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· **Invited Review** ·

Signaling in Plant Disease Resistance and Symbiosis

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Abstract

Interactions between plants and microbes result in plant disease and symbiosis. The former causes considerable economic damage in modern agriculture, while the latter has produced great beneficial effects to our agriculture system. Comparison of the two interactions has revealed that a common panel of signaling pathways might participate in the establishment of the equilibrium between plant and microbes or its break-up. Plants appear to detect both pathogenic and symbiotic microbes by a similar set of genes. All symbiotic microbes seem to produce effectors to overcome plant basal defenses and it is speculated that symbiotic effectors have functions similar to pathogenic ones. Signaling molecules, salicylic acid (SA), jasmonic acid (JA) and ethylene (ET), are involved in both plant defense and symbiosis. Switching off signals contributing to deterioration of disease symptom would establish a new equilibrium between plant and pathogenic microbes. This would facilitate the development of strategies for durable disease resistance.

Key words: calcium signals; disease resistance; effector; pathogen-associated molecular patterns; symbiosis.

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Plants in the natural environment are confronted with the challenges of various microbes, which result in the establishment of symbiosis, parasitism and saprophytism. Protein sequence analyses indicate that major lineages of fungi were present 1 000 million years ago (Ma) and that land plants appeared approximately 700 Ma, although the first fossil land plants and fungi appeared 460–480 Ma (Heckman et al. 2001). It was postulated that a partnership between two basically aquatic protists, a green alga and a "phycomycetous" fungus, started in the initial step of land plant evolution, suggesting that plants have coevolved with microbes since their first appearance on land (Gehrig et al. 1996). Although one can only speculate about subsequent events, the evolution of land plants has been shaped by interactions with pathogenic and symbiotic microbes (Chisholm et al. 2006).

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Interactions between plants and fungi may result in biotrophic or necrotrophic diseases and arbuscular mycorrhizal (AM) symbiosis. Also, interactions between plants and bacteria may cause bacterial diseases and nodule symbiosis. Pathogens rob nutrients such as carbohydrates, sometimes resulting in severe disease symptoms. Plant diseases cause considerable economic damage in modern agriculture. On the other hand, symbiotic microbes provide mineral nutrients or nitrogen by bargaining carbohydrates with the hosts, which has produced great beneficial effects to our agriculture system. Two symbioses are of critical importance in sustainable agriculture, which are AM association and root nodule symbiosis. Most (80%–90%) land plants have established association with AM fungi, which are obligate symbionts and obtain carbon from the hosts, whose main contribution is to assist the plants with the acquisition of mineral nutrients, particularly phosphorus (Harrison 1999; Parniske 2000). Root nodule symbiosis was a more recent evolutionary event (~60–70 Ma) (Remy et al. 1994) compared to AM association that originated more than 400 Ma (Soltis et al. 1999).

Pathogenic bacteria invade plants through wounds or natural pores, while rhizobia enter legume plants by infection threads. However, azorhizobia can infect via cracks in the epidermis in *Sesbania rostrata* (Capoen et al. 2005). It is believed that fungi penetrate the plant cell wall by using physical force in combination with hydrolytic enzyme attack. The haustorial or arbuscular complex is actively formed by the host cell after the

cell wall is crossed, except for some fungal pathogens which do not form haustoria. The intracellular complex is accommodated in a host-derived membrane and substance as the primary cell wall, which separate fungi from the host cell in topology. The infection thread shares similar features to the arbuscular complex so it has been hypothesized that the nitrogen-fixing symbiosis may have recruited functions from the ancient AM symbiosis.

Different pathogenic (or symbiotic) microbes associate with different hosts. The hosts are partly determined by chemicals from the wound sites in *Agrobacterium* plant interaction. Host legumes of rhizobia are thought to be discriminated from non-hosts partly on the basis of the specific flavonoids that they release (Brencic and Winans 2005). AM fungal spores can germinate and grow in the absence of a host, but their hyphal growth is very limited. However, the hyphae of AM fungi in the vicinity of host roots show extensive branching before formation of the appressorium. The 5-deoxy-strigol, isolated from the root exudates of *Lotus japonicus*, induced extensive hyphal branching in germinating spores of the AM fungus, *Gigaspora margarita*, at very low concentrations (Akiyama et al. 2005).

A recent review (Kogel et al. 2006) comparing interaction procedures and symptoms between plant disease resistance and symbiosis has suggested that the endophyte was a balanced state between plant and microbes. If the interaction becomes unbalanced, disease symptoms appear or the fungus is excluded by induced host defense reactions. Symbioses of plants with beneficial or neutral endophytes share many common attributes with plant interactions with pathogens. In this review, comparisons were focused on signaling pathways between plant disease resistance and symbiosis. The molecular basis of plant defense and symbiosis is complex, but the interactions between plants and microbes can be described in three steps: detection, signaling and responses.

Detection of Microbes in Plant Disease Resistance and Symbiosis

PAMP recognition

Plants can recognize both pathogenic and symbiotic microbes by detection of pathogen-associated molecular patterns (PAMPs) via extracellular receptor-like kinases (RLKs) (Figure 1). PAMPs such as flagellin, cold shock proteins, elongation factor Tu (EF-Tu), evolve slowly and are highly conserved. Also there are non-protein PAMPs including lipopolysaccharides from Gram-negative bacteria, chitin and ergosterol from higher fungi, β-heptaglucosan from *Phytophthora megasperma* and other oomycetes (Garcia-Brugger et al. 2006). It was believed that induced systemic resistance (ISR) mediated by plant growth-promoting rhizobia is relevant to PAMP perception.

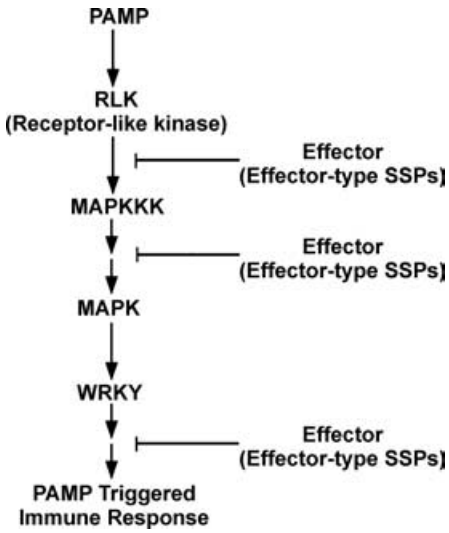

Figure 1. Pathogen-associated molecular patterns (PAMP)-triggered immunity in both plant defense and symbiosis.

Plants recognize both pathogenic and symbiotic microbes by identifying PAMPs via extracellular receptor-like kinases (RLKs). Perception of PAMP swiftly triggers PAMP-triggered immunity (PTI), which requires signaling through mitogen-activated protein kinase (MAPK) cascades and WRKY transcription factors. Pathogenic (or symbiotic) microbes deliver effectors (or effector-type small secreted proteins, SSPs) into host cells to overcome PTI.

Flagellin is a widely-studied bacterial PAMP, which is recognized by At-FLS2 in *Arabidopsis* (Gómez-Gómez and Boller 2000). Perception of flagellin promptly triggers defense responses in various plants. EF-Tu is detected by At-EFR, an LRR-kinase (Zipfel et al. 2006). *At-Efr* mutants showed higher transient transformation frequency in *Agrobacterium*-based transformation experiments. Treatment with a conserved EF-Tu peptide induces expression of a gene set nearly identical to that induced by flg22, which is a synthetic 22-amino-acid peptide from a conserved domain within the flagellin N-terminus. Hence, the responses to PAMPs converge on a limited number of pathways and lead to a common set of outputs (Jones and Dangl 2006).

Detection of signaling molecules from symbiotic microbes

An AM fungus-derived diffusible signaling molecule that induces plant gene activation has been confirmed by experiments (Kosuta et al. 2003), while the molecule and its receptor (Myc-receptor) in plant are still unclear. However, a lipophilic signal that was characterized as lysophosphatidylcholine (LPC) from root extracts of mycorrhizal plants is capable of inducing the phosphate transporter genes *St-PT3* and *St-PT4* of potato

(*Solanum tuberosum*). These two genes are specifically induced in roots colonized by AM fungi (Drissner et al. 2007).

In *Medicago truncatula*, Nod factor (NF, lipochitooligosaccharide) perception requires two LysM receptor kinases (LYKs), Mt-LYK3 and Mt-LYK4 (Zhu et al. 2006) (Figure 2). The LysM domains have been implicated in binding polysaccharides, particularly glucosamine chains that are similar to the NF backbone (Bateman and Bycroft 2000), which contain a N-acetylglucosamine backbone, but the direct binding of NFs remains to be elucidated. In addition to NFs, extracellular polysaccharides, lipopolysaccharides and secreted proteins from rhizobia are also recognized by host plants. Recently, two symbiotic, photosynthetic, *Bradyrhizobium* strains, BTAi1 and ORS278, have been completely sequenced, but canonical *nodABC* genes encoding enzymes for NF biosynthesis have not been found in the whole genome. NFs are not required for nodule formation between some legumes and BTAi1 (or ORS278), which indicates that other signals can trigger nodule organogenesis (Giraud et al. 2007). However, signaling molecules delivered by symbiotic microbes were not discovered in any pathogenic microbes so far. Nod factors may be structurally similar to chitin. Also, putative chitin receptors required for fungal recognition have been found (Wan et al. 2008).

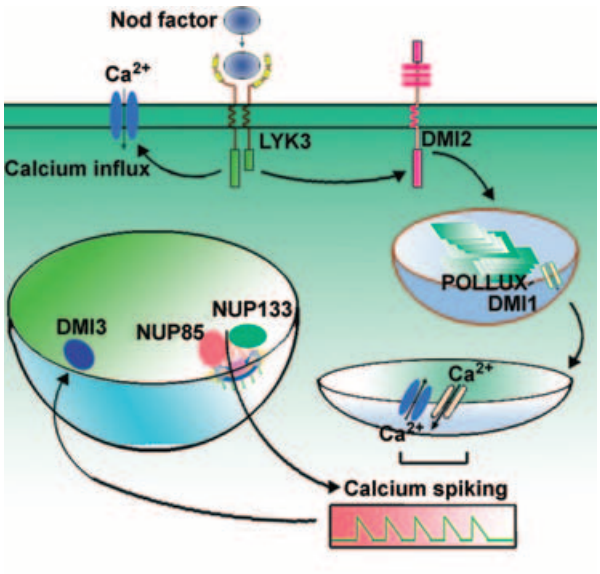

Figure 2. Nod factor (NF) perception and calcium signals.

NF perception requires two LysM receptor kinases (LYKs), Mt-LYK3 and Mt-LYK4, in *Medicago truncatula*, and elicits two separable calcium responses, a Ca^{2+} influx and a Ca^{2+} spiking (Esseling et al. 2004). *Mt-DMI1* and *Mt-DMI2* act upstream of calcium spiking, while *Mt-DMI3* lies downstream of calcium spiking (Zhu et al. 2006). *Lj-NUP133* and *Lj-NUP85*, two nucleoporin genes, are required for the Ca^{2+} spiking, indicating that the components needed for Ca^{2+} spiking must translocate from nuclear to cytoplasm via nucleopore.

Signaling in Disease Resistance and Symbiosis

PAMP-triggered immunity

There exists an innate immune system in plant, which comprises PAMP-triggered immunity (PTI) and effector-triggered immunity (ETI). Plants perceive PAMPs via RLKs, and then trigger PTI (Figure 1). The whole process requires signaling through mitogen-activated protein kinase (MAPK) cascades and transcriptional reprogramming mediated by plant WRKY transcription factors. Pathogens overcome PTI and ETI by secreting effectors that are recognized by specific disease resistance (R) genes (Jones and Dangl 2006).

There are 74 WRKY proteins in *Arabidopsis* (Eulgem et al. 2000). It was reported that 49 were induced in treatment with salicylic acid (SA) or *Pst* (*Pseudomonas syringae* pv. *tomato*) in 72 tested WRKY genes (Dong et al. 2003). At-WRKY11 and At-WRKY70 had a pivotal role in co-ordination SA and jasmonic acid (JA) signal cascades (Journot-Catalinoa et al. 2006; Li et al. 2004, 2006) (Figure 3). Both *At-PEN2* (Lipka et al. 2005)

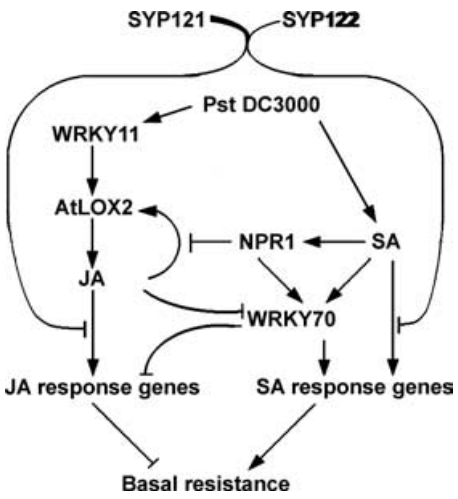

Figure 3. Cross-talk between salicylic acid (SA) and jasmonic acid (JA) pathway.

Both WRKY70 and NPR1 modulate cross-talk between SA and JA–ethylene (ET) signaling in plant basal resistance elicited by *Pst*. Both SYP121 and SYP122 are negative regulators of SA and JA–ET pathways. WRKY11 regulates expression of LOX2 (Journot-Catalinoa et al. 2006), a JA biosynthetic enzyme. WRKY70 is negatively controlled by JA and positively controlled by SA (Li et al. 2004). NPR1 suppresses JA biosynthesis. Thus, NPR1 and WRKY70 function as integrators of the mutually antagonistic JA and SA pathways.

and *At-PEN3* (Stein et al. 2006), non-host resistance genes, are induced by flg22, indicating that they might be involved in PTI. At-PEN2 is a peroxisomal glucosyl hydrolase, and *At-PEN3* encodes a plasma membrane ABC transporter (Lipka et al. 2005; Stein et al. 2006).

Although it still remains unknown which are active downstream of LRR-receptor kinase (or NB-LRR protein) to activate resistance responses after detecting PAMPs (or effectors), transcription of RLK and NB-LRR genes are more likely induced by PAMPs in the way of feedback amplification instead of a linear pathway. Investigation of barley Hv-MLA10 (R protein) shed light on the convergent nodes of both PTI and ETI. Recognition of A10 (effector) by Hv-MLA10 induces nuclear associations between receptor and WRKY transcription factors. The identified WRKY proteins act as repressors of PAMP-triggered basal defense. Hv-MLA appears to interfere with the WRKY repressor function, thereby de-repressing PAMP-triggered basal defense (Shen et al. 2007).

Similar to perception of pathogenic PAMPs, recognition of PAMPs by symbiotic hosts also results in PTI. For example, ectomycorrhizal and AM fungi secreted chitin elicitors to induce a defense response (Salzer and Boller 2000). When pea Myc^{-} (non-mycorrhizal) mutant plants were challenged with AM fungi, a stronger defense response has been observed (Gollotte et al. 1993). Expression of defense-related genes is partially activated during early stages of AM fungal penetration (García-Garrido and Ocampo 2002).

Effectors in pathogenic and symbiotic microbes

Plants evolved a PAMP-triggered immune system to defend pathogens, while the latter developed effectors to suppress the defenses. It is reasonable to speculate that many pathogenic and symbiotic microbes have effector genes for suppressing PTI.

Plant pathogenic microbes deliver effectors into host cells to overcome PTI. Some effectors can be recognized by specific disease R genes directly or indirectly to induce resistance and are hence termed avirulence (Avr) proteins. Pathogenic bacteria such as *P. syringae* can deliver approximately 20–30 effectors via the type III secretion system (TTSS) during infection (Petnicki-Ocwieja et al. 2002). ETI is activated in the presence of a cognate R gene product.

Features of fungus effectors are gradually revealed by analyzing of secreted proteins from the flax rust fungi, *Melampsora lini* (Catanzariti et al. 2005), and the leaf-mold fungi, *Cladosporium fulvum* (Rivas and Thomas 2005). The common features of many fungal effectors are cystein-rich and less than 300 amino acid residues in size. CfAvr2 from *C. fulvum* is one of shortest effectors with only 58 amino acid residues. It is suggested that the processed form is even smaller. Pathogens also produce small molecule toxins to enhance virulence, such as coronatine secreted by *P. syringae* (Brooks et al. 2005), gibberellin made by the fungus *Gibberella fujikuroi*, and cytokinin synthesized by plasmodia of *Plasmodiophora brassicae* (Siemens et al. 2006).

Recently, the genome sequence of the ectomycorrhizal basidiomycete, *Laccaria bicolor* (a symbiosis fungus), was published, which contains 20 614 predicted protein-encoding genes. Twelve predicted proteins showed a similarity to known haustoria-expressed secreted proteins of the basidiomycetous rusts, *Uromyces fabae* and *M. lini*, which are involved in pathogenesis. There are 2 931 proteins predicted to be secreted by *L. bicolor*. Within this set, a large number of genes encode cystein-rich products that are less than 300 amino acids. Two-hundred and seventy-eight proteins are classified as small secreted proteins (SSPs). Transcript profiling revealed that the expression of several SSP genes is specifically induced in the symbiotic interaction. Five of the 20 most highly upregulated fungal transcripts in ectomycorrhizal root tips encode for SSPs. Within the mycorrhiza-induced cystein-rich SSPs (MISSPs), there are a family of secreted proteins with a CFEM domain (INTERPROIPR014005), as previously identified in the plant pathogenic fungi, *M. lini* and *Magnaporthea grisea* (Martin et al. 2008). Although these effector-type SSPs cannot be ascribed a function at present, they may play a role similar to pathogenic effectors.

Calcium signals

Calcium^{2+} is one of the most important second messengers in plants. Ca^{2+} signaling has a pivotal role in signals of disease resistance and symbiosis. Ca^{2+} specificity is due to the time course of $(Ca^{2+})_{cyt}$ variations, and the location of the $(Ca^{2+})_{cyt}$ increase (Hetherington and Brownlee 2004).

Pathogen-associated molecular pattern (or effector) perception is followed rapidly by a Ca^{2+} influx and intracellular Ca^{2+} signals, which in turn could activate calcium-dependent protein kinases (CDPKs) (Romeis 2001). But direct connections between Ca^{2+}, CDPKs and MAPKs remain to be deciphered.

In fact, Nod factors elicit two separable calcium responses in *M. truncatula* root hair cells, a Ca^{2+} influx and a Ca^{2+} spiking (Figure 2). Ca^{2+} influx is one of the first responses in the root epidermis after NF perception via LYKs. Ca^{2+} spiking represents repeated increases in cytoplasmic Ca^{2+}, particularly around the nucleus, and appears approximately 10–20 min after addition of Nod factors to legume roots. It was suggested that approximately 36 consecutive Ca^{2+} spikes are sufficient to induce ENOD11-GUS expression in root hairs (Miwa et al. 2006). Except for LYKs, *Mt-DMI1*, *Mt-DMI2*, *Lj-NUP133* and *Lj-NUP85* are required for the Ca^{2+} spiking. *Mt-DMI1*, *Mt-DMI2* and *Mt-DMI3* are *M. truncatula* genes needed for both AM and nodulation symbioses (Catoira et al. 2000). *Mt-DMI1* and *Mt-DMI2* act upstream of calcium spiking, while *Mt-DMI3* lies downstream of calcium spiking (Wais et al. 2000). Both

L j-NUP133 and *L j-NUP85* are plant nucleoporin genes in *L. japonicus*. Mutation of *Nup133* results in a temperature-sensitive nodulation-deficient phenotype and absence of mycorrhizal colonization (Kanamori et al. 2006), while *nup85-2* mutation confers a weak and temperature-sensitive symbiotic phenotype (Saito et al. 2007).

It has been verified that calcium flux and calcium spiking act as symbiosis signaling (Esseling et al. 2004; Shaw and Long 2003). Both calcium signals may intervene and inhibit plant defense responses that are triggered by rhizobia PAMPs.

SA and JA-ET signaling

It has been demonstrated that three endogenous plant signaling molecules, SA, JA and ethylene (ET), are involved in plant defense. Systemic acquired resistance (SAR) and ISR are two widely-studied plant resistances to pathogenic microbes. SAR requires both local and systemic SA accumulation, while ISR generally needs JA and ET. Besides At-WRKY70, At-NPR1 also modulates cross-talk between SA and JA-ET signaling (Figure 3). At-SYP121 (PEN1) and At-SYP122 are negative regulators of SA and JA-ET pathways (Zhang et al. 2007).

There are two JA-ET signaling pathways in plants (Figures 3, 4). JA synergistically induces the expression of pathogen-response genes with ET. On the other hand, JA is responsible for activating wound response genes that are negatively regulated by ET. Mt-ERF1 (ethylene response factor 1) is proposed to act as a converging point between synergistic signaling in ISR and antagonistic interaction in ET and JA-induced wound response (Lorenzo et al. 2003, 2004). JA inhibits the plant responses to rhizobial bacteria (Figure 4). JA not only inhibits calcium spiking but also suppresses the frequency of calcium oscillations when applied at lower concentrations. This effect of JA is amplified in the ET-insensitive mutant, *Mt-skl*, indicating an antagonistic interaction between JA and ET for NF signaling. ET, signaling through Mt-SKL, acts downstream to antagonize JA signaling to limit its effect on the frequency of calcium spiking. However, both JA and ET act synergistically to inhibit nodulation (Sun et al. 2006).

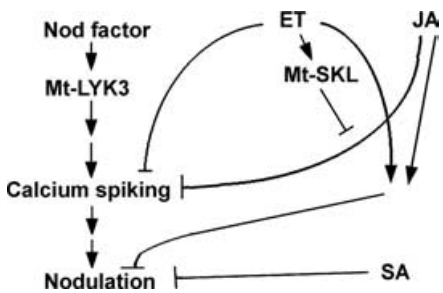

Figure 4. Salicylic acid (SA) and jasmonic acid (JA)-ethylene (ET) inhibit nodulation.

Antagonistic JA-ET signaling inhibits frequency of calcium spiking, while synergistic JA-ET signaling inhibits nodulation (Sun et al. 2006). Ethylene suppresses the initiation of calcium spiking alone. SA only suppresses nodulation without influencing calcium spiking.

Ethylene has been shown to be involved in nodulation: it regulates the formation of the infection thread and the placement of the nodule primordium in the root by inhibiting cell division. It also could have a direct effect on the NF perception pathway that defines the nodule number. ET inhibits some early responses in legume plants, including the expression of *RIP1* and *ENOD11* which are the two of the earliest genes to be induced by NFs, and the initiation of calcium spiking (Oldroyd et al. 2001).

Exogenous SA specifically affects the physiological state of indeterminately nodulating plants and inhibits indeterminate-type nodulation. The inhibitory effect of SA did not appear to result from obvious differential effects on root growth, root hair growth or root hair formation. Exogenous SA did not inhibit determinate-type nodulation (Spronsen et al. 2003). Nevertheless, NahG (salicylate hydroxylase) expression in both *M. truncatula* and *L. japonicus* plants led to enhanced nodulation and infection (Figure 4). These data point to an important role for SA-mediated plant defense pathways in controlling of nodule formation on both determinate and indeterminate nodule-forming hosts (Stacey et al. 2006).

Cytokinin signals

Infection of obligate biotrophic protist *P. brassicae* results in clubroot in the family Brassicaceae, a disease with symptoms of stunted growth and gall formation in the root system (Ludwig-Müller et al. 1999). There are two hormones involved in clubroot development: auxins produced by the host owing to stimulation of the pathogen, and cytokinins that are synthesized by plasmodia. At-NIT1 and At-NIT2 are the nitrilase isoforms predominantly expressed in *Arabidopsis* clubroot tissue. Root galls are smaller in *At-nit1-3* plants compared with the wild type (Grsic-Rausch et al. 2000). Cytokinin homeostasis (cytokinin synthases and cytokinin oxidases/dehydrogenases) are strongly downregulated during the early infection. Cytokinin oxidase/dehydrogenase overexpressing lines are disease resistant, which indicates the importance of cytokinin as a key factor in clubroot disease development (Siemens et al. 2006). Infection by *P. brassicae* might occur in non-*Brassica* species, leading to the potential formation of resting spores, but without gall formation (Ludwig-Müller et al. 1999).

It has been hypothesized that the common ancestor of Eurosid I clade had acquired a “predisposition to nodulate” (Soltis et al. 1995), which was validated with a gain-of-function mutation, *snf2* (spontaneous root nodule formation 2), in a cytokinin receptor that triggers spontaneous root nodule organogenesis and develops white rhizobia free nodules in the absence of

Mesorhizobium loti in *L. japonicus*, that do not need Ca^{2+} spiking. A single nucleotide transition (C to T) resulting in substitution of a conserved leucine 266 by phenylalanine (L266F) identifies *snf2* as an allele of a Lotus histidine kinase (*LHK1*) gene. Comparative analysis defines Lj-LHK1 as a member of the cytokinin receptor family, which has 64% identity with the *Arabidopsis* cytokinin histidine kinase receptor AHK4, and 49% and 45% identity with AHK2 and AHK3, respectively. *HIT1 (HYPERINFECTED 1)*, a loss-of-function allele of *Lj-LHK1*, suppresses *L. japonicus har1*-1 hypernodulation phenotype. The large number of infection threads that formed in the *hit1*-1 *har1*-1 mutant roots originated within curled root hairs but the root cortex failed to initiate a nodule primordium (Tirichine et al. 2007). Indeed, in some actinorhizal and legume symbioses, rhizobia are restricted to the infection threads without nodulation (Naisbitt et al. 1992; Gualtieri and Bisseling 2000). The above evidences indicate that cytokinin signals contribute to initiation of nodulation.

Hence, it is presumable that there also existed a "predisposition to clubs" in the mutual ancestor of the family *Brassicaceae*. Lack of corresponding auxin and cytokinin signals would be the reason for no club formation in some non-*Brassica* species. Shutting off those signals in *Arabidopsis* would make *P. brassicae* friendly to its host, because the plasmodia synthesize trehalose and secrete it to the host cell (Brodmann et al. 2002), which would augment its host's resistance to drought.

Plant Defense Response and its Depression in Symbiosis

Plant defense responses include the expression of the pathogenesis-related (PR) genes, cell wall reinforcement, antibiotic production and the programmed cell death (the hypersensitive response, HR). The local HR can, in turn, trigger SAR in whole plant. In addition, E3 ubiquitin ligases are involved in different defense responses including early defense reactions, R gene resistance and induced disease resistance (Delauré et al. 2008).

The At-PEN1 (SYP121) syntaxin acts via a pre-invasion nonhost resistance pathway (Collins et al. 2003). At-PEN1 together with At-SNAP33 and vesicle-associated molecular patterns (VAMPs) form a ternary SNARE complex that secretes vesicle cargo to fungal invasion spots, contributing to formation of cell wall appositions (Kwon et al. 2008). PEN1-dependent disease resistance acts *in vivo* mainly through functionally redundant At-VAMP721 and At-VAMP722, which contribute to a wider range of defense responses than PEN1. Pathogen-induced *de novo* cell-wall biosynthesis beneath fungal appressoria is delayed in *pen1*-1 plants compared with wild type. The incidence of callose formation in transgenic lines, in which both At-VAMP721 and At-VAMP722 were constitutively co-silenced, was also lower relative to wild type at all inspected time points (Kwon et al. 2008).

Callose deposition usually can be detected within infection spots of pathogens but cannot be observed in normal symbiosomes. It indicates the suppression of host defense responses in the symbiosis.

Depression of the plant defense occurs in both PAMP perception and signal transduction in symbiosis. In the late stages of AM fungi penetration, differential regulation of chitinase and chitosanase could be responsible for degradation of AM fungus PAMPs and attenuation of plant defense. The cyclic β-glucans from *Bradyrhizobium japonicum* USDA110 compete efficiently with the hepta-β-glucans derived from the cell wall of the phytopathogenic *Phytophthora sojae* for the same receptor binding site. This indicates that induced or suppressed plant defense might be regulated based on the ratio of receptor occupancy by the two signaling compounds (Mithöfer 2002). Host defense responses may also be inhibited by effector-type SSPs in symbiotic associations.

Concluding Remarks

Plants have shaped a hostile relationship with pathogens. PAMPs perception triggers PTI which is then suppressed by pathogenic effectors. Effectors can be recognized by R genes and then trigger ETI. Natural selection results in new effectors and R genes. Competition between plant and pathogenic microbes is a never ceasing marathon. Detailed comparison enables better understand of the signaling pathways in both plant disease resistance and symbiosis. A common panel of signaling pathways may participate in the establishment of the equilibrium between plant and microbes or its breakup. Plants appear to detect both pathogenic and symbiotic microbes by a similar set of genes. All symbiotic microbes seem to encode effectors to overcome plant basal defense. It is speculated that symbiotic effectors have functions similar to pathogenic ones. Signaling molecules, SA, JA and ET, are involved in plant defense and symbiosis.

Knowledge of pathogenic effectors would contribute to the study of effector-type SSP function in symbiosis. On the other hand, investigation of effector-type SSPs would give us more detailed answers as to how pathogenic effectors evolve and work, which have a significant importance to developing cultivars with durable disease resistance. Effectors are the results of the coordinated evolution between plant and pathogenic microbes. Until now, only a few effectors have been cloned from a small number of microbes. Whether pathogen delivers RNA-based effectors remains unknown. However, it is clearer that there exists some common features for effectors. Sequencing the whole genomes of the most important crop pathogens and symbiotic microbes will provide a basis for prediction and identification of pathogen effectors through a bioinformatic approach.

Appearance of disease symptoms is a result of an unbalanced association between plant and microbes. Switching off signals contributing to deterioration through disease symptoms would establish a new equilibrium between plant and pathogenic microbes. This would facilitate development of strategies for durable disease resistance.

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