*}]. Although root pathogens also need to be tested in these mutants to rule out any specificities of these LysM-RLKs functioning between leaves and roots, the conclusions of this report indicate that fine genetic dissection can likely sift functions among the members of the multigenic LysM receptor family.

Common host genes control signalling and responses to pathogens and symbionts: same genes but different functions?

Following their recognition, rhizobia and AM fungal ingress are tightly regulated by host plants [7^{**},16,20], notably through the so-called common symbiosis signalling pathway (CSSP). While the CSSP is seemingly not involved in the regulation of pathogen colonisation, a number of other symbiotic host genes can modify plant resistance level to parasites. The *M. truncatula* small GTPase ROP9 positively controls rhizobial infection but hinders mycorrhiza formation and oomycete infection by regulating a membrane-associated NADPH-oxidase and its resulting reactive oxygen species (ROS) production [40]. The *LATERAL DEFICIENCY (LATD)* transporter, involved in nodule organogenesis, enhances susceptibility to *Phytophthora palmivora* root inoculation [7^{**}]. Conversely, the E3-Ligase Lumpy INfection (*LIN*) and the transcription factor ERF Required for Nodulation 1 (*ERN1*) which are both implicated in rhizobial infection of root hairs are also both positive actors of plant resistance to this oomycete [7^{**}]. The AM symbiosis mutant *ram2* (Required for Arbuscular Mycorrhiza 2) shows higher invasion by oomycetes [7^{**}]. *MtRAM2* encodes an endoplasmic reticulum-located glycerol-3-phosphate acyl transferase involved in the biosynthesis of cutin monomers [41]. The formation of hyphopodia by AM fungi and appressoria by *P. palmivora* is triggered upon cutin release at the rhizodermis [41]. However, further infection stages inside *ram2* roots are different between AM symbiosis and the oomycete. The former cannot form arbuscules nor fully develop in *ram2* tissues [42,43^{**},44^{*}] while *P. palmivora* develops intracellular haustoria and invades the root cortex [7^{**}]. Hence, cutin monomers produced by RAM2 have different functions: they act solely as a surface signal for *P. palmivora* penetration while they have a nutritional function for AM fungi to support arbuscules formed in the root cortex [42,43^{**},44^{*},45].

Legume transcription factors (TF) can also have dual functions in biotic interactions. MtEFD (Ethylene response factor required for nodule differentiation) is a TF induced by *S. meliloti* and the pathogenic bacteria

Ralstonia solanacearum. It is a positive regulator for the infection of these two types of bacteria and also makes a link with cytokinin signalling [9]. The TF MtNF-YA1 (Nuclear Factor — Y) [46^{*},47^{*},48,49] and the GRAS protein MtRAD1 (Required for Arbuscule Development 1) [50–53] were primarily implicated in nitrogen fixing and mycorrhizal symbiosis respectively. Nonetheless, they act as susceptibility factors to *A. euteiches* for MtNF-YA1 [46^{*}] and to *P. palmivora* for MtRAD1 [54^{*}]. MtNF-YA1 is a constitutive repressor of root immunity, high defence responses under standard culture condition were indeed detected in a transcriptomic analysis of the *nf-ya1-1* mutant [46^{*}]. Interestingly, NF-YA1 is a direct activator of *ERN1* in the NFS and an *ern1* mutant was more susceptible to *P. palmivora* [7^{**},48]. Finally, MtNF-YA1 and MtRAD1 interact with DELLA GRAS proteins which are crucial for both rhizobial [47^{*},55,56] and mycorrhizal [50,55,57,58] endosymbiosis, prompting the need to address the role of DELLAs with pathogens. Such a study, would help to assess whether these actors are able to alter legume immune responses by modulating salicylic acid (SA)/jasmonic acid (JA) balance as they did in some monocot species, increasing susceptibility to biotrophs and enhancing resistance to necrotrophs [59,60].

Shared hormonal and metabolic nodes for symbiont accommodation and pathogen control in legume roots

Salicylic acid (SA), jasmonic acid (JA) and ethylene (ET), are well known to play major roles in plant adaptation to their biotic environment [61]. However, the lack of characterised hormone-related mutants in model legumes explains our limited knowledge about the precise functions of hormonal pathways in legume root–microbe interactions. An exception is *MtSKL*, the orthologous gene of *EIN2* in Arabidopsis, which participates in ET signalling and negatively regulates both mutualistic and pathogenic interactions [62]. The impaired regulation of the isoflavonoid pathway by ET in the *Mtskl* mutants is one of the major determinant that leads to increased infection with microbes [3]. Among the few other characterised hormonal components in legumes stands the Histidine Kinase receptor CYTOKININ RECEPTOR 1 (MtCRE1) which controls the formation of nitrogen fixing nodules but also promotes the colonisation of pathogenic bacteria and oomycetes [9,63]. Hence this receptor appears to mediate compatibility of the interaction with rhizobia and bacterial or fungal pathogens, but does not intervene to facilitate the AM symbiosis [9,63]. Finally the role of Strigolactones (SLs) in promoting the AM symbiosis has been clearly defined [64] but conflicting reports suggest they are either positively involved or unrelated to colonisation processes by various pathogens [65–67].

Finally, plant responses to pathogenic and mutualistic microbes also intersect at the level of secondary metabolism. The phenylalanine ammonia lyase (PAL) is the first

enzyme that initiates synthesis of flavonoids, some of them being hallmarks of plant defence activation. A recent report showed that the *L. japonicus* *PAL1* also controls the NFS, likely by inducing lignin modification and by regulating endogenous SA [68**]. Another connection with flavonoid pathways came with chalcone-O-methyltransferase genes (ChOMTs) that control the production of 2'-O-methylisoliquiritigenin, a powerful inducer of nodulation by *S. meliloti* on the one hand (by inducing the production of rhizobial LCOs), but that is also able on the other hand to display antimicrobial properties against oomycetes [2]. These two recently described examples of genes or products illustrate well the opposite actions of flavonoids on symbionts and pathogens and confirm the known key role played by this pathway in legume–microorganism interactions. Among the other secondary metabolite families produced by legumes, it would be also worth assessing whether some actors of the mevalonate pathway, recently described as crucial in the early signalling of both rhizobial and mycorrhizal symbioses [69], can also regulate legume responses to pathogens.

Conclusions

Plant mutualism can be considered as a stage in evolution, derived from a pathogenic relationship [20], in which plant and microbe cohabit by providing reciprocal nutritional and developmental benefits to each other. Plant genes primarily involved in mutualist symbiosis and then found to be associated to plant–pathogen interactions significantly enriched our understanding of plant disease resistance. Moreover, such findings foster the concept of continuum between pathogenic to beneficial components of the plant microbiome. In parallel to the commonalities in plant genes mediating interactions with microbes, beneficial Rhizobia and AM fungi similarly use pathogen tricks. This includes MAMP masking strategies and secretion of extracellular and intracellular proteins as well as injection by bacterial Type Three Secretion System (TTSS) of effectors to reprogram host cells during their infection process [70]. Given the common strategies of infection shared by pathogens and mutualistic symbionts, it is not surprising that plants exploit some genes or molecular components to control them both. These commonalities between immunity and symbiosis should indeed help plants to adapt more quickly to a changing biotic environment. While common actors can constitute the backbone of plant signalling in response to different microbes, supplementary interactors must achieve the plant response specificity to pathogens or symbionts. Identifying these molecular switches is a major goal for the coming years.

Hitherto, our insights into the genetic of plant–microbe interactions have mainly been gained in axenic biological systems with plants treated with purified signals or challenged with single microorganisms. Using cocktails of

molecules and mixes of microbes to unravel the mechanisms used by plants to integrate simultaneous and multiple signals from various microorganisms will probably be one of the next challenges to gain supplementary insights into plant adaptation to a complex and changing biotic environment.

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References and recommended reading

Papers of particular interest, published within the period of review, have been highlighted as:

- of special interest
- of outstanding interest

1. Zipfel C, Oldroyd GED: **Plant signalling in symbiosis and immunity**. *Nature* 2017, **543**:328–336.
2. Badis Y, Bonhomme M, Lafitte C, Huguet S, Balzergue S, Dumas B, Jacquet C: **Transcriptome analysis highlights preformed defences and signalling pathways controlled by the *prAe1* quantitative trait locus (QTL), conferring partial resistance to *Aphanomyces euteiches* in *Medicago truncatula***. *Mol Plant Pathol* 2015, **16**:973–986.
3. Liu Y, Hassan S, Kidd BN, Garg G, Mathesius U, Singh KB, Anderson JP: **Ethylene signaling is important for isoflavonoid-mediated resistance to *Rhizoctonia solani* in roots of *Medicago truncatula***. *Mol Plant Microbe Interact* 2017, **30**:691–700.
4. Ben C, Debellé F, Berges H, Bellec A, Jardinaud MF, Anson P, Huguet T, Gentzbittel L, Vaillau F: **MtQRRS1, an R-locus required for *Medicago truncatula* quantitative resistance to *Ralstonia solanacearum***. *New Phytol* 2013, **199**:758–772.
5. Nishimura MT, Dangl JL: **Arabidopsis and the plant immune system**. *Plant J* 2010, **61**:1053–1066.
6. Rey T, Nars A, Bonhomme M, Bottin A, Huguet S, Balzergue S, Jardinaud M-F, Bono J-J, Cullimore J, Dumas B *et al.*: **NFP, a LysM protein controlling Nod factor perception, also intervenes in *Medicago truncatula* resistance to pathogens**. *New Phytol* 2013, **198**:875–886.
7. Rey T, Chatterjee A, Buttay M, Toulotte J, Schornack S: ***Medicago truncatula* symbiosis mutants affected in the interaction with a biotrophic root pathogen**. *New Phytol* 2015, **206**:497–500.
8. Ben C, Toueni M, Montanari S, Tardin MC, Fervel M, Negahi A, Saint-Pierre L, Mathieu G, Gras MC, Noël D *et al.*: **Natural diversity in the model legume *Medicago truncatula* allows identifying distinct genetic mechanisms conferring partial resistance to *Verticillium* wilt**. *J Exp Bot* 2013, **64**:317–332.
9. Moreau S, Fromentin J, Vaillau F, Vernié T, Huguet S, Balzergue S, Frugier F, Gamas P, Jardinaud MF: **The symbiotic transcription factor MteFD and cytokinins are positively acting in the *Medicago truncatula* and *Ralstonia***

This study reports the role of NFP in resistance fungal and oomycete root pathogen by the interplay of cellular processes at the transcriptomic level rather than classic immune responses.

This article is the first comprehensive screening of mutualist defective mutant with a biotrophic root pathogens. It showed that the CSSP does not control *per se* the interactions with pathogens but other individual symbiotic genes can act in resistance or compatibility with the disease. Mutualistic genes acting independently of the CSSP can also affect interaction with pathogens.

- solanacearum* pathogenic interaction. *New Phytol* 2014, **201**:1343-1357.
10. Zhang X, Dong W, Sun J, Feng F, Deng Y, He Z, Oldroyd GE, Wang E: **The receptor kinase CERK1 has dual functions in symbiosis and immunity signalling.** *Plant J* 2015, **81**:258-267.
 11. Buendia L, Wang T, Girardin A, Lefebvre B: **The LysM receptor-like kinase SILYK 10 regulates the arbuscular mycorrhizal symbiosis in tomato.** *New Phytol* 2016, **210**:184-195.
 12. Tanaka K, Cho S-H, Lee H, Pham AQ, Batek JM, Cui S, Qiu J, Khan SM, Joshi T, Zhang ZJ *et al.*: **Effect of lipochitooligosaccharide on early growth of C4 grass seedlings.** *J Exp Bot* 2015, **66**:5727-5738.
 13. Liang Y, Cao Y, Tanaka K, Thibivilliers S, Wan J, Choi J, Kang C, Qiu J, Stacey G: **Nonlegumes respond to rhizobial Nod factors by suppressing the innate immune response.** *Science* 2013, **341**:1384-1387.
- The authors expand the role of Nod factors from plant reprogramming for mutualism toward defence suppression.
14. Carotenuto G, Chabaud M, Miyata K, Capozzi M, Takeda N, Kaku H, Shibuya N, Nakagawa T, Barker DG, Genre A: **The rice LysM receptor-like kinase OsCERK1 is required for the perception of short-chain chitin oligomers in arbuscular mycorrhizal signaling.** *New Phytol* 2017, **214**:1440-1446.
- This article shows how OsCERK1 senses chitooligosaccharides of different polymerisation degree and mediates either immunity or mutualistic signalling.
15. Genre A, Chabaud M, Balzergue C, Puech-Pagès V, Novero M, Rey T, Fournier J, Rochange S, Bécard G, Bonfante P *et al.*: **Short-chain chitin oligomers from arbuscular mycorrhizal fungi trigger nuclear Ca²⁺ spiking in *Medicago truncatula* roots and their production is enhanced by strigolactone.** *New Phytol* 2013, **198**:190-202.
 16. Gourion B, Berrabah F, Ratet P, Stacey G: **Rhizobium-legume symbioses: the crucial role of plant immunity.** *Trends Plant Sci* 2015, **20**:186-194.
 17. Domonkos Á, Kovács S, Gombár A, Kiss E, Horváth B, Kovács GZ, Farkas A, Tóth MT, Ayaydin F, Bóka K *et al.*: **NAD1 controls defense-like responses in *Medicago truncatula* symbiotic nitrogen fixing nodules following rhizobial colonization in a BacA-independent manner.** *Genes* 2017, **8**:387-408.
 18. Fuechtbauer W, Yunusov T, Bozsóki Z, Gavrin A, James EK, Stougaard J, Schornack S, Radutoiu S: **LYS12 LysM receptor decelerates *Phytophthora palmivora* disease progression in *Lotus japonicus*.** *Plant J* 2017, **93**:297-310.
 19. Shinya T, Nakagawa T, Kaku H, Shibuya N: **Chitin-mediated plant-fungal interactions: catching, hiding and handshaking.** *Curr Opin Plant Biol* 2015, **26**:64-71.
 20. Cao Y, Halane MK, Gassmann W, Stacey G: **The role of plant innate immunity in the legume-rhizobium symbiosis.** *Annu Rev Plant Biol* 2017, **68**:535-561.
 21. Desaki Y, Kouzai Y, Ninomiya Y, Iwase R, Shimizu Y, Seko K, Molinaro A, Minami E, Shibuya N, Kaku H, Nishizawa Y: **OsCERK1 plays a crucial role in the lipopolysaccharide-induced immune response of rice.** *New Phytol* 2017, **217**:1042-1049.
 22. Miyata K, Kozaki T, Kouzai Y, Ozawa K, Ishii K, Asamizu E, Okabe Y, Umehara Y, Miyamoto A, Kobae Y *et al.*: **The bifunctional plant receptor, OsCERK1, regulates both chitin-triggered immunity and arbuscular mycorrhizal symbiosis in rice.** *Plant Cell Physiol* 2014, **55**:1864-1872.
- This article provides the first example of a single LysM-RLK contributing oppositely to pathogenic and mutualistic plant-microbe interactions.
23. Miyata K, Hayafune M, Kobae Y, Kaku H, Nishizawa Y, Masuda Y, Shibuya N, Nakagawa T: **Evaluation of the role of the LysM receptor-like kinase, OsNFR5/OsRLK2 for AM symbiosis in rice.** *Plant Cell Physiol* 2016, **57**:2283-2290.
 24. Liu T, Liu Z, Song C, Hu Y, Han Z, She J, Fan F, Wang J, Jin C, Chang J *et al.*: **Chitin-induced dimerization activates a plant immune receptor.** *Science* 2012, **336**:1160-1164.
 25. Hayafune M, Berisio R, Marchetti R, Silipo A, Kayama M, Desaki Y, Arima S, Squeglia F, Ruggiero A, Tokuyasu K *et al.*: **Chitin-**
- induced activation of immune signaling by the rice receptor CEBiP relies on a unique sandwich-type dimerization. *Proc Natl Acad Sci U S A* 2014, **111**:404-413.
26. Le MH, Cao Y, Zhang XC, Stacey G: **LIK1, a CERK1-interacting kinase, regulates plant immune responses in Arabidopsis.** *PLoS One* 2014, **9**:e102245.
 27. Shinya T, Yamaguchi K, Desaki Y, Yamada K, Narisawa T *et al.*: **Selective regulation of the chitin-induced defense response by the Arabidopsis receptor-like cytoplasmic kinase PBL27.** *Plant J* 2017, **79**:56-66.
 28. Yamada K, Yamaguchi K, Shirakawa T, Nakagami H, Mine A, Ishikawa K, Fujiwara M, Narusaka M, Narusaka Y, Ichimura K *et al.*: **The Arabidopsis CERK1-associated kinase PBL27 connects chitin perception to MAPK activation.** *EMBO J* 2016, **35**:2468-2483.
 29. Espinoza C, Liang Y, Stacey G: **Chitin receptor CERK1 links salt stress and chitin-triggered innate immunity in Arabidopsis.** *Plant J* 2017, **89**:984-995.
- This suggests that a LysM-RLK receptor may together with ANNEXIN control salt stress responses in a way reminiscent of biotic stress responses.
30. Ben Amor B, Shaw SL, Oldroyd GE, Maillet F, Penmetsa RV, Cook D, Long SR, Denarie J, Gough C: **The NFP locus of *Medicago truncatula* controls an early step of Nod factor signal transduction upstream of a rapid calcium flux and root hair deformation.** *Plant J* 2003, **34**:495-506.
 31. Czaja LF, Hogekamp C, Lamm P, Maillet F, Martinez EA, Samain E, Denarie J, Küster H, Hohnjec N: **Transcriptional responses toward diffusible signals from symbiotic microbes reveal MtNFP- and MtDMI3-dependent reprogramming of host gene expression by arbuscular mycorrhizal fungal lipochitooligosaccharides.** *Plant Physiol* 2012, **159**:1671-1685.
 32. Buendia L, Wang T, Girardin A, Lefebvre B: **The LysM receptor-like kinase SILYK10 regulates the arbuscular mycorrhizal symbiosis in tomato.** *New Phytol* 2016, **210**:184-195.
 33. Gough C, Jacquet C: **Nod factor perception protein carries weight in biotic interactions.** *Trends Plant Sci* 2013, **18**:566-574.
 34. Moling S, Pietraszewska-Bogiel A, Postma M, Fedorova E, Hink MA, Limpens E, Gadella TW, Bisseling T: **Nod factor receptors form heteromeric complexes and are essential for intracellular infection in *Medicago* nodules.** *Plant Cell* 2014, **26**:4188-4199.
 35. Pietraszewska-Bogiel A, Lefebvre B, Koini MA, Klaus-Heisen D, Takken FL, Geurts R, Cullimore JV, Gadella TW: **Interaction of *Medicago truncatula* lysin motif receptor-like kinases, NFP and LYK3, produced in *Nicotiana benthamiana* induces defence-like responses.** *PLoS One* 2013, **8**:e65055.
 36. Madsen EB, Antolín-Llovera M, Grossmann C, Ye J, Vieweg S, Broghammer A, Krusell L, Radutoiu S, Jensen ON, Stougaard J *et al.*: **Autophosphorylation is essential for the in vivo function of the *Lotus japonicus* Nod factor receptor 1 and receptor-mediated signalling in cooperation with Nod factor receptor 5.** *Plant J* 2011, **65**:404-417.
 37. Larraínzar E, Riely BK, Kim SC, Carrasquilla-García N, Yu HJ, Hwang HJ, Oh M, Kim GB, Surendrarao AK, Chasman D *et al.*: **Deep sequencing of the *Medicago truncatula* root transcriptome reveals a massive and early interaction between nodulation factor and ethylene signals.** *Plant Physiol* 2015, **169**:233-265.
- This article connects signaling events mediated by mutualistic receptors MtNFP and MtLYK3 to the biotic stress hormone ethylene.
38. Maillet F, Poinot V, Andre O, Puech-Pagès V, Haouy A, Gueunier M, Cromer L, Giraudet D, Formey D, Niebel A *et al.*: **Fungal lipochitooligosaccharide symbiotic signals in arbuscular mycorrhiza.** *Nature* 2011, **469**:58-63.
 39. Bozsóki Z, Cheng J, Feng F, Gysel K, Vinther M, Andersen KR, Oldroyd G, Blaise M, Radutoiu S, Stougaard J: **Receptor-mediated chitin perception in legume roots is functionally separable from Nod factor perception.** *Proc Natl Acad Sci U S A* 2017, **114**:8118-8127.
- This article identified LysM-RLKs controlling chitin triggered immunity that are distinct from receptors involved in mutualist symbiosis. In the

meantime, CO4s that are known to promote mycorrhizal associations are shown to induce defence responses.

40. Kiirika LM, Bergmann HF, Schikowsky C, Wimmer D, Korte J, Schmitz U, Niehaus K, Colditz F: **Silencing of the Rac1 GTPase MtROP9 in *Medicago truncatula* stimulates early mycorrhizal and oomycete root colonizations but negatively affects rhizobial infection.** *Plant Physiol* 2012, **159**:501-516.
 41. Wang E, Schornack S, Marsh JF, Gobbato E, Schwessinger B, Eastmond P, Schultze M, Kamoun S, Oldroyd GE: **A common signaling process that promotes mycorrhizal and oomycete colonization of plants.** *Curr Biol* 2012, **22**:2242-2246.
 42. Luginbuehl LH, Menard GN, Kurup S, Van Erp H, Radhakrishnan GV, Breakspear A, Oldroyd GED, Eastmond PJ: **Fatty acids in arbuscular mycorrhizal fungi are synthesized by the host plant.** *Science* 2017, **356**:1175-1178.
 43. Bravo A, Brands M, Wewer V, Dörmann P, Harrison MJ: **Arbuscular mycorrhiza-specific enzymes FatM and RAM2 fine-tune lipid biosynthesis to promote development of arbuscular mycorrhiza.** *New Phytol* 2017, **214**:1631-1645.
- This article further reinforces the understanding of the contribution of RAM2 to the AM symbiosis, suggesting that this gene may have different functions than that detected during root colonisation by a pathogenic oomycete.
44. Jiang Y, Wang W, Xie Q, Liu N, Liu L, Wang D, Zhang X, Yang C, Chen X, Tang D *et al.*: **Plants transfer lipids to sustain colonization by mutualistic mycorrhizal and parasitic fungi.** *Science* 2017, **356**:1172-1175.
- This article suggests that common lipid-based nutrients transferred from host plants to mycorrhizal fungi or obligate biotrophs are crucial to sustain microbial colonisation.
45. Keymer A, Pimprikar P, Wewer V, Huber C, Brands M, Bucerius SL, Delaux P-M, Klingl V, von Röpenack-Lahaye E, Wang TL *et al.*: **Lipid transfer from plants to arbuscular mycorrhiza fungi.** *eLife* 2017, **6**:e29107.
 46. Rey T, Laporte P, Bonhomme M, Jardinaud MF, Hugué S, Balzergue S, Dumas B, Niebel A, Jacquet C: **MtNF-YA1, a central transcriptional regulator of symbiotic nodule development, is also a determinant of *Medicago truncatula* susceptibility toward a root pathogen.** *Front Plant Sci* 2016, **7**:1837.
- This article demonstrates that inducible a mutualistic transcription factor can constitutively act to suppress plant defence responses to a root pathogen.
47. Fonouni-Farde C, Tan S, Baudin M, Brault M, Wen J, Mysore KS, Niebel A, Frugier F, Diet A: **DELLA-mediated gibberellin signalling regulates Nod factor signalling and rhizobial infection.** *Nat Commun* 2016, **7**:12636.
- This article links DELLA proteins to nitrogen fixing symbiosis and highlights links with transcription factors involved in nodule development such as NF-YA1, which was recently highlighted as a negative regulator of plant defence.
48. Baudin M, Laloum T, Lepage A, Rípodas C, Ariel F, Frances L, Crespi M, Gamas P, Blanco FA, Zanetti ME *et al.*: **A phylogenetically conserved group of nuclear factor-Y transcription factors interact to control nodulation in legumes.** *Plant Physiol* 2015, **169**:2761-2773.
 49. Laporte P, Lepage A, Fournier J, Catrice O, Moreau S, Jardinaud MF, Mun JH, Larrainzar E, Cook DR, Gamas P *et al.*: **The CCAAT box-binding transcription factor NF-YA1 controls rhizobial infection.** *J Exp Bot* 2014, **65**:481-494.
 50. Floss DS, Lévesque-Tremblay V, Park HJ, Harrison MJ: **DELLA proteins regulate expression of a subset of AM symbiosis-induced genes in *Medicago truncatula*.** *Plant Signal Behav* 2016, **11**:e1162369.
 51. Park HJ, Floss DS, Lévesque-Tremblay V, Bravo A, Harrison MJ: **Hyphal branching during arbuscule development requires reduced arbuscular mycorrhiza.** *Plant Physiol* 2015, **169**:2774-2788.
 52. Xue L, Cui H, Buer B, Vijayakumar V, Delaux PM, Junkermann S, Bucher M: **Network of GRAS transcription factors involved in the control of arbuscule development in *Lotus japonicus*.** *Plant Physiol* 2015, **167**:854-871.
 53. Kim G-B, Nam Y-W: **A novel GRAS protein gene MtSymSCL1 plays a role in regulating nodule number in *Medicago truncatula*.** *Plant Growth Regul* 2013, **71**:77-92.
 54. Rey T, Bonhomme M, Chatterjee A, Gavrin A, Toulotte J, Yang W, André O, Jacquet C, Schornack S: **The *Medicago truncatula* GRAS protein RAD1 supports arbuscular mycorrhiza symbiosis and *Phytophthora palmivora* susceptibility.** *J Exp Bot* 2017, **68**:5871-5881.
- This article highlights an unsuspected role for the GRAS protein RAD1 in seedling elongation and susceptibility toward a root pathogen.
55. Jin Y, Liu H, Luo D, Yu N, Dong W, Wang C, Zhang X, Dai H, Yang J, Wang E, Zeng L *et al.*: **A DELLA protein complex controls the symbiotic rhizobial and mycorrhizal signalling pathways.** *Nat Commun* 2016, **7**:12433.
 56. Tatsukami Y, Ueda M: **Rhizobial gibberellin negatively regulates host nodule number.** *Sci Rep* 2016, **6**:27998.
 57. Yu N, Luo D, Zhang X, Liu J, Wang W, Jin Y, Dong W, Liu H, Yang W, Zeng L *et al.*: **A DELLA protein complex controls the arbuscular mycorrhizal symbiosis in plants.** *Cell Res* 2014, **24**:130-133.
 58. Takeda N, Handa Y, Tsuzuki S, Kojima M, Sakakibara H, Kawaguchi M: **Gibberellins interfere with symbiosis signaling and gene expression and alter colonization by arbuscular mycorrhizal fungi in *Lotus japonicus*.** *Plant Physiol* 2015, **167**:545-557.
 59. De Bruyne L, Höfte M, De Vleeschauwer D: **Connecting growth and defense: the emerging roles of brassinosteroids and gibberellins in plant innate immunity.** *Mol Plant* 2014, **7**:943-959.
 60. De Vleeschauwer D, Seifi HS, Filipe O, Haec A, Huu SN, Demeestere K, Höfte M: **The DELLA protein SLR1 integrates and amplifies salicylic acid- and jasmonic acid-dependent innate immunity in rice.** *Plant Physiol* 2016, **170**:1831-1847.
 61. Berens ML, Berry HM, Mine A, Argueso CT, Tsuda K: **Evolution of hormone signaling networks in plant defense.** *Annu Rev Phytopathol* 2017, **55**:401-425.
 62. Penmetza RV, Uribe P, Anderson J, Lichtenzweig J, Gish JC, Nam YW, Engstrom E, Xu K, Sckisel G, Pereira M *et al.*: **The *Medicago truncatula* ortholog of Arabidopsis EIN2, sickle, is a negative regulator of symbiotic and pathogenic microbial associations.** *Plant J* 2008, **55**:580-595.
 63. Laffont C, Rey T, André O, Novero M, Kazmierczak T, Debelle F, Bonfante P, Jacquet C, Frugier F: **The CRE1 cytokinin pathway is differentially recruited depending on *Medicago truncatula* root environments and negatively regulates resistance to a pathogen.** *PLoS One* 2015, **10**:e0116819.
 64. Besserer A, Puech-Pagès V, Kiefer P, Gomez-Roldan V, Jauneau A, Roy S, Portais JC, Roux C, Bécard G, Séjalon-Delmas N: **Strigolactones stimulate arbuscular mycorrhizal fungi by activating mitochondria.** *PLoS Biol* 2006, **4**:e226.
 65. Piisilä M, Keceli MA, Brader G, Jakobson L, Jösaar I, Sipari N, Kollist H, Palva ET, Kariola T: **The F-box protein MAX2 contributes to resistance to bacterial phytopathogens in *Arabidopsis thaliana*.** *BMC Plant Biol* 2015, **15**:53.
 66. Foo E, Blake SN, Fisher BJ, Smith JA, Reid JB: **The role of strigolactones during plant interactions with the pathogenic fungus *Fusarium oxysporum*.** *Planta* 2016, **243**:1387-1396.
 67. Marzec M: **Strigolactones as part of the plant defence system.** *Trends Plant Sci* 2016, **21**:900-903.
 68. Chen Y, Li F, Tian L, Huang M, Deng R, Li X, Chen W, Wu P, Li M, Jiang H *et al.*: **The phenylalanine ammonia lyase gene *ljal1* is involved in plant defense responses to pathogens and plays diverse roles in *Lotus japonicus* rhizobium symbioses.** *Mol Plant Microbe Interact* 2017, **30**:739-753.
- These finding demonstrates that common secondary metabolism genes of plant can shape divergent plant-microbe interactions complementarily to host signalling.
69. Venkateshwaran M, Jayaraman D, Chabaud M, Genre A, Balloon AJ, Maeda J, Forshey K, den Os D, Kwiecien NW, Coon JJ *et al.*: **A role for the mevalonate pathway in early plant**

- symbiotic signaling.** *Proc Natl Acad Sci U S A* 2015, **112**:9781-9786.
70. Le Fevre R, Evangelisti E, Rey T, Schornack S: **Modulation of host cell biology by plant pathogenic microbes.** *Annu Rev Cell Dev Biol* 2015, **31**:201-229.
 71. Nars A, Lafitte C, Chabaud M, Drouillard S, Mélida H, Danoun S, Le Costaouéc T, Rey T, Benedetti J, Bulone V *et al.*: **Aphanomyces euteiches cell wall fractions containing novel glucan-chitosaccharides induce defense genes and nuclear calcium oscillations in the plant host *Medicago truncatula*.** *PLoS One* 2013, **8**:e75039.
 72. Nadal M, Sawers R, Naseem S, Bassin B, Kulicke C, Sharman A, An G, An K, Ahern KR, Romag A *et al.*: **An N-acetylglucosamine transporter required for arbuscular mycorrhizal symbioses in rice and maize.** *Nat Plants* 2017, **3**:17073.
 73. Sun J, Miller JB, Granqvist E, Wiley-Kalil A, Gobbato E, Maillet F, Cottaz S, Samain E, Venkateshwaran M, Fort S *et al.*: **Activation of symbiosis signaling by arbuscular mycorrhizal fungi in legumes and rice.** *Plant Cell* 2015, **27**:823-838.
 74. Sánchez-Vallet A, Mesters JR, Thomma BP: **The battle for chitin recognition in plant-microbe interactions.** *FEMS Microbiol Rev* 2015, **39**:171-183.
 75. Limpens E, van Zeijl A, Geurts R: **Lipochitooligosaccharides modulate plant host immunity to enable endosymbioses.** *Annu Rev Phytopathol* 2015, **53**:311-334.