



BEST JOURNAL 13(1):

Date received: 27/03/2016

Date accepted: 05/05/2016

Printed in Nigeria

MOLECULAR BASIS OF PLANT-PATHOGEN INTERACTIONS AND CONSEQUENCES ON FOOD SECURITY: A REVIEW.

Chejara, N.,¹ Animasaun, D. A.,^{1,2*} Krishnamurthy, R.¹ and Ingalthalli, R. S.¹

¹C.G. Institute of Biotechnology, UkaTarsadia University, Bardoli, Surat, Gujarat, India.

²Department of Plant Biology, Faculty of Life Sciences, University of Ilorin, Nigeria. P.M.B.1515, Ilorin, Kwara State, Nigeria

*Corresponding author: biostanleydayor@yahoo.com.au, animasaun.ad@unilorin.edu.ng
+2348060264429

ABSTRACT

Plant diseases is a major cause of yield losses and have impacted significantly on the well-being of humans and animals. Plants are engaged in continuous co-evolutionary struggle to get dominance over common pathogens. Understanding the Plant-Pathogen interaction constitutes major concern and strategy in curbing global food. Concise knowledge of plant pathogen-host mechanism could help in the developing of robust plant protection strategy to prevent food shortage due to yield loss, infection and spoilage in crop plants. The knowledge of such interactions would include the various mechanisms of plant defense systems and pathogenesis by different types of pathogens, which have major impact on agricultural and crop production. The frontline of plant defense against non-viral pathogens such as bacteria, fungi and oomycetes is provided by transmembrane pattern. The receptor mechanism recognize and detect conserved Pathogen Associated Molecular Patterns (PAMPs), such as Lipopolysaccharides (LPS) in Gram negative bacteria which activates the pattern-triggered immunity (PTI). To counter this plant innate defense, pathogens usually deploy effector proteins with a primary function to suppress PTI. The efficiency of PTI could be suppressed by pathogen virulence effectors; Effector Triggered Susceptibility (ETS). In response to the pathogen effector proteins, plants have developed surveillance proteins (R-protein) to either directly or indirectly sense the presence of the pathogen effector proteins and the mechanism activates immunity against the pathogen. There is therefore continuous struggle between plant and associated pathogen for survival. Consequently plant have evolved in such a way that it can switch between its hypersensitive response with respect to Necrotrophs as well as Biotrophs as a mean of surviving virulent pathogens.

Keyword: Defence mechanism, effector proteins, pathogenesis, plant immunity, plant susceptibility.

INTRODUCTION

Food security has become an issue of global importance, and foremost price hike of food is due to loss in production to plant infection and diseases (Orkeet *et al.*, 1994). A vast number of plant pathogens from viroids of a few hundred nucleotides to higher plants cause diseases in our crops. Their effects range from mild symptoms to catastrophes in which large areas planted to food crops are destroyed. Catastrophic plant disease exacerbates the current deficit of food supply in which at least 800 million people are inadequately fed (Strange and Scott, 2005). With continued population growth, rapid income growth, and changes in lifestyles, demand for food materials would be on continual increase in particular in the developing countries.

Food production will not keep pace with demand in developing countries and an increasing portion of the developing world's food consumption will have to be met by imports from the developed world due to massive loss to pest and diseases in crop production (Andersen, 2001). Plant pathogens are difficult to control because their populations are variable in time, space, and genotype. Most insidiously, they

evolve, often overcoming the resistance from chemicals, so the ability of the plant to develop an in-built mechanism for suppressing infection is imperative. The ability of plant to detect and repress pathogenic microbes has been dominant to the evolution and developmental success of modern day plants. On the basis of fossil record, the first plant to be established on the land occurred almost 480 million years ago. However, molecular clock guesses propose that the plants evolved more than 700 million years ago (Aked and Galan, 2005).

Plants do not have any movable defender cells and a somatic adaptive immune system, but the presence of physical barriers, like waxy epidermal cuticles, and bark. These substances not only protect the plant from invasion, they also give the plant strength and rigidity. In addition to preformed barriers, virtually all living plant cells have the ability to detect invading pathogens and respond with inducible defences including the production of toxic chemicals, pathogen-degrading enzymes, and deliberate cell suicide (Freeman and Beattie, 2008). The generation of toxic secondary metabolites are sufficient to stall the efforts of attacker to establish infection (Liao *et al.*, 2000; Guimaraseet *et al.*, 2004).



Fungi are most essential pathogens of plants and cause more noteworthy yield loss than bacteria and viruses. The development of new and innovative ways to diagnose, predict and restrict plant disease has therefore become a constant challenge for the science of Plant Pathology(Nuss, 1996).This interdisciplinary field has progressed dramatically in the last decade in parallel with the transition of biological sciences as a whole, in large part due to the introduction of various molecular markers and genomic tools in the study and analysis of host pathogen interaction(Jonsthan *et al.*, 2006). This review will assess the basic mechanisms of plant pathogen interaction, and specifically focus on molecular mechanisms and evolutionary aspects of effector proteins from different groups such as fungi, oomycetes, nematodes and bacteria.

Plant defence system

Plants use a vast array of signals originating from micro-organisms and the environment to recognise pathogens and elicit plant defence responses. Non-

specific elicitors of biotic and abiotic origin induce host defences in a broad range of host species(Freeman and Beattie, 2008).Plants display inducible systemic acquired resistance, which occurs when previous exposure to a pathogen activates signalling pathways acting via molecules such as jasmonate, ethylene, and salicylic acid (Figures 1a-c). These small and sometimes volatile molecules spread throughout the plant or even the plant population(Sexton and Homolelt, 2006). This triggers responses such as the expression of "Pathogenesis Related Proteins"(PRP), such as chitinases or glucanases, which can lead to the increased resistance of the whole plant against a subsequent pathogen attack. Apart from these, plants use two innate immune systems to respond to pathogen infection, Pathogen-Associated Molecular Pattern (PAMP)-triggered innate immunity (PTI) and Effector-triggered immunity mechanisms (ETIM)(Pieterse and Loon, 2004).

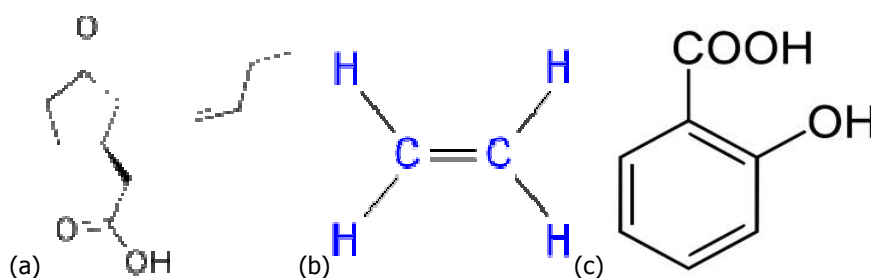


Fig 1: Biochemical structure of (a) Jasmonate (b) Ethylene and, (c) Salicylic acid

PAMP-triggered innate immunity is induced by recognition of PAMPs by transmembrane receptors and gives early responses to pathogen infection, while Effector-triggered immunity involves resistance (R) proteins as receptors that specifically recognize pathogen effectors, either directly or indirectly, and

usually induces hypersensitive cell death(Osheroov and May, 2001). The major R- proteins are intracellular receptors and contain nucleotide binding site (NBS) and leucine-rich repeat (LRR) domains. The total system of plant defence as well as susceptibility can be shown by a zig zag model.(Fig 2) as postulated by (Jones and Dangl, 2006)

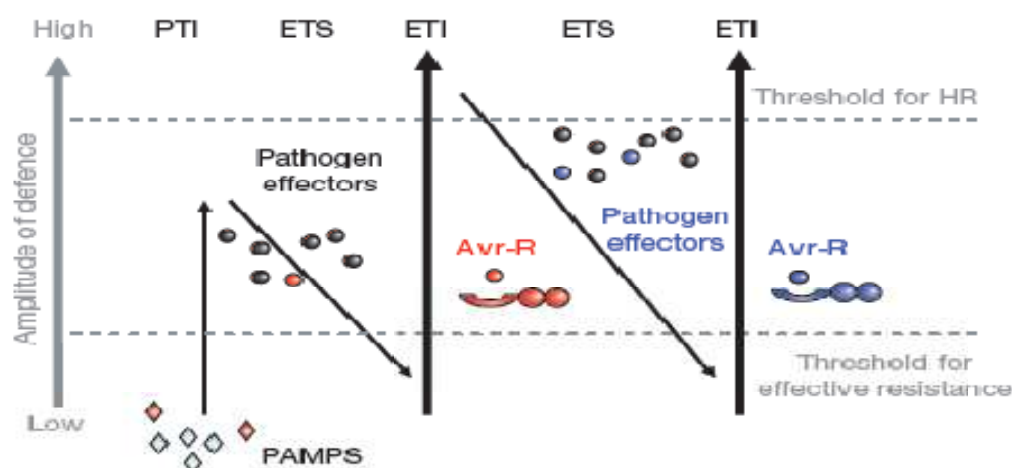


Fig 2: Illustration of Zig zag model of plant defensive mechanism(Jones and Dangel, 2006)



PAMP pathogen-associated molecular pattern
MAMP microbial-associated molecular pattern
PTI PAMP-triggered immunity
ETS effector-triggered susceptibility
ETI effector-triggered immunity
HR hypersensitive cell death response
Avr-R Avrulence disease resistance

Pathogen-Associated Molecular Patterns(PAMP) to Pattern-Triggered Immunity (PTI)

The frontline of plant defense against non-viral pathogens such as bacteria, fungi and oomycetes is provided by transmembrane pattern recognition receptors that detect conserved pathogen-associated molecular patterns (PAMPs), leading to pattern-triggered immunity (PTI). To counteract this innate defense, pathogens deploy effector proteins with a primary function to suppress PTI (Thomma *et al.*, 2011; Zverena and Pooggin, 2012). Usually PTI is initiated upon recognition of conserved microbial features by plant cell-surface receptors, and its induction is associated with MAP-kinase signalling, transcriptional induction of pathogen-responsive genes, production of reactive oxygen species, and deposition of calluses to reinforce the cell wall at sites of infection, all of which contribute to prevention of microbial growth. PAMPs fulfil a function critical to the lifestyle of the organism, are highly structurally conserved across a wide range of microbes, and are not normally present in the host. For example, plants respond to chitin and ergosterol, major constituents of the cell wall of higher fungi (Fillinger *et al.*, 2002; Doehlemann *et al.*, 2006).

Effector-Triggered Immunity (ETI)

Once plants activate a PAMP-triggered immune system enabling the detection of PAMPs, some pathogens evolved the ability to evade this type of resistance. It is

likely that some pathogenic microbes encode effectors that suppress PAMP triggered defences, but the best characterized come from phytopathogenic bacteria. Gram-negative bacterial pathogens acquired a type III secretion system (TTSS) through either horizontal gene transfer or adaptation of the flagellar apparatus (Idnurm and Howlett, 2002). Unlike Gram-negative bacteria, no TTSS has been discovered for fungal pathogens, and their effectors may be delivered from haustoria into the plant intercellular space (apoplast). Both fungal and bacterial effector proteins that are delivered to plants can possess enzymatic materials. These enzymes are responsible for modifying host proteins to enhance pathogen virulence and evade detection (Zverena and Pooggin, 2012).

Additionally, while many fungal effectors are small peptides that directly caused pathogenicity in plants, viral effectors involved the suppression of host's RNA, silence the host defence mechanism and subsequently infected the host by trigger of silencing code in the double-stranded RNA. The majority of plant viruses have RNA genomes, and double-stranded viral secondary structures or replication intermediates may trigger host silencing of the entire viral genome, preventing systemic viral spread. Once pathogens acquired the capacity to suppress primary defences, plants developed a more specialized mechanism to detect microbes, referred to as Effector-triggered immunity (ETI). (Thomma *et al.*, 2011). Effector-triggered immunity involves the direct or indirect recognition of the very microbial proteins used to subvert PTI by plant resistance (R) proteins. The mechanism involved is illustrated in Fig.3.

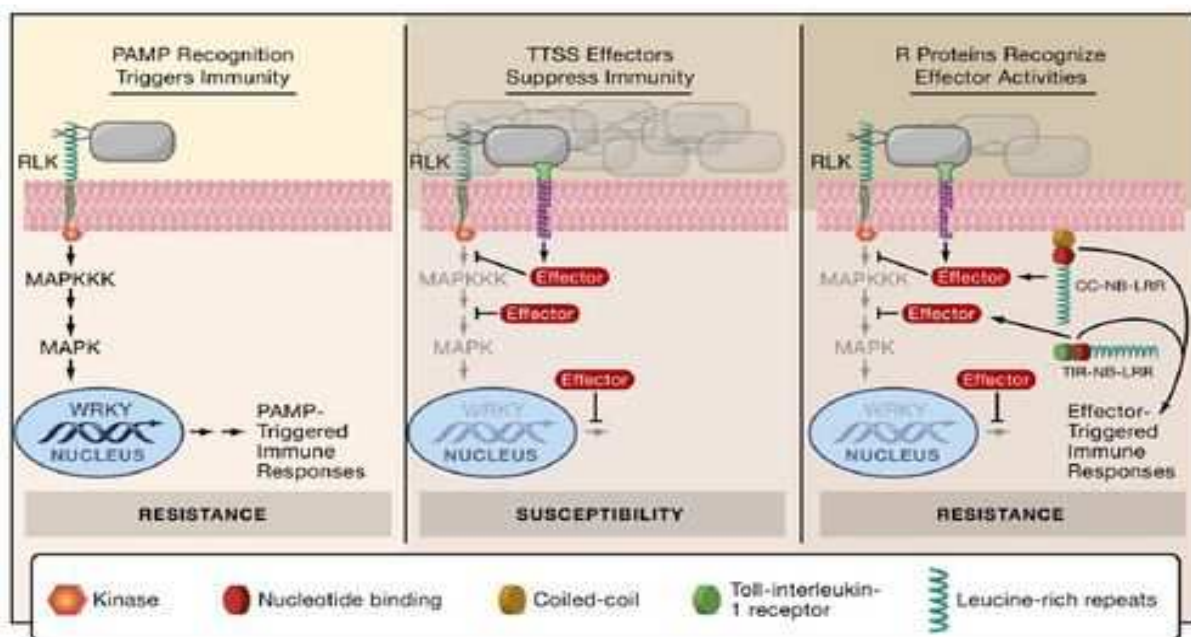


Fig 3: Effector-triggered immunity involves the direct or indirect recognition of the very microbial proteins used to subvert PTI by plant resistance (R) proteins (Thomma *et al.*, 2011).



Plant resistance gene and avirulence gene

The R-gene basically known as resistance gene generally recognised the effector proteins of pathogens. It has Nucleotide Binding Leucine Rich Repeat(NB-LRR), the molecular structure of the conserved region as well as the specific nucleotides and leucine (Fig 3). Plants contains thousands of R- genes with specificities for particular viral, bacterial, fungal, or nematode pathogens. Although there are differences in the defence responses induced during different plant-pathogen interactions, some common themes are apparent among R- gene-mediated defences (Pooggin *et al.*, 2006). Most significantly, the function of a given R gene is dependent on the genotype of the pathogen. An *Avr*gene (pathogen gene) expression causes the pathogen to produce a signal that triggers a strong defence response in a plant with the appropriate R-gene. However, expressing an *Avr*gene does not stop the pathogen from being virulent on hosts that lack the corresponding R-gene. The discovery of matched

specificity between single host R genes and single pathogen *Avr*genes was believed to be the source of the term gene-for-gene resistance. A single plant can have many R genes, and a pathogen can have many *Avr*genes (Solomon *et al.*, 2004).

A strong resistance response is induced when an *Avr*gene and an R gene of matched specificity are expressed. A distinguishing hallmark of most gene-for-gene interactions is the activation of a hypersensitive response (HR) in which plant cells in the immediate vicinity of the pathogen undergo programmed cell death as part of the overall defence response. Other features of the resistance response include induced synthesis of antimicrobial metabolites (often referred to as phytoalexins) such as capsidiol, terpenoid, lanosteroid (Fig 4) and alkaloids; synthesis of enzymes that can be harmful to the pathogen (such as chitinases and glucanases) and reinforcement of plant cell walls in the infected area (Lengeler *et al.*, 2000).

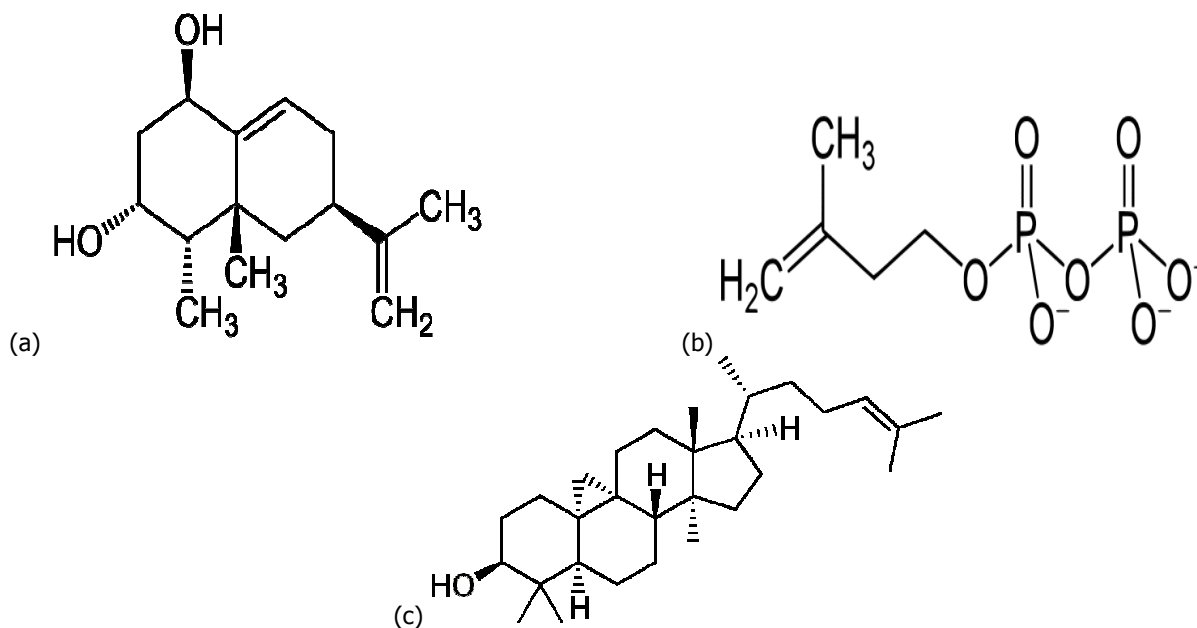
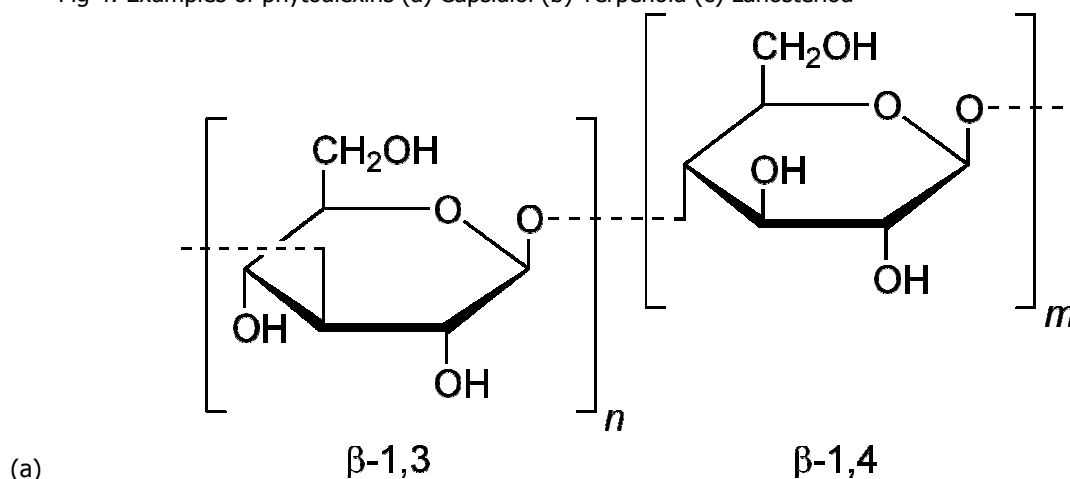
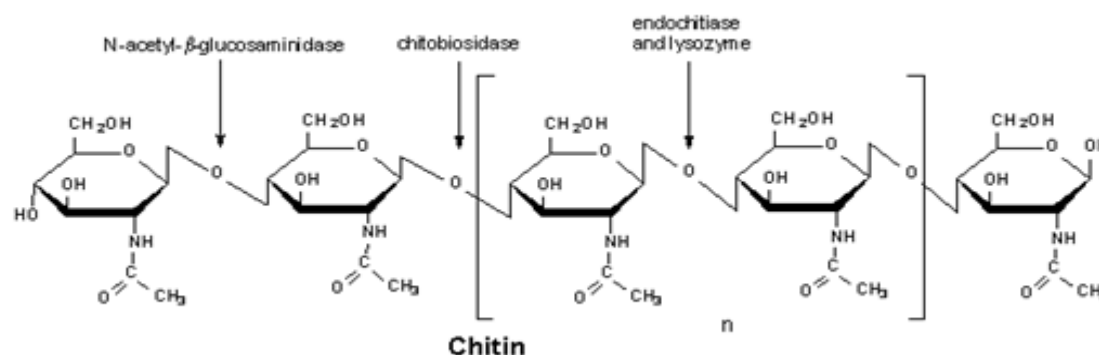


Fig 4: Examples of phytoalexins (a) Capsidiol (b) Terpenoid (c) Lanosteroid





(b)

Fig 5: Enzymes that are harmful to pathogens (a) Glucanase from glucan (b) Chitinase from chitin

In addition, responses are generated that have been postulated or proven to be involved in defence signal transduction. These include Ca^{2+} ion influx, specific changes in protein phosphorylation, the generation of activated oxygen species such as superoxide, and the production or release of salicylic acid (Cessna *et al.*, 2003).

Induced Immune response

Plants are constantly being challenged by aspiring pathogens, but resulting in disease in some cases. There are three reasons for pathogen failure. Either (A) the plant is unable to support the niche requirements of a potential pathogen and is thus a non-host; or (B) the plant possesses preformed structural barriers or toxic compounds that confine successful infections to specialized pathogen species; or (C) upon recognition of the attacking pathogen, defence mechanisms are elaborated and the invasion remains localized (Guimarase *et al.*, 2004).

All of the approximately 300,000 species of flowering plants are attacked by pathogenic fungi. However, a single plant species can be host to only a few fungal species, and similarly, most fungi usually have a limited host range (Winnerburge *et al.*, 2006). The evolution of fungal phyto-pathogens toward a high degree of specialization for individual plant species may be reflected in the different levels of specialization observed in extant plant-fungal interactions. Race-specific pathogen recognition is hypothesized to result from the direct or indirect interaction of the product of a dominant or semi-dominant plant resistance (R)-gene with a product derived from the corresponding dominant pathogen avirulence (Avr) gene. Subsequent signal transduction events are assumed to coordinate the activation of an array of defence responses (Wang *et al.*, 2003).

Various induced defence responses encountered by invading microbes are depicted as follows.

Hypersensitive response-(HR)

Classically, hypersensitive response (HR) is the death of host cells within a few hours of pathogen contact. The

HR has been proposed to play a causal role in disease resistance (Prussee *et al.*, 2004). In interactions with obligate biotrophic fungi that form intimate haustorial associations with host cells, plant cell death would deprive the pathogen of access to further nutrients (Pieterse and Loon, 2004). In interactions involving hemibiotrophic and necrotrophic fungi, the role of the HR is less clear because these pathogens can obtain nutrients from dead plant cells. However, cellular de-compartmentalization may lead to the release of harmful preformed substances that are stored in the vacuole. Several R-Avr gene-mediated resistances appear not to involve an HR. These include barley resistance against all races of *Erysiphegraminis hordei*, which is conferred by the *mlogene* and the potato *Rx* gene-mediated resistance to potato virus (Nurnberger *et al.*, 2004).

Reactive oxygen species-(ROS)

The production of reactive oxygen species probably plays a key role in plant defence against pathogen. Often the first response activated in many incompatible interactions, it may be the trigger that initiates the HR. We were the first to report that superoxide anions (O_2^-) were produced in incompatible interactions, initially between potato and *Phytophthora infestans* (late blight fungus) and then between tobacco and tobacco mosaic virus (TMV) (Kim *et al.*, 2005).

From recent studies involving plant cell culture, it appears extremely likely that plants contain a mechanism for producing O_2^- that involves an NADPH oxidase analogous to that used in mammalian neutrophils. Both O_2^- and H_2O_2 are only moderately reactive, however, and the cellular damage by ROS appears to be due to their conversion into more reactive species. Protonation of O_2^- , which occurs more readily at low pH, yields the hydroperoxyl radical (Cessna *et al.*, 2000). Because HO_2^- is less polar than O_2^- , it should be able to cross biological membranes about as effectively as does H_2O_2 .



Unlike O_2^- , HO_2^- can attack fatty acids directly and has been shown to convert linolenic, linoleic, and arachidonic acids to lipid peroxides. Thus, under appropriate conditions, O_2^- generation, leading to HO_2^- formation, could result in membrane damage (Talbot *et al.*, 1996).

Benzoic acid (BA) and Salicylic acid (SA)

Incompatible pathogens, whether fungi, viruses, or bacteria, frequently provoke the accumulation of both free BA and SA and their respective glucoside conjugates, with the highest concentrations forming in

the immediate vicinity of the infection site. The induction of these compounds is commonly associated with the hypersensitive response. The biochemical pathway leading to SA biosynthesis during the defence response is now relatively well established, but its regulation may differ between plant species (Pieterse and Loon, 2004). The Salicylic acid is derived from the phenylpropanoid pathway (Fig 6), but it appears (at least in tobacco) that SA synthesis is not regulated at the level of Phenylalanine ammonia-lyase (PAL) transcription.

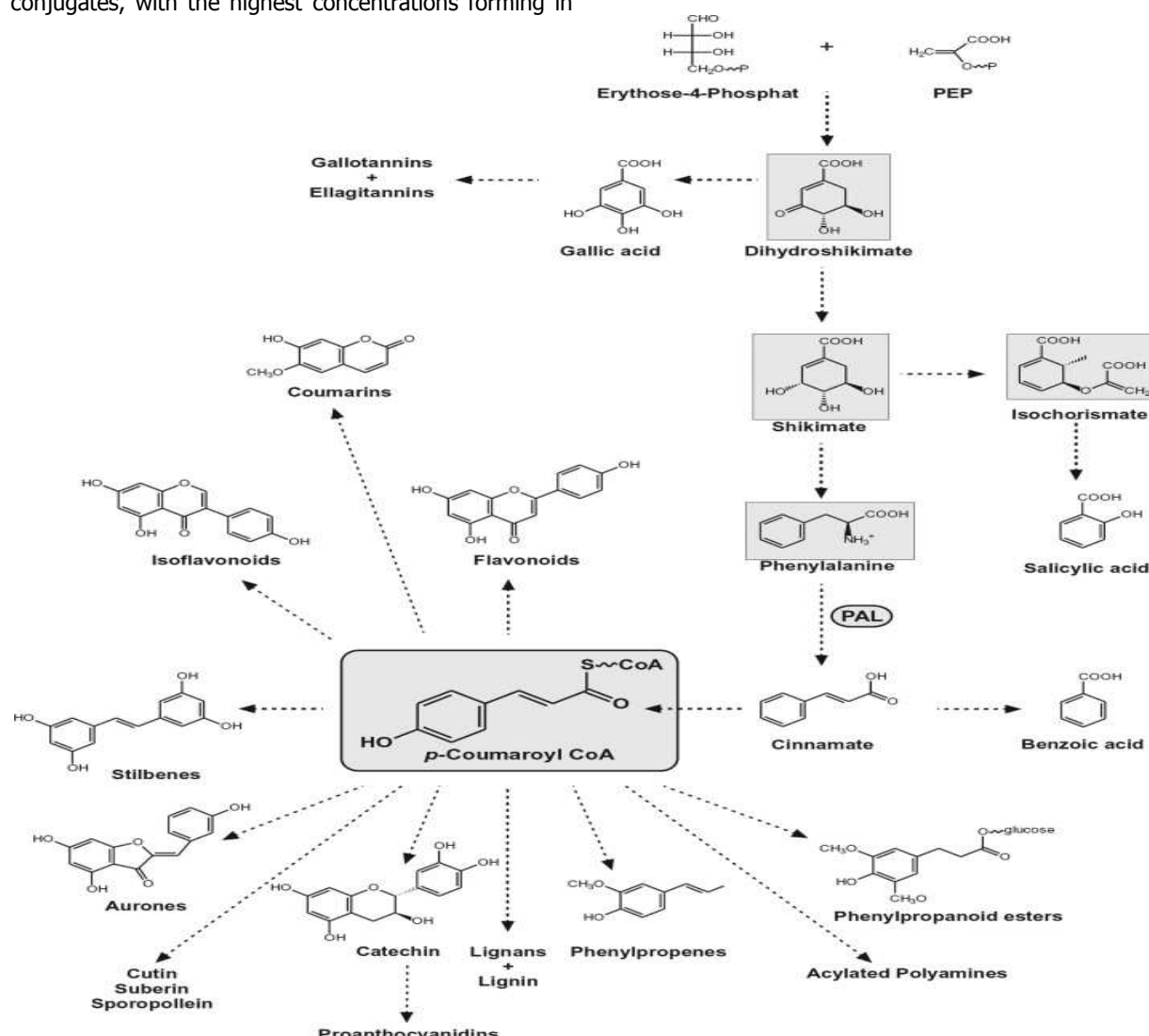


Figure 6: Diversification of Phenylpropanoids Based on the General Phenylpropanoid Pathway.

The metabolites of the shikimate pathway and the central metabolite, 4-coumaroyl CoA, are shaded in gray (Vogt, 2010).

Instead, the release of BA from a preformed BA conjugate induces a soluble cytochrome P_{450} monooxygenase (BA2-H) that converts BA to SA. BA2-H enzyme activity is strongly induced before the appearance of the HR. However, in *Arabidopsis* and other species, the pre-existing BA conjugate may be

absent. In these cases, increased SA levels require increases in PAL activity. Interestingly, oxidative stress caused by ozone or ultraviolet light also triggers SA biosynthesis in tobacco, perhaps by chemical release of BA from its conjugated form (Perpetua *et al.*, 1996).



Jasmonic acid (JA) and Ethylene mediated defence

Overlapping requirements for jasmonate, ethylene and camalexin in resistance are obvious. Several independent analyses have now established a requirement for the plant wound response regulator, Jasmonic Acid, in defences against certain pathogens. The involvement of another plant hormone, ethylene, in plant-pathogen interactions has also been vigorously debated. Recently, however, it has become evident that participation of ethylene may lie more in the control of disease symptom expression than in determining absolute plant resistance or susceptibility phenotypes (Perpetua *et al.*, 1996). For example, reduced ethylene-sensitive soybean mutants produced less severe chlorotic symptoms when challenged with virulent strains of *P. syringae*, whereas virulent strains of the fungi *Septoria glycines* and *Rhizoctonia solani* caused more severe symptoms.

Phytoalexins

Phytoalexins are low molecular weight, lipophilic, antimicrobial compounds that accumulate rapidly around sites of incompatible pathogen infections and in response to an extensive array of biotic and abiotic elicitors. Phytoalexin biosynthesis occurs after a diversion of primary metabolic precursors into novel secondary metabolic pathways. This diversion often arises from the de novo induction of enzymes, such as PAL, that control key branch points in the biosynthetic pathway (Solomon *et al.*, 2004). However, because the synthesis of most phytoalexins requires the activity of numerous enzymes, highly coordinated signalling events must be required in the attacked cells to establish successfully this type of defence response (Gomez *et al.*, 2009). Interestingly, common sequence elements have been identified in the promoters of several genes encoding enzymes required for different steps in the biosynthesis of flavonoid Phytoalexins (Bagga and Straney, 2000).

Various sugars (sucrose, glucose and fructose) acting as endogenous signals, have been reported to regulate the biosynthesis and accumulation of phytoalexins (Formela *et al.*, 2014). Also, over expression of non-expressor of pathogenesis-related genes which play a critical role in the systemic acquired resistance was reported to induce the biosynthesis of the cotton phytoalexin gossypol (Parkhi *et al.*, 2010). The efficaciousness *in vivo* of Phytoalexins to reduce green mold symptoms caused by *Penicillium digitatum* on oranges was reported (Sanzani *et al.*, 2014). In the same way, phenolic Phytoalexins such as resveratrol, scopoletin and umbelliferones significantly inhibited the growth of *Penicillium expansum* and patulin accumulation in apples (Sanzani *et al.*, 2009). Knowledge of the regulatory mechanisms of phytoalexin biosynthesis thus paves the way for metabolic engineering of plants for disease resistance.

However, some phytopathogenic fungi evolved mechanisms of insensitivity or resistance to protect

themselves against phytoalexins. One of such is extruding toxic compounds out of the cell through transporters, conferring them protection against plant defense products. In fungi, the role of ATP-binding cassette (ABC) transporters in the efflux of natural and synthetic toxicants is known (Del Sorbo *et al.*, 2000). In addition, several genes encoding ABC transporters involved fungal virulence on plant hosts and a number of phytoalexins and other toxic compounds induced expression of these fungal transporters (Schoonbeek *et al.*, 2001).

Genetic approaches addressing Phytoalexin and other plant metabolites production for disease resistance have provided direct and indirect proofs of their implication in plant-pathogen interactions. The first report of increased disease resistance resulting from foreign phytoalexin expression in plant was carried out by transfer of grapevine stilben synthase (STS) genes (*Vst 1* and *Vst 2*) into tobacco [77]. Introduction of these two genes confer higher resistance to *B. cinerea*. Subsequently, a number of transformations were completed in alfalfa, rice, barley, wheat and tomato using the same STS genes or those from other plant origins, conferring resistance to various pathogens (Jeandet *et al.*, 2013). Thus, phytoalexins could act as determinant factors in the expression of the defense mechanisms of plants against phytopathogenic microorganisms

CONCLUSION

The growing evidence that innate immunity as confers by PTI and ETI and RNA silencing function are known in natural defense of plants against pathogens. In order to break through these plant defense line and establish infection in susceptible hosts, pathogens have evolved effectors with a primary function to suppress both PTI/ETI innate responses and RNA silencing. However, in most resistant hosts (resistant plants) there is presence of protein which recognized the microbial effectors or Avr protein, activate complex mechanism (ETI/PCD) thereby developing resistance to pathogens. In case of viral pathogen, the effectors may be protein or viral RNA-based. Likewise, innate immunity may be suppressed or silenced by effectors or RNA that serves as a decoy engaging critical components of the silencing machinery. There is considerable conservation of defense signaling mechanisms among plant species because several different classes of R genes also confer resistance when expressed in heterologous plant species. As a result of continuous coevolution between plant and pathogen, a wealth of plant perception systems for microbe-derived molecules has been shaped that reliably fulfills roles in mediating the establishment of plant immunity. Therefore, exciting times lie ahead with several R genes cloned. But do different R proteins activate distinct resistance mechanisms? It still is a big question that require in-depth understanding of the population biology of pathogen effectors, and their co-evolving host genes.



REFERENCES

- Akeda, Y. and Galan, J.E. (2005). Chaperone release and unfolding of substrates in type III secretion. *Nature* 437: 911–915.
- Andersen, P. (2001). The future world food situation and the role of plant diseases. *The Plant Health Instructor*. DOI: 10.1094/PHI-1-2001-0425-01
- Bagga, S., and Straneys D. (2000). Modulation of cAMP and phosphodiesterase activity by flavonoids which induce spore germination of *Nectria haematococca* MP VI (*Fusarium solani*). *Physiol. Mol. Plant Pathol.* 56:51–61.
- Cessna, S., Sears, V., Dickman, M. and Low, P. (2000). Oxalic acid, a pathogenicity factor for *Sclerotinia sclerotiorum*, suppresses the oxidative burst of the host plant. *Plant Cell*, 12:2191–2200.
- Cessna, Kim, J., Ann T. and Taylor, S. (2013). Cytosolic Ca^{2+} pulses and protein kinase activation in the signal transduction pathways leading to the plant oxidative burst. *Journal of Plant Biology*, 46: 215
- Del Sorbo, G., Schoonbeek, H. J. and de Waard, M.A. (2000). Fungal transporters involved in efflux of natural toxic compounds and fungicides. *Fungal Genet. Biol.* 30: 1–15.
- Doehlemann, G., Berndt, P. and Hahn, M. (2006). Different signalling pathways involving a G α protein, cAMP and a MAP kinase control germination of *Botrytis cinerea* conidia. *Mol. Microbiol.* 59:821–835.
- Fillinger, S., Chaverroche, M. K., Shimizu, K., Keller, N. and d'Enfert, C. (2002). cAMP and RAS signalling independently control spore germination in the filamentous fungus *Aspergillus nidulans*. *Mol. Microbiol.* 44:1001–1016.
- Formela, M., Samardakiewicz, S., Marczak, L., Nowak, W., Narozna, D., Waldemar, B., Kaspruwicz-Maluski, A. and Morkunas, I. (2014). Effects of endogenous signals and *Fusarium oxysporum* on the mechanism regulating genistein synthesis and accumulation in yellow lupine and their impact on plant cell cytoskeleton. *Molecules*, 19: 13392–13421
- Freeman, B. C. and Beattie, G. A. (2008). An overview of plant defence against pathogen and herbivores. *The Plant Health Instructor*. DOI: 10.1094/PHI-1-2008-0226-01
- Gómez, G., Martínez, G. and Pallás, V. (2009) Interplay between viroid-induced pathogenesis and RNA silencing pathways. *Trends Plant Sci.* 14: 264–269.
- Guimaraes, R. L. and Stotz, H. U. (2004). Oxalate production by *Sclerotinia sclerotiorum* deregulates guard cells during infection. *Plant Physiol.* 136:3703–3711.
- Idnurm, A. and Howlett, B. J. (2002). Isocitrate lyase is essential for pathogenicity of the fungus *Leptosphaeria maculans* in canola (*Brassica napus*). *Eukaryot. Cell* 1:719–724.
- Jeandet, P., Clément, C., Courrot, E. and Cordelier, S. (2013). Modulation of phytoalexin biosynthesis in engineered plants for disease resistance. *Int. J. Mol. Sci.*, 14: 14136–14170.
- Jonsthan, D., Jones G. and Jeffery, L. (2006). The plant immune system. *Nature* 444: 323–329
- Jones, J. D. G. and Dangl, J. L. (2006). Plant Immune System. *Nature*, 444: 323–329 (doi:10.1038/nature05286)
- Kim, S., Ahn, I., Rho, H. and Lee, Y. (2005). *MHP1*, a *Magnaporthe grisea* hydrophobin gene, is required for fungal development and plant colonization. *Molecular Microbiology*, 57: 1224–1237.
- Lengeler, K. B., Davidson, R. C., D'Souza, C., Harashima, T., Shen, W. C., Wang, P., Pan, X., Waugh, M. and Heitman, J. (2000). Signal transduction cascades regulating fungal development and virulence. *Microbiology and Molecular Biology Review*, 64:746–785.
- Liao, D. I., Basarab, G., Gatenby, A. A. and Jordan, D. B. (2000). Selection of a potent inhibitor of trihydroxynaphthalene reductase by sorting disease control data. *Bioorg. Med. Chem. Lett.*, 10:491–494
- Nurnberger, T., Brunner, F., Kemmerling, B., and Piater, L. (2004). Innate immunity in plants and animals: striking similarities and obvious differences. *Immunology Review*, 198: 249–266.
- Nuss, D. L. (1996). Using hypoviruses to probe and perturb signal transduction processes underlying fungal pathogenesis. *Plant Cell*, 8:1845–53
- Orke, E. C., Dehne, H. W., Schonbeck, F. and Weber, A. (1994). *Crop production and crop protection: Estimated losses in major food and cash crops*. Elsevier, Amsterdam. pp 14–21
- Oshero, N. and May, G. (2001). The molecular mechanisms of conidial germination. *FEMS Microbiology Letters*, 199:153–160.
- Parkhi, V., Kumar, V., Campbell, L.M., Bell, A.A., Shah, J. and Rathore, K.S. (2010). Resistance against various fungal pathogens and reniform nematode in transgenic cotton plants expressing Arabidopsis *NR1*. *Transgenic Res.*, 19: 959–975.
- Perpetua, N. S., Kubo, Y., Yasuda, N., Takano, Y. and Furusawa, I. (1996). Cloning and characterization of a melanin biosynthetic THR1 reductase gene essential for appressorial penetration of *Colletotrichum lagenarium*. *Molecular Plant-Microbe Interaction*, 9:323–329.



- Pieterse, C. M. and Van-Loon, L. (2004). NPR1: the spider in the web of induced resistance signalling pathways. *Current Opinion in Plant Biology*, 7:456–464
- Pooggin, M. M., Ryabova, L. A., He, X., Fütterer, J. and Hohn, T. (2006). Mechanism of ribosome shunting in Rice tungro bacilliform pararetrovirus. *RNA*, 12: 841–850.
- Pruss, G. J., Lawrence, C. B., Bass, T., Li, Q. Q., Bowman, L. H. and Vance, V. (2004). The potyviral suppressor of RNA silencing confers enhanced resistance to multiple pathogens. *Virology*, 320: 107–120.
- Sanzani, S. M., de Girolamo, A., Schena, L., Solfrizzo, M., Ippolito, A. and Visconti, A. (2009). Control of *Penicillium expansum* and patulin accumulation on apples by quercetin and umbelliferone. *Eur. Food Res. Technol.* 228: 381–389.
- Sanzani, S., Schena, L., and Ippolito, A. (2014). Effectiveness of phenolic compounds against citrus green mould. *Molecules*, 19: 12500–12508
- Schoonbeek, H. J., del Sorbo, G., and de Waard, M. A. (2001). The ABC transporter BcatrB affects the sensitivity of *Botrytis cinerea* to the phytoalexin resveratrol and the fungicide fenpiclonil. *Mol. Plant-Microbe Interact.* 14: 562–571.
- Sexton, A. C. and Homolelt, B. J. (2006) Parallels in fungal pathogenesis on plant and animal hosts. *Eukaryotic cell*. 5(15): 1941-1949
- Solomon, P., Lee, R., Wilson, T. and Oliver, R. (2004). Pathogenicity of *Stagonosporano dorum* requires malate synthase. *Molecular Microbiology*, 53:1065–1073.
- Strange, R. N and Scott, P. R. (2005). Plant disease: a threat to global food security. *Annual Revision of Phytopathology*, 43: 83-116
- Talbot, N., Kershaw, M. J., Wakley, G. E., De Vries, O. M. H., Wessels, J. G. H. and Hamer, J. (1996). *MPG1* encodes a fungal hydrophobin involved in surface interactions during infection-related development of *Magnaporthe grisea*. *Plant Cell*, 8:985–999.
- Thomma, B. P. H. Nurmberger, T. and Joosten, M. H. J. (2011). Of PAMPs and Effectors: the blurred PTI-ETI. *The Plant Cell*, 23(1): 4-15
- Vogt, T. (2010). Phenylpropanoid biosynthesis. *Molecular Plant*, 3(1): 2-20
- Wang, Z. Y., Thornton, C. R., Kershaw, M. J., Debaio, L. and Talbot, N. J. (2003). The glyoxylate cycle is required for temporal regulation of virulence by the plant pathogenic fungus *Magnaporthe grisea*. *Molecular Microbiology*, 47:1601–1612.
- Winnenburg, R., Baldwin, T. K., Urban, M., Rawlings, C., Köhler, J. and Hammond-Kosack K. E (2006). PHI-base: a new database for pathogen host interactions. *Nucleic Acids Research*, 34:D459–D464.
- Zverena, A. S. and Pooggin, M. M. (2012). Silencing and innate immunity in plant defence against viral and non-viral pathogens. *Virus*, 4: 2578-2579 (doi:10.3390/v4112578)