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CHAPTER : 07

Host-Microbe Interplay to Exhibit Immune Response against the Phytopathogens

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Abstract

The constant battle between plants and pathogenic microbes has led to the evolution of various defence mechanisms in plants. These include physical barriers such as thickening of cell walls, chemical defences like antimicrobial compounds and molecular responses triggered by identification of pathogen-associated molecular patterns. Plants also rely on friendly microbes, such as mycorrhizal fungi and rhizobia, to enhance nutrient uptake and provide protection against pathogens through competition or production of antimicrobial compounds. In addition, some plants have developed symbiotic relationships with specific microbes that can triggered systemic resistance against a broad range of pathogens. Plants have also evolved sophisticated signalling pathways that allow them to mount a rapid and specific defence response upon pathogen detection. These signalling pathways involve the activation of defence-related genes, the production of signalling compounds like salicylic acid and jasmonic acid and the deployment of defence proteins such as pathogenesis-related proteins. Furthermore, plants can communicate with neighbouring plants through airborne signals or root exudates, enabling them to prime their defences in anticipation of potential threats. Overall, the intricate interplay between plants and pathogenic microbes highlights the dynamic and complex nature of plant defence mechanisms. Understanding the intricate interactions among plants and microbial organisms is crucial for developing sustainable agricultural practices which minimize the use of chemical pesticides while ensuring crop productivity and food security. Research in plant-microbe interactions continues to uncover new insights into the complex networks that govern these relationships, offering potential solutions for managing plant diseases in an environmentally friendly manner.

Keywords DAMPs, PAMPs, NLR, Signal transduction, PRRs, WAKs, MAPK, ROS, Signalling pathways

1. Introduction

Phytopathological investigations in the past ancient times such as 3rd or 4th centuries B.C. in the findings of Aristotle's disciple Theophrastus. Many plant diseases that were documented in ancient times were frequently attributed to spiritual sources. With the advent of compound microscopes, microbiology

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throughout the enlightenment allowed for the systematic classification of pathogenic organisms. The effectiveness of fungicides, for example the Bordeaux mixture of calcium oxide and copper sulfate, was established in the first studies conducted in the 19th century. Heinrich Anton de Bary proved that pathogenic microorganisms were the source of plant illnesses later in the 1800s. During early 20th century witnessed the development of genetic and heritability notions, which made it possible for scientists to pinpoint the resistance genes (R genes), or sources of transmissible resistance.

Harold Henry Flor's revolutionary gene-for-gene approach provided additional information on R genes, which are correlated with avirulence genes that the pathogen possesses and which elicit an incompatible response (Flor, 1942). Later in the 20th century, with discoveries in chemistry and molecular biology, mechanisms for resistance *via* R genes were subsequently clarified. Several gene families that encode regulators of susceptibility and resistance to disease were identified in the early 21st century as a result of advancements in genomics and molecular biology. It was discovered that R genes were just one group of players in a network of interdependent elements. Beyond the basic framework of H. H. Flor's gene-for-gene model, recent molecular research has shown that plant resistance depends on a complex regulatory mechanism that governs plant defensive responses. Various aspects of the plant immune system are involved in defensive response, signal transduction and pathogen detection (Dangl *et al.*, 2013). According to the zig-zag model, selection forces drive the evolution of infectious agents with sophisticated escape tactics and plants with intricate detection systems.

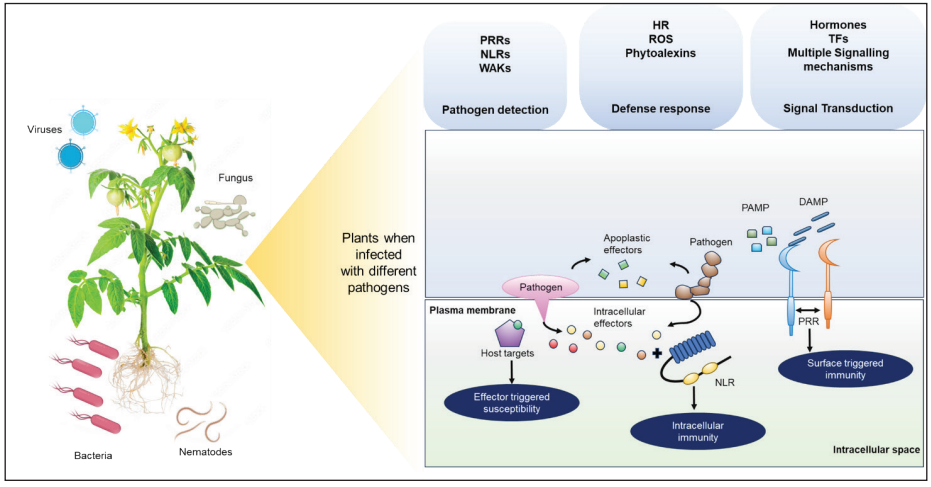

Figure 1: Various components involved in plant immunity against phytopathogens

2. Detection and Response are preliminarily Steps Exhibited by Plant Immune System

Examining the molecular basis of pathogen resistance reveals a group of cellular receptors that are capable of directly detecting toxic substances (Niehl *et al.,* 2016) recognition receptors (PRRs) in the cell membrane identify pathogen-associated molecular patterns (PAMPs), whereas wall-associated kinases (WAKs) identify damage-associated molecular patterns (DAMPs) brought on by cellular damage during infection. Leucine-rich repeats (NLRs) and nucleotide-binding domain receptors (NDRs) recognize effectors that pathogens employ to spread infection (Prince *et al.*, 2014). NLRs, PRRs and WAKs start one of the numerous signalling cascades that are still being fully understood. The expression of genes associated to pathogenesis is regulated by a number of factors, including transcription factors (TFs), G-proteins, ubiquitin, calcium, hormones and epigenetic alterations. This results in a range of reactions that stop the infection from spreading, such as the hypersensitive response (HR), the release of reactive oxygen species (ROS), alteration of the cell wall, stomata closure, or the synthesis of different antimicrobial proteins and molecules. Plant pathogen resistance requires a variety of organelles and classes of protein and non-protein molecules, all of which are necessary for regulating the defence response, as are now known *via* molecular approaches. Abiotic reaction to stress and growth are two examples of additional signalling systems that are impacted by variables in each of these roles. Enhancing our understanding of plant-pathogen interaction requires a detailed characterization of these molecular interactions that take place when a compatible pathogen interacts with plant tissue (Toruño *et al.*, 2016).

3. Detection of Plant Pathogen by the Host

3.1. PAMPs and DAMPs are Prey of PRRs and WAKs

PRRs can identify a wide range of microorganisms, including fungal polysaccharides, viral nucleic acids, and bacterial proteins (Monaghan and Zipfel, 2012). These receptors often contain leucine-rich repeats (LRRs) that bind to external ligands, transmembrane domains necessary for their placement in the plasma membrane, and cytoplasmic kinase domains responsible for signal transduction via phosphorylation. LRRs' significant divergence is associated with their ability to bind to a broad variety of elicitors. Many PRRs need on the regulatory protein brassinosteroid insensitive 1-associated receptor kinase 1 (BAK1) and other somatic embryogenesis receptor-like kinases (SERKs) to operate. When activated, some PRRs release kinase domains that enter the nucleus and trigger transcriptional reprogramming, but not all of them initiate significant signaling.

Insect (elicitors originating from aphids), oomycete (glucan and elicitins), fungal (chitin, xylanase), bacterial components and viral (double stranded RNA) molecules are among the various molecules discovered by PRRs (Jonge *et al.*, 2010). Through the identification of fungal PAMPs, wheat PRRs

TaLRK10, TaRLP1.1 and TaRLK-R1-3 have been linked to resistance to rust (fungi of the genus Puccinia), despite the fact that majority of these findings were carried out to clarify specific molecular relationships in Arabidopsis. Some receptors sense damage by identifying cellular compounds that have been upset by infectious enzymes, in contrast to PRRs that identify non-self pathogens molecules during infection. This has been demonstrated in Arabidopsis by the sensing of extracellular ATP by DORN1/LecRK-I.9 or oligogalacturonides by WAK1.

In addition to cytoplasmic kinase domains that resemble PRR structures, WAKs have an N-terminal external galacturonan-binding domain to interacts with cell wall pectins. WAK1 and WAK2 are able to detect oligogalacturonic acid, which is produced when fungal enzymes break down the pectin in plant cell walls (Decreux and Messiawn, 2005). Plant lectins are capable of identifying carbohydrates that caused from injury or damage sustained during the pathogen infection or damage formation by pathogen. Several PAMPs and DAMPs, including lectin receptor kinases, are identified by PRRs/WAKs with lectin motifs because they include carbohydrates, such as lipopolysaccharides, peptidoglycans, oligogalacturonides and cellulose. Many extracellular substances, including extracellular DNA, ATP and NAD(P), are detected by plants as indicators of pathogen infection. Pathogens have developed to impede PAMP detection and limit effectiveness during PTI. Avr4 and Slp1, respectively, are chitin-binding proteins produced by *Cladosporium fulvum* and *Magnaporthe oryzae* that inhibit plant sensing. As the zig-zag model illustrates, pathogens also create effectors to defy numerous aspects of plant immunity, which plants have evolved defence mechanisms against (Jones and Dangl, 2006). Plants use another, larger class of proteins to identify these effectors of pathogens that facilitate infection.

3.2. Pathogen Effectors are Detected by Action of NLRs

Perhaps the gene families that evolve the fastest are NLRs, sometimes referred to as R genes. When pathogenic effectors are detected, their products change configuration, going from a compacted, ADP-bound state to an open, ATP-bound state with exposed N-terminal domains, which triggers downstream signalling (Zhang *et al.,* 2012). An evolutionarily preserved domain with a Nucleotide-Binding site found in Apoptotic protease-activating factor, R proteins and *Caenorhabditis elegans* death-4 protein (NB-ARC) comes before N-terminal Toll/interleukin-1 receptor-like (TIR) or coiled-coil (CC) domains, which are followed by an exceptionally variable LRR. While TIR-NBS-LRR genes (TNL genes) are unique to dicots, CC-NBS-LRR genes (CNL genes) are present in both types of animals. Similar to PRRs, these receptors may distinguish between different effector structures due to variations in the LRR. NLRs have LRRs at the C-terminal end and are often found in the cytoplasm, in contrast to PRRs (Zipfel, 2014). P-loop or Walker-A, resistant nucleotide-binding site A (RNBS-A), Kinase-2 and MHDV are among the several conserved motifs found in the NB-ARC. GLPL and MHDV are termed after the preserved amino acids. Nevertheless, not every motif is necessary

for function; the rice Pb1 CNL protein, for example, is not a P-loop. Owing to reports, NLRs function in networks and distinguish between sensor and helper NLRs as well as NLRs necessary for NRCs. As sophisticated sensors capable of detecting a wide range of alterations through both modified-self and non-self recognition, NLRs have come to light. NLR mismatches in hybrids can lead to auto-immunity, therefore NLR interactions are not always beneficial. Similar to the proteins found in NLRs, NB-ARCs are present in a wide range of organisms, including humans, nematodes and *Streptomyces coelicolor*, the latter two of which are also implicated in programmed cell death. High rates of chromosomal recombination occur in extra-pericentromeric clusters, where a large number of NLR genes are found. Through repetitions, chromosomal rearrangements and uneven crossing over, these genes rapidly change. Additionally, transposable elements contribute to the evolution of regulatory sequences such as promoters. The possibility of functional diversity is increased by the translocation of NLR genes to unlinked sites. Many effector-NLR interactions in *Arabidopsis* have been clarified, much like PRRs. When pathogen effectors directly interact with NLRs, or whether the effector's target protein, a target-mimicking decoy protein, or the NLR itself is modified, the NLR is activated. One of the most well researched NLR-effector interactions is the NLRs RPM1 and RPS2, which identify the targeting of resistance negative regulatory RIN4 by *Pseudomonas syringae* effectors. Since their keeper, RIN4, is also attached to the plasma membrane, RPS2 and RPM1 are located inside it, unlike other NLRs. RPM1 promotes the expression of resistance responses by attaching to the promoter-binding AtTIP49a negative regulator after activation.

NLRs contain a variety of topologies, some of which may have integrated decoy domains, such as TF sequences, that function as effector targets. This WRKY domain is altered by the *Ralstonia solanacearum* effector PopP2, which causes the NLR to become activated. NLRs can also form monomers; in rice, this is demonstrated by the CNL proteins RGA5 and RGA4, where RGA5 binds directly to the *Magnaporthe oryzae* effectors Avr-Pia and Avr1-Co39. Like PRRs, which are dependent on BAK1, NLRs also need other proteins to send messages. Non-race-specific disease resistance 1 and enhanced disease susceptibility 1 proteins are associated with CNLs and TNLs, respectively. Furthermore, NLRs have the ability to localize to certain regions of the cell, including the nucleus or endosomes. *Phytophthora infestans* effector Avr3aKI triggers the potato CNL protein R3a, which then shuttles to endosomes and enlists other effectors. Barley CNL MLA proteins build up in the nucleus and disrupt WRKY TFs, which suppresses immune response. Additionally, exocytosis is used by plants to produce antimicrobial compounds and transfer immunological receptors to the plasma membrane. Certain pathogen effectors affect the generation of antimicrobial compounds *via* interfering with the release of proteases, vesicular trafficking through proteasome degradation and endocytosis. The effectors SnTox1 and PtrToxA of *Penicillium nodorum* and *P. tritici-repentis* utilises the susceptibility genes Snn1 and Tsn1, which encode the WAK and NLR proteins, respectively. Through the development of

reactive oxygen species (ROS), necrotrophic infections are able to induce HR by seizing control of immune components. Defence responses are initiated by PRRs, WAKs and NLRs through intricate signalling pathways. TFs, hormones, MAPKs and other elements are important in this signal transduction process.

4. Signal Transduction

4.1. Involvement of Various Signalling Mechanisms for Imparting Resistance

Receptors trigger signalling pathways that are involved in numerous physiological functions, such as calcium fluctuations, ubiquitin, G-proteins and MAPKs. Membrane-bound proteins called Ras aid in the process of conversion of GTP to GDP in the general model of MAPK signalling, phosphorylating MAPKK (MEK) proteins are phosphorylated by MAPKKK (Raf) proteins, which results in the proteins called MAPK (ERK) are phosphorylated. MAPK's participation in numerous biological functions has resulted in the recognition of the 60 MAPKKKs, 10 MAPKKs and MAPK genes in Arabidopsis and 20 MAPKs. PRRs FLS2 and elongation factor interaction, which is started by bacterial flagellin, When EFR dimerizes with BAK1, MAPK signalling is initiated (Sun *et al.*, 2013). An MAPK cascade is also triggered by pathogen pectin degradation which are detected by WAK1 and WAK2detect. Investigation on tomatoes has revealed that MAPK genes are also involved in the signal transduction of NLR perception. MAPK signalling has the ability to downregulate defence responses as well and infections have created effectors that obstruct MAPK signalling in order to stifle resistance responses. Comparably, because of its role in several biological processes, the heterotrimeric G-protein and G-protein-coupled receptor system (GPCR) has been extensively researched. Extracellular ligands attach to the transmembrane GPCR, causing the GDP in the G-protein complex's α subunit to become substituted for GTP. This results in the further initiation of signals of the α subunit from the b- g subunit complex begins further signalling. The subunits then reassociate as a result of the α subunit hydrolyzing GTP. G-protein signalling is more prevalent in metazoan systems; nonetheless, G-proteins also play roles in stomatal closure and HR. Proteasome-mediated protein breakdown following ubiquitination is also involved in other signalling pathways, including defence Components are regulated either negatively by targeted deterioration or positively by suppressing their degradation. In an effort to impede infection by interfering with the ubiquitin proteasome machinery, pathogens have developed effectors. Plants also use small ubiquitin-like modifiers (SUMOs) to regulate their response and pathogenic agents equivalently obstruct this signalling also.

Receptors that cause alterations in the concentration of calcium ions (Ca2+) serve as signalling pathways that initiate defences against harmful or symbiotic bacteria. In order to activate many families of transcription factors (TFs), including calmodulin-binding transcription activators (CAMTAs), calcium is detected by calcineurin B-like proteins, calcium-dependent

protein kinases (CDPKs) and calcineurin (CaM). CaM contributes to the generation of ROS by initiating the MAPK cascade (Lecourieux *et al.*, 2006). Hormone activation and the expression of the proteins NDR1 and EDS1 are regulated by calcium signalling. To phosphorylate the WRKY TFs implicated in RPS2 and RPM1 ETI, CDPKs migrate to the nucleus. Hormones that play a variety of roles in stress and developmental responses can communicate this chemical information. Hormonal variations cause defensive response genes to express differently, just like calcium signalling does. Transient MAPK activity during PTI is highly dependent on hormone signalling, whereas less dependence on hormonal regulation is made possible by MAPK activation during ETI. Temporary MAPK activation during PTI is highly dependent on hormone signalling, whereas prolonged MAPK activation during ETI allows for less reliance on hormonal regulation (Meng *et al.*, 2013).

4.2. Initiation of Plant Hormones to Repress Resistance

A further layer of regulation is provided by hormones that function downstream of pathogen detection. In addition to influencing a wide range of developmental and response processes, including as interactions with other hormones, SA is essential for both systemic and local defences against several diseases. MAPK and SA cascades can operate in parallel, with certain cascades starting MAPK cascades and others starting SA activity. Signaling from receptors is carried out via SA by NDR1 for CNL receptors and an assortment of EDS1 and phytoalexin deficient 4 (PAD4) for TNL receptors. By means of intricate interplay, SA communicates the existence of a pathogen by means of TFs that trigger the expression of genes responsible for defence. Following signalling, SA causes thioredoxins to break down disulfide bonds within the oligomer protein nonexpressor of pathogen resistance gene 1 (NPR1), permitting its constituent monomers to enter the nucleus from the cytosol. They subsequently attach with the TF TGA and upregulate resistance-related genes. Using this mechanism, the pathogenic effector of *Cochliobolus victoriae*, called victorin, aims the thioredoxin TRX-h5, which is accompanies in the monomerization of NPR1 and causes cell death by activating the susceptibility protein in Arabidopsis i.e., LOV1. Major hormones of the plant immunity against necrotrophic diseases include JA and ET. Studies states that the signalling mechanism of ET synthesis is enhanced by bacterial flagellin. In the absence of ET,EIN3 is broken down by a proteasome and ubiquitination reactions process driven by the F-box proteinaction. ET causes the constitutive triple response1 (CTR1) protein to stop working and disable receptors. The inhibition of EIN2 and EIN3, which permits the expression of defence through the increase of ET signalling necrotrophic resistance and genes. Pathogen interference also targets this, as the XopD the tomato pathogen *Xanthomonas euvesicatoria* effector desumoylates the TF SIERF4 in order to obstruct hormone signalling, in particular the inhibition of ET derived resistance. Deployment of the important functions of many hormones in immunity and development demonstrate the tight, frequently inverse relationships between defence and

growth.ABA plays a role in several plant stressors, including suppressing and encouraging resistance reactions both in the presence and absence ofabiotic stress, in that order. In order to control water loss, ABA signalling is involved in stomata closure. Exchange of gases and entry of pathogens into tissue. Deficits in GA and ascorbic acid (AA) result in improved defence. Given that systemic regulators constitute the general definition of hormones, peptides can additionally serve as phytohormones. It has recently been demonstrated that the short peptide hormone system in has a role in the system herbivory response, changing the expression of some genes, particularly those of nearby plants that are not subjected to the biotic stress. This suggests that plant hormones can boost defence responses by causing individual plants to communicate with one another.

5. Defence Response

5.1. Cell Wall Reinforcement, HR and ROS Imparts Resistance against Pathogen Attack

As one of the most often employed immune responses, HR results in the targeted death of cells in the vicinity of an outbreak of infection. For diseases that involve living tissue (biotrophs), this creates a quarantine zone to prevent the infection from spreading. The generation of ROS, which are employed in several facets of the resistance response, is initiated by pathogen infection, which also causes the synthesis of peroxidases. Superoxide is produced by NADPH oxidases and is used by peroxidases to produce hydrogen peroxide (H2O2). One NADPH oxidase, RBOHD, binds to PRRs EFR and FLS2 and BIK1 phosphorylates it, which causes ROS to be produced. When ROS cause programmed cell death, hydrogen peroxide spreads to nearby cells to start the synthesis of substances that stop oxidative damage. It came to light that transgenic plants with impaired detoxification of ROS compounds reacted more strongly to pathogens that cause HR. In addition to aiding in HR, ROS are employed in an oxidative burst, a process that renders surroundings suboptimal for pathogen survival and reproduction. Consequently, ROS directly interfere with signal transduction and the plant immunity to produce defence response, which prevents the germination of fungal spores. Apart from peroxidases and NADPH oxidase, additional enzymes that generate reactive oxygen species (ROS) are amine and oxalate oxidases. The necrotrophic fungus *Sclerotinia sclerotiorum* infects numerous species and secreates oxalic acid, which inhibits plant oxidative burst during the initiation stage of infection but promotes ROS generation after establishment. The oxalate oxidase proteins, or germins, that wheat and barley generate increase their resistance to infections by degrading oxalic acid. Crops that were transgenic and have oxalate oxidase genes in wheat or barley shown heightened resilience against *Sclerotiorum* and other pests.

Glycoprotein crosslinking, mediated by ROS, fortifies cell walls. The requirement for various pathogens to pierce the cell wall inhibits pathogen mobility and restricts accessibility to their food required for normal

reproduction. Because they are devoid of a few degradation enzymes that majority fungi have, pathogenic bacteria utilise stomata and wounds to obtain nutrients from plants. Stomatal guard cells use SA and ABA signalling to cause stomatal closure in order to inhibit entry after identifying lipopolysaccharides and bacterial PAMPs, such as flg22. *P. syringae* reacts to this by producing coronatine, which mimics phytohormones and interferes with hormone biosynthesis to cause closed stomata to open again. It has been shown that stomata regulation includes a complicated defence machinery besides its response to stress. Previously, this process was thought to be a passive means of pathogen access into plant tissue. Apart from oxidase synthesis, various other substances are produced by plants and pathogens that disrupt the functioning of lipids, proteins and carbohydrates.

5.2. Phytoalexins and Symbionts Elevate Defence Responses in Plants

Organic substances known as phytoalexins are generated in response to invasive pests and aim to interfere with growth, metabolism and reproduction. Originally, phytoalexins were studied as defence mechanisms against *P. infestans* that safeguarded potatoes. Phytoanticipins are a class of plant compounds that are constitutively generated and exhibit pesticide activity. Camalexin is produced as response to various disease and is also a model phytoalexin in *Arabidopsis* uses.. Camalexin is controlled by WRKY TFs and MAPK cascades. This substance can be detoxified by certain pathogens that are adaptable. Avenanthramides found in oats and diterpenoids in rice are two further phytoalexins found in cereals. The oat root epidermis produces avenacin A-1, a phytoanticipin of the saponin group, which interacts with fungal membrane sterols to generate pores in the membranes. The capacity to detoxify avenacin A-1 has evolved in *G. graminis* var. *avenae*. Numerous species include phytoalexins, which are known to have allelopathic effects. However, certain signalling pathways that lead to the creation of these compounds are yet unknown. Additionally, phytoalexins might be beneficial in medicinal settings. Crop vulnerability to exogenous chemicals, such as herbicides containing glyphosate, could rise incidence of disease.

Certain symbionts help their host fight against pathogens in addition to giving the plant access to nutrients. Through the synthesis of antibiotic compounds, rhizobacteria in case of wheat exhibit responses against the pathogen *G. graminis*, while rice arbuscular mycorrhiza stimulates enhanced host defences. In corn, mycorrhizae have the capacity to increase DIMBOA production. It has been demonstrated that symbionts influence resistance responses by inhibiting JA-mediated defence or interfering with the generation of ROS and b-1,3-glucanase. These interactions show how the immune system in plants is complex.

6. Conclusion and Future Directions

With improvements in molecular biology and computing resources, the arena of plant-microbe communications will not stop to flourish through the twenty-first century. Phyto-pathology or plant pathology for say like

other scientific disciplines, will continue to develop as further information regarding pathogen-plant interplay become available. Research will be driven by a number of factors which will raise the necessity for crops to have long-lasting pathogen resistance. The field of plant immunity research will progress and agricultural genetics will be modified for enhanced resistance. To acquire resistance, it is generally ideal to continuously switching up the receptors needed to initiate defence responses. NLRs possess the ability to be an extremely effective biotechnology tool that may be employed to alter the functioning of the CRISPR/Cas9 system and develop immunity to infections. Despite the limits of current technology, subsequent studies will likely produce crops with distinct R-genes that might not directly transplanted among various species. With the goal to trigger the most efficient defence response, it will also be necessary to align receptors with the appropriate signal transduction mechanism for designing novel resistance routes against different pathogens. Subsequent investigations will likewise focus on understanding such ideas. More resistance regulation and response mechanisms that may be useful in agricultural systems may be found in the upcoming years. A deeper comprehension of plant immunology and disease resistance will greatly increase agricultural productivity by reducing crop loss. It will also have wide applications to many biological systems and advance our knowlegde of the molecular relationships and coevolution that underlie this field.

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