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Receptor-Mediated Signalling

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Receptor-Mediated Signalling in Plants – Molecular Patterns and Programs

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SUMMARY

A highly evolved surveillance system in plants is able to detect a broad range of signals originating from pathogens, damaged tissues, or altered developmental processes, initiating sophisticated molecular mechanisms that result in defense, wound healing, and development. Microbe associated molecular pattern molecules (MAMPs), damage associated molecular pattern molecules (DAMPs), virulence factors, secreted proteins and processed peptides can be recognized directly or indirectly by this surveillance system. Nucleotide binding-leucine rich repeat proteins (NB-LRR) are intracellular receptors and have been targeted by breeders for decades to elicit resistance to crop pathogens in the field. Receptor-like kinases (RLKs) or receptor like proteins (RLPs) are membrane bound signalling molecules with an extracellular receptor domain. They provide an early warning system for the presence of potential pathogens and activate protective immune signalling in plants. In addition, they act as a signal amplifier in the case of tissue damage, establishing symbiotic relationships, and effecting developmental processes. The identification of several, important ligands for the RLK-type receptors provided an opportunity to understand how plants differentiate, how they distinguish beneficial and detrimental stimuli, and how they coordinate the role of various types of receptors under varying environmental conditions. Here we examine the diverse roles of extra-and intracellular plant receptors, reviewing recent findings on how they promote defense and development.

Keywords: RLK, RLP, DAMPs, MAMPs, defense, development

It is humankind's duty to respect all life, not only animals have feelings but also trees and plants. Michel de Montaigne (French Philosopher and Writer. 1533-1592)

INTRODUCTION

Plants are immobile organisms, capable of receiving and responding to endogenous and exogenous signals. Discriminating beneficial or detrimental stimuli and initiating an appropriate response has emerged over a long evolutionary history. Endogenous stimuli, generally derived from stressed, damaged or malfunctioning cells (damage associated molecular pattern molecules; DAMPs) (Lotze et al., 2007) promote responses in both animal and plant cells. Exogenous stimuli comprise a) pathogen- or microbe associated molecular pattern molecules (PAMPs or MAMPs); virulence factors such as toxins (Friesen et al., 2008), enzymes (Beliën et al., 2006) and effector molecules (Kamoun, 2006; Tör, 2008), and b) non-microbial or abiotic stress inducers such as toxic compounds, pollutants, UV-B light, injury, or ozone.

Receptors that have an affinity within the low nM range for ligands (Ogawa et al., 2008) exist across the individual kingdom, play a significant role in the detection of stimuli and activation of programs that direct development and defense. Animals rely on a limited number of Pattern Recognition Receptors (PRRs) including membrane bound Toll-like receptors (TLRs), cytoplasmic NOD-like proteins (NLRs) and RIG-I-like receptors (RLRs) for the activation of innate immunity (Lotze et al., 2007), which promotes the development of an adaptive immune response. Plants, however, lack an adaptive immune system and rely solely on innate immune mechanisms. In addition, each plant cell is surrounded by the cell wall matrix that acts as a barrier as well as nutrient source for would-be pathogens. Pathogens overcoming this barrier are under molecular surveillance by the plant cell, usually by receptors that reside at the cell surface or within the cytoplasm. Membrane bound plant PRRs include receptor-like kinases (RLKs) (Shiu et al., 2003) that have an extracellular domain such as leucine rich repeats (LRRs), lectin, lysine motif (LysM) or wall associated kinases (WAK) with a single transmembrane spanning region and a cytoplasmic kinase domain; receptor-like proteins (RLPs) (Wang, G et al., 2008) that posses

an extracellular LRR domain and a C-terminal membrane anchor but lack the cytoplasmic kinase domain, and polygalacturanase inhibiting proteins (PGIP) (Di Matteo et al., 2003) that have only an extracellular LRR domain. Intracellular plant PRRs are NB-LRR proteins (nucleotide binding site–leucine–rich repeats) (Meyers et al., 2003) that are encoded by the so-called disease resistance genes (**Figure 1**). Functions for several PRRs have been assigned for a number of plants including rice, tomato and *Arabidopsis thaliana*. Recent findings have increased our understanding of the role of PRRs in diverse biological settings and we have focused on these more novel findings in the studies reviewed below.

RLP-type receptors rely on others to communicate the message

The number of RLP-type receptors predicted from genomic sequences varies according to the plant species studied. *Arabidopsis* has 57 while rice has more than 90 (Wang G et al., 2008; Fritz-Laylin et al., 2005). Some of these receptors also contribute to development or defense. For example, *Arabidopsis* CLAVATA2 (CLV2, AtRLP10) and Too Many Mouths (TMM, AtRLP17) proteins play a significant role in meristem and stomatal development, respectively (Jeong et al., 1999; Nedeau et al., 2002). Conversely, in the tomato, the RLP-encoding *Cf* and *Ve* genes confer race specific resistance to *Cladosporium fulvum* and *Verticillium* spp isolates, respectively (Kruijt et al., 2005; Kawchuk et al., 2001). Recently, in collaboration with several other laboratories, we have identified homozygous T-DNA insertion lines for all the *Arabidopsis* RLP-encoding genes. These were subjected to a wide range of stress inducers including adapted and non-adapted pathogens, MAMPs and abiotic stimuli. We have also investigated if the mutation in these RLP-type receptors causes altered plant growth or development (Wang G et al., 2008). A number of novel developmental phenotypes were observed for the *clv2* and *tmm* insertion mutants. These were slow growth, more rosette leaves, shorter stems and late flowering for the *Atrlp10-1* T-DNA insertion line, and chlorosis and reduced growth for the *Atrlp17-1* and *tmm-1* mutants upon abscisic acid (ABA) treatment (Wang G et al., 2008). *Atrlp30* and, in addition, *Atrlp18* were found to be more susceptible to the non-adapted bacterial bean pathogen *Pseudomonas syringae* pv. *phaseolicola*. Similarly, we confirmed that *AtRLP52* confers resistance to the non-adapted fungal pathogen *Erysiphe cichoracearum* (Ramonell et al.,

2005). Mutation in the *AtRLP41* gene leads to enhanced sensitivity to ABA, the plant hormone that integrates and fine-tunes abiotic and biotic stress-response signalling networks both in plants and animals (Asselbergh et al., 2008; Nagamune et al., 2008).

It is surprising that a biological role has been found for only a few of the defined *AtRLP* genes. This may be attributed to several factors; a) the approach taken may have been biased towards the pathogens and mainly race-specific resistance may have been investigated, b) no insects or nematodes were included in our screen, c) the assay used may not have been sensitive enough to discover some of the roles that these proteins may play, d) these receptors may be involved in the recognition of DAMPs, which were not addressed in our study, or e) there may be functional redundancy. In many ways, this is similar to the abundance of NLRs in the animal genome without known functions. The *Arabidopsis* genome harbours 24 loci containing a single *AtRLP* gene and 13 loci comprising multiple *AtRLP* genes (Wang G et al., 2008; Fritz-Laylin et al., 2005). Most homologous *AtRLP* genes reside at the same locus and the identification of a T-DNA insertion mutation in one gene may, because of the functional redundancy, not be enough to uncover the role of those genes. In addition, generation of double mutants by crossing individual T-DNA lines would be impossible. In order to overcome the problem of functional redundancy and further investigate the role of RLP-type proteins in *Arabidopsis*, Ellendorf et al (2008) used an RNA interference (RNAi) approach and confirmed some of the phenotypes observed before. However, no new phenotype has been identified.

Since RLP-type receptors lack a cytoplasmic catalytic domain, one of the intriguing questions concerning RLP-mediated signalling is how the message is transmitted from the extracellular matrix to the intracellular space. Although RLP-type receptors in tomato recognize some pathogen effectors indirectly, it is not known how this message is internalized. The most facile explanation could be similar to that suggested for CLV2 and TMM where these RLPs may function in combination with RLK-type receptors CLAVATA1 and ERECTA, respectively, thus relaying the message (Waites et al., 2000; Shpak, 2005). Although it has not been reported, it is tempting to speculate that AtRLP41 may

also interact with an RLK such as RPK1 (Osakabe et al., 2005) to regulate abscisic acid signalling in *Arabidopsis*.

RLK-type receptors are the primary communicators

RLK-type receptors comprise the largest family of receptors in plants. The *Arabidopsis thaliana* genome is predicted to contain >600 of such members while rice (*Oryza sativa*) has more than 1100 (Shiu et al., 2004) The structural features of the extracellular domain of plant RLKs have been used to classify them into subfamilies including LRR, Lectin, self-incompatibility locus (S-Locus), lysine motif (LysM), wall associated kinase (WAK), tumour necrosis factor receptor (TNFR), PR5-like receptor kinase (PR5K) and receptor-like cytoplasmic kinase (RLCK, **Figure 1**). The majority of these RLKs phosphorylate serine or threonine residues of the cytoplasmic kinase domains (Torii et al., 2000; Walker, 2004; Narusaka et al., 2007).

The diverse structures in the receptor domains suggest that there are likely to be several biological functions of these proteins (**Table 1**). The roles of some of these receptors in the perception of self or non-self molecules are described below.

Perception of MAMPs and virulence factors: Despite the large numbers of bacterial, viral, fungal and oomycete plant pathogens, only limited numbers of MAMPs have been discovered. By contrast, hundreds of virulence factors including effectors from pathogens have been identified, and some of their functions have been uncovered. The reason for the discrepancy between the number of MAMPs and effectors could be attributed to a) the conserved nature of MAMPs, b) radical impact of effectors on agriculture where they suppress immune system of host plant, c) amenability of effectors to rapid evolutionary change, and d) delivery of the effectors by the pathogen into plant cells, all of which may have contributed to identification and characterisation of a wide range of effectors (Tör, 2008).

Chitin, xylanase, and ergesterol from fungi, transglutaminase (Pep-13) from oomycete, lipopolysaccharide (LPS), flagellin (flg22), cold shock protein (CSP) and elongation factor Tu (EF-Tu) from bacteria have been studied as MAMPs in

plant pathogen interactions (Ingle et al., 2006; Tör, 2008). FLS2 (Flagellin Sensing 2) and EFR (Ef-Tu receptor), LRR-RLKs, have been identified as receptors for flg22 and Ef-Tu, respectively, and their physical interactions with the receptors have been demonstrated (Zipfel et al., 2004; Zipfel et al., 2006). The FLS2 and flg22 interaction has become one of the best-characterised systems in the activation of innate immunity in plants. Although flagellin has been portrayed as an invariant MAMP, data are accumulating to suggest that variation occurs within species as well as within pathovars limiting defense eliciting activity of flagellin (Sun et al., 2006). Therefore, we would expect to see further co-evolutionary studies in MAMP-receptor interactions.

Race-specific pathogen-encoded virulence factors (effectors) are secreted from the bacterial pathogens into host cells via the Type III secretion system (TTSS), bind to a protein and thereby alter the activity of that protein (Mudgett, 1998). This finding helped the establishment of a common link between the mechanisms of pathogenicity of the plant and animal pathogens. In addition, it has also brought a change in our thinking. Rather than killing the host cell from outside, pathogens delivers effector proteins as virulence factors into the host cell to adapt to a particular niche (Medzhitov, 2007) and manipulate it for its own purpose (Xiao et al., 2007). When these effectors are recognized by the cytoplasmic receptors (described below), they are termed avirulence (AVR) proteins (Jones and Dangl, 2006). Although there are studies on apoplastic effectors from *Cladosporium fulvum* (syn. *Passalora fulva*) (Kruijt et al., 2005), the majority of effectors from this pathogen are recognized indirectly by RLP-type receptors (Shabab et al., 2008). The rice LRR-RLK-type protein Xa21 functions similarly to cytoplasmic receptors in that they confer race–specific resistance to secreted molecules including in this instance the AvrXa21 from *Xanthomonas oryzae*, the causal agent of bacterial blight disease of rice (Lee et al., 2008).

The effector protein (Dsp)A/E of *Erwinia amylovora* (causal agent of fire blight on apple, pear and other Rosaceae plant) is absolutely required for its pathogenicity (Gaudriault et al., 1997). It is delivered by TTSS inside the cell and interacts specifically and directly with the cytoplasmic kinase domain of at least 4 different LRR-RLK-type receptors, DIPM1 to 4, (DspA/E-interacting proteins of *Malus x domestica*) to induce disease (Meng et al., 2006). This

finding suggests that a) these putative receptors may act as compatibility factors or b) pathogens may use their effectors to target these receptors to block the signal transmission and evade recognition. Recent findings with the AvrPto and AvrPtoB from *Pseudomonas syringae* support the anti-receptor strategy of the pathogens (Xiang et al., 2008). Shan et al (2008) demonstrated that when expressed in Arabidopsis, AvrPto and AvrPtoB interact with BAK1 (brassinosteroid-receptor 1 associated kinase 1) (He et al., 2007), which acts as an adaptor or co-receptor with FLS2 and EFR (Chinchilla et al., 2007; Heese et al., 2007), and interferes with the ligand promoted association of FLS2 with BAK1.

Perception of DAMPs: Mechanical injury, insect or herbivore damage releases specific signals, which have been known as wound inducing proteins in plants. However, these molecules are also released during programmed cell death (PCD), or hypersensitive reaction (HR), or trailing necrosis, the term "damage associated molecular pattern molecules (DAMPs)" would be more precise. DAMPs are generated at the damage site and signals arising from them are delivered to other undamaged part of the plant in a systemic manner. PRRs at the cell surface of the healthy cells can then recognize these DAMPs in a similar fashion to MAMPs and activate the defense signalling cascade.

DAMP molecules differ according to the plant species investigated. For example, systemin is only found in solaneceous species such as tomato. In damaged tomato leaf, systemin, an 18-aa peptide, derived from a 200-aa precursor protein, can travel over long distances activating a defense response (Pearce et al., 1991; Scheer et al., 2002). Systemin binds the LRR-RLK, SR160/BRI1 (Systemin receptor 160kDa/ brassinosteroid insensitive 1), however, SR160/ BRI1 mutant plants are still capable of eliciting a systemin induced defense response (Holton et al., 2007), suggesting that additional systemin receptor(s) are present. Indeed, other systemin binding proteins including SBP50 (systemin binding protein 50kDa) have been identified (Schaller et al., 1994). BRI1 also binds and participates in brassinosteroid (BR) signalling through BRI1, in a synergistic interaction with other LRR-RLKs including BAK1 and BKK1 (BAK1-LIKE1) (He et al., 2000). It should be noted

that BAK1 and BKK1 have been reported to have dual physiological roles: positively regulating a BR-dependent plant growth pathway, and negatively regulating a BR-independent cell-death pathway (Kemmerling et al., 2007; He et al., 2007).

Arabidopsis has six PROPEP proteins that are precursors for peptides that act as DAMPs. AtPep1, a 23-aa peptide derived from PROPEP1, can be found in the apoplast. PEPR1 is an LRR-RLK-type PRR, which directly interacts with AtPep1 and initiates defense signalling (Yamaguchi et al., 2006). Interestingly, the PROPEP proteins can be induced by their own peptides, MAMPs such as flg22 and elf18, salicylic acid, jasmonic acid or ethylene. AtPep1 has been suggested to act as a signal amplification loop for the innate immune response in plants (Ryan et al., 2007). In the animal systems, High mobility group box1 (HMGB1) protein is the best-characterized DAMP molecule and binds to receptors (TLR2/4, RAGE) on the cell membrane or inside the cell (TLR9) and triggers innate immunity (Lotze et al., 2007). There are several orthologues of HMGB1 in *Arabidopsis* but it is not known if they activate the immune system in plants by binding to the PRRs, in a similar fashion to that observed in animals. Their role in regulating autophagy in response to stressors is also under investigation.

Perception of developmental cues: Brassinosteroids (BRs) are one of the best-characterized examples of hormones in plants that regulate growth processes such as cell expansion, cell elongation, vascular differentiation, pollen tube formation, and acceleration of senescence (Gendron et al., 2007) and the receptors, BRI, BAK1, and BKK1 involved in the BR signalling (Karlova et al., 2006; Albrecht et al., 2008) are discussed above.

Plant cells can be dedifferentiated and proliferate *in vitro* as totipotent cells, called calli. Phytosulfokine (PSK), a five-residue peptide, is the growth factor that induces the dedifferentiation and callus growth with the help of auxin and cytokinin, two well-studied hormones in plants that regulate root and shoot formations (Matsubayashi et al., 1996). PSK triggers cell proliferation by binding directly to an LRR-RLK-type receptor, PSKR (Phytosulfokine receptor) (Matsubayashi et al., 2002).

Mutation in the *Arabidopsis CLAVATA1* (CLV1) gene causes a variety of morphological phenotypes, including club-shaped gynoecia. Mutation in two other genes, CLV2 and CLV3 also produce similar phenotypes. CLV1 is an LRR-RLK, CLV2 is an LRR-RLP and CLV3 is a secreted protein that acts as a ligand for CLV1. Interactions of these three proteins regulate the size of the meristem (Clark et al., 1997; Fletcher et al., 1999). Recently, a novel receptor kinase, CORYNE, has been shown to act synergistically with CLV2 but independently of CLV1 to transmit CLV3 signalling (Muller et al., 2008; Miwa et al., 2008).

INFLORESCENCE DEFICIENT IN ABSCISSION (IDA) is another secreted protein that acts as a potential ligand for LRR-RLK-type receptors, HAESA (HAE) and HAESA-LIKE2 (HSL2) in *Arabidopsis*. These receptors and the putative ligand are involved in the regulation of abscission of the floral organs (Stenvik et al., 2008; Cho et al., 2008).

There are other RLK-type receptors such as members of *Arabidopsis* ERECTA (Shpak et al., 2005) and STRUBBELIG family proteins (Eyüboglu et al., 2007) that are involved in plant development. However, the ligands for these receptors are not yet known. Their roles and orthologues in other plants have been reviewed extensively by others (Morillo and Tax, 2006).

Recognition of signals that determine self-incompatibility: Many plants have the capacity to recognize pollen from close relatives, and reject these nominally to prevent inbreeding and maintain genetic diversity within a species, a system that is known as self-incompatibility (SI). In *Brassica* species, a soluble extracellular protein, the S-locus glycoprotein (SLG), and a membrane bound receptor SRK (S-locus receptor kinase), an RLK with an S-locus extracellular domain at the stigma surface have been identified (Stein et al., 1991; Yamakawa et al., 1994). Further studies led to the identification of SCR/SP11 (S-locus cysteine rich protein or S-locus protein 11) that is expressed predominantly in the anther and interacts directly with SRK resulting in SI (Shiba et al., 2001). When pollen and pistil share the same allele, a ligand-receptor interaction induces a signalling cascade in the female papillar cell, which then signals back to the pollen and inhibits its germination. Some other S-locus RLKs are up-regulated

in response to pathogen recognition, MAMPs and wounding, indicating a similarity between perception of self and non-self molecules and activation of downstream signalling (Sanabria et al., 2008).

Perception of beneficial microbes: Nitrogen is essential for plant growth and certain plant species such as legumes can utilise gaseous N_2 in the atmosphere symbiosing with nitrogen fixing bacteria of the *Rhizobiaceae* family. In the interaction between plants and nitrogen fixing bacteria, flavonoid compounds from plants attract rhizobial bacteria, which are triggered to produce nodulation (Nod) factors, lipochito-oligosacharides. When the plant detects this signal, a series of events, especially in root development, occur leading to encapsulation of bacteria and formation of nodules where the bacteria fix nitrogen in return for nutrients derived from the plant (Trevaskis et al., 2002). Receptors that play a significant role in the regulation of nodule formation include LRR-RLK-type receptors such as the nodulation receptor kinase (NORK) in alfalfa (Endre et al., 2002), symbiosis receptor-like kinase (SYMRK) in lotus and pea (Stracke et al., 2002) and hypernodulation receptor (HAR1) in Lotus (Nishimura et al., 2002) and LysM-RLK-type receptors, such as Nod-factor receptor kinase (NFR1 and NFR5) in lotus (Madsen et al., 2003; Radutoiu et al., 2003).
What happens to the MAMP-activated immunity in symbiotic relations? Lipopolysaccharide (LPS), a MAMP that triggers innate immunity in animals and plants, plays a positive role in the establishment of symbiosis by suppressing the oxidative burst. Alterations in the LPS structure result in delayed nodulation, abortion of infection threads, formation of nonfixing nodules, and induction of plant defense reactions (Tellström et al., 2007), suggesting a necessity for bacterial LPS for the bacteria to form its symbiotic relation with the host plant. Not a dissimilar response is noted in the setting of NK (Natural killer) recognition of paternal allogantigens in implantation of the mammalian fetus (Eastabrook et al., 2008).

Conveying the message: ligand binding activates RLKs: Since there are several RLKs with known ligands, the question as to how these receptors are activated and transmit the message from the extracellular space into the cell arises. From recent studies on several RLK-type PRRs described above, it has become clear that ligand binding a) promotes heterodimerization among

members of CLAVATA, ERECTA and BRI family proteins as well as between FLS2 and BAK1; b) increases activating phosphorylation of these proteins; c) promotes conformational changes that generate docking sites for adaptor molecules such as BAK1 for BRI1; d) promotes phosphorylation of residues at the juxta-membrane domain, the region between kinase domain and the transmembrane, which act as docking sites for downstream signalling or regulatory molecules such as membrane bound receptors including cytoplasmic kinases (RLCK), which in turn may also promote phosphorylation (Waites et al., 2000; Shiu et al., 2003; Russinova et al., 2004; Shpak et al., 2005; Wang et al., 2005; Wang X et al., 2008; Karlova et al., 2008). Once cytoplasmic signalling molecules, such as Rho GTPase in the case of CLV1, receive the message from RLKs, it is distributed further within the cell via a canonical MAPK signalling cascade (Trotochaud et al., 2004).

It should be noted that these receptors are under strict regulation of phosphorylation inhibitors, phosphatases such as KAPP (kinase associated protein phospatase), endocytosis, ubiquitin-mediated protein degradation and possibly of autophagy (Tör et al., 2003; Robatzek et al., 2006; Wang et al., 2006; Park et al., 2008; Trujillo et al., 2008; Todde et al., 2009). Once the message is conveyed, they are downregulated by some of the same mechanisms.

Intracellular receptors.

Plant NB-LRR proteins (nucleotide-binding site-leucine-rich repeats) have been studied in detail and some members are well characterized as immune receptors. They are traditionally referred to as disease resistance proteins or *R*-genes and form the bridge between molecular cell biology in plant immunity and plant breeding for agriculture. They form one of the largest gene families in plants. There are more than 140 predicted members in *Arabidopsis* and more than 400 in rice. Their gene products promote resistance to viral, bacterial, fungal and oomycete pathogens.[5] Their tripartite structure is very similar to the mammalian CLR, a central nucleotide binding site, carboxyl LRR domain (hence NB-LRR) and a variable, TIR or coiled-coil N-terminal domain (DeYoung et al., 2008).

NB-LRR proteins recognize pathogen specific signals, most often effector molecules responsible for virulence, either directly or indirectly. Recognition of

either modified host protein or a pathogen-derived protein leads to conformational changes in the amino-terminal and LRR domains of these receptor proteins. Such conformational alterations promote the exchange of ADP for ATP by the NB domain, which activates a signalling cascade in turn, promoting resistance to the pathogen (DeYoung et al., 2006). Although these proteins reside within the cytoplasm, they are also mobile and can translocate into the nucleus, chloroplast or mitochondria. For example, barley MLA, tobacco N and *Arabidopsis* RPS4 translocate into the nucleus. In such cases, it has been proposed that these NB-LRR proteins de-repress basal defense by associating with WRKY transcription factors in the nucleus (Shen et al., 2007).

Activation of defense responses by extracellular and intracellular PRRs have been defined as primary and secondary immune responses, respectively (Shen et al., 2007). In both cases, a localized hypersensitive response (HR, a kind programmed cell death of the infected cell) has been reported (Naito et al., 2008), and the main differences between these responses have been reviewed (Jones and Dangl, 2006; Tör, 2008;). Recent studies demonstrated that individual effectors could be recognized by the same intracellular receptor, especially by those that recognize incoming effectors indirectly (de Wit, 2007). In addition, not only do some NB-LRR proteins act additively to provide a resistance response (Marathe and Dinesh-Kumar, 2003; Sinapidou et al., 2004), but also some NB-LRR type receptors are required for RLP-mediated defense responses (Gabriëls et al., 2007).

Nearly all NB-LRRs proteins have been reported to function as disease resistance proteins, however, exceptions do occur. Recently Sweet et al (2008) reported that *LOV1* (*LOCUS ORCHESRATING VICTORIN EFFECTS1*), a CC-NB-LRR gene, show natural and induced variation and confer victorin sensitivity and disease susceptibility in Arabidopsis indicating that the NB-LRR genes could also have diverse roles.

NB-LRR proteins are also strictly regulated by mechanisms including repression by the chromosomal structure, feedback amplification from the receptor protein, and repression by their negative regulators at the transcriptional level (Li et al., 2007) or ubiquitin-mediated degradation (Tör et al., 2003).

Conclusions

Plants have many proteins that act as pattern recognition receptors [PRRs] at the cell surface or within the cytoplasm. They have a crucial role in the plant's life and its response to stress elicited by microorganisms or damage; the means of transmitting the signal is exceedingly complex and equally fascinating. Whether primary or secondary defense responses, wound healing or developmental processes ensue, the outcome is dictated by the presence and type of exogenous and endogenous inducers including MAMPs, DAMPs, effectors, secreted proteins and processed peptides. Despite large numbers of receptor proteins having been identified at the cell surface, only a small numbers of ligands have been identified. Recent studies on effectors that are delivered inside the cell uncovered a vast number of putative virulence molecules. Although a few examples of effectors that are delivered into the apoplast are known, more information on these type of molecules are needed to develop a clearer picture of their recognition at the cell surface.

Homo- or hetero-dimerization of RLK-type receptors to initiate an appropriate response is currently known for only a few members and we expect additional candidates to be identified. Similarly, the mobility of NB-LRR proteins within several intracellular locations brought attention to the convergence of MAMP-triggered and effector-triggered immunity.

DAMPs have been regarded as wound inducing proteins in plants and have not received the same attention as their counterparts in animal systems. Although, plants can easily dispense with dying or dead cells, there is still a lot to learn from the process of responding to damage or injury and there may be ancient prototypical recognition systems such as the hydrophobic portions of molecules (Hyppos) that unify some aspects of plant and animal immunity (Seong et al., 2004).

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