INTRODUCTION

Phytopathogens have coexisted with their host plants from the beginning of their existence. Plant pathogens rely entirely on their hosts for shelter and nutrients to survive. This total reliance has led to a constant attack of host plants by phytopathogens, resulting in physiological dysfunction in host plants, leading to a diseased condition (Shittu et al., 2017). On the other end of the spectrum, host plants have developed receptors to recognize the presence of pathogens and PAMPs (Pathogen-Associated Molecular Patterns) from the pathogens. In a counter attack, host plants have developed mechanisms for the suppression of ETI. In some plant-pathosystems, the plants are winning, while in others, the pathogens are winning. Phytopathological research should therefore be directed towards assisting susceptible plants to defeat phytopathogens, in order to ensure food security.

Keywords: Arms race, Phytopathogen, Strategies, MAMP, PAMP, PTI, ETI

ARMS RACE BETWEEN PLANTS AND PHYTOPATHOGENS

During evolutionary periods, phytopathogens have learnt to rely entirely on plants for shelter and nutrients. This total reliance has led phytopathogens to develop strategies (arms) to constantly attack host plants. Plants have also developed strategies (arms) to defend themselves against pathogen attack, thus leading to constant and dynamic attack-counter attacks, known as “arms race”. This “arms race” plays a vital role in the evolution of new and well adapted species of phytopathogens and plants.

Pathogen attack: Evolution of physical and biochemical weapons by phytopathogens

Phytopathogens have developed strategies to break the protective barrier of host plants. Pathogens that penetrate the host plant directly exert a mechanical force on the host surface to enhance their penetration. For example, the formation of appressoria by some fungal phytopathogens such as Colletotrichum, Verticillium and the powdery mildew fungi enhanced the penetration of the host plant (Agrios, 2005). The successful penetration of the host plant is immediately followed by colonization, thereby resulting to a diseased condition. Accumulation of melanin in the apoplastic wall of some fungi such as Cochliobolus, Colletotrichum, Gaumannomyces and Magnaporthe enhances the penetration of the host plant (Agrios, 2005). In Magnaporthe griseae, single gene mutations at loci encoding melanin biosynthetic enzymes resulted in non-melanized appressorium that are unable to generate turgor, thereby making the organism non-pathogenic (Howard and Valient, 1996; Money and Howard, 1996). Pathogenicity of a non-melanin producing albino mutant of the cucumber pathogen, Colletotrichum lagenarium, could be restored by transformation with a melanin biosynthetic gene (Kubo et al., 1991). Also, appressoria from melanin mutant strains of Magnaporthe griseae as well as wild-type appressoria after treatment with a melanin synthesis inhibitor displayed much lower glycerol levels (De Jong et al., 1997). Therefore, glycerol appears to be the major compound generating the turgor pressure and melanin deposition is required for efficient build-up of turgor by rendering the appressorial walls impermeable to glycerol. Parasitic nematode such as Meloidogyne javanica that causes root knot diseases physically penetrates the host surface by thrusting its stylet to and fro (Agrios, 2005). The nematode first sticks to the plant surface by the pressure that develops when its fused lips contact with the host plant. Unlike fungal phytopathogens that produce appressoria, bacteria phytopathogens are unable to penetrate the host plant directly, but rather enter the host usually through natural openings such as the stomata, and they also secrete cell wall-softening and degradative enzymes.

Phytopathological weapons of phytopathogens include secretion of enzymes, growth regulators, polysaccharides and toxins (Shittu et al., 2017). Enzymes such as cutinases, cellulases, pectolytic enzymes and xylanase are secreted by phytopathogens to enhance the penetration of the host plant (Agrios, 2005). The secretion of enzymes seems to be the most important attack strategy (arms) in some diseases such as the soft rot, caused by Erwinia carotovora (Agrios, 2005). Growth regulators are synthesized endogenously by host plants and they are effective at minute concentrations. Elevated levels of these growth factors caused by pathogens often create an imbalance in the hormonal system of the host plant, thereby bringing about abnormal growth responses incompatible with the healthy development of a plant (Agrios, 2005). The most important groups of plant growth regulators that are implicated in plants diseases include auxins, gibberellins,
cytokinins and ethylene. Increased auxin levels have been reported in plants infected with some phytopathogens such as A. tumefaciens (causing crown gall), Ustilago maydis (causing corn smut), and Fusarium oxysporum f. cubense (causing banana wilt) (Agrios, 2005). These increases in growth regulators could be attributed to direct production by the pathogen, through the action of a regulatory system or inhibition of enzymes such as IAA oxidase by the pathogen (Agrios, 2005). The foolish seedling disease of rice, in which rice seedlings infected with the fungus Gibberella fujikuroi grow rapidly and become abnormally taller than the healthy plant could be attributed to a considerable extent, to the gibberellin secreted by the pathogen (Agrios, 2005). Ethylene is produced by several plant pathogenic fungi and bacteria such as Ralstonia solanacearum (Agrios, 2005).

Infection by phytopathogens using physical and biochemical weapons is aided by the inability of the host plants to recognize the presence of pathogen-associated molecular patterns (PAMPs). These PAMPs are recognized by membrane receptive sensors that are evolutionarily period and also give the organism an adaptive advantage (Boyd et al., 2018). These structures are also referred to as microbe-associated molecular patterns (MAMP) because they could be inherent in non-pathogenic microbes. Examples of PAMPs include bacterial flagellin, bacterial elicitation factor (EF-Tu), glucan and glycoproteins from oomycetes, chitin from fungal cell wall, lipopolysaccharides of Gram-negative bacteria and chitin and cold shock proteins, with the latter two known as orphan PAMPs (Boyd et al., 2018). Some PAMPs are able to suppress defence response in the host plant, for example, lipopolysaccharide (LPS) suppresses plant defence by chelating calcium (Ca++) ions which plays a very important role in host plant defence and signal transduction (Newman et al., 2007).

Plant counterattack: Development of PAMP-triggered immunity (PTI)

In a counter attack, host plants have developed receptors known as pattern recognition receptors (PRRs) localized in the plasma membrane to recognize or perceive the presence of PAMPs in order to activate a defence response (Boller and Felix, 2009; Zipfel, 2016). Examples of PRRs include flagellin sensitive 2 (FLS2), elongation factor receptor (EFR), elicitor binding protein and glucan binding protein which recognize a conserved epitope of flagellin (flg22), bacterial elongation factor (EF-Tu), chitin and glucan respectively (Zhang and Zhou, 2010). The flagellin two are Lecine-Rich-Repeat (LRR) receptor-like kinases that are capable of auto phosphorylation (Zhang and Zhou, 2010). Plants possessing the appropriate PRR are able to detect the presence of the pathogen at very low concentrations (Boller and Felix, 2009). Recognition of PAMPs serves as an early system warning for the presence of a potential pathogen and it is followed by the activation of a form of immunity known as PAMP-triggered immunity (PTI). PTI is the first line of innate immunity in the host plant defence that is activated following PAMP or pathogen perception and it is also known as basal resistance (Nicaisse et al., 2009). Different plant species respond to different PAMPs. For example, tobacco responds to cold-shock protein, while Arabidopsis does not, and only members of the Brassicaceae have so far been shown to respond to EF-Tu (Felix and Boller, 2003). The possibility of engineering plants to possess different PRRs that recognize different PAMPs could therefore play a role in plant improvement against phytopathogens. The most well-known PAMP--PRR system involves the perception of a stretch of the bacterial flagellin through a 22-amino acid epitope known as flg22 by the cognate PRR, FLS2 (Gomez-Gomez and Boller, 2000). A good example of a plant that uses this mechanism to defend itself against pathogen attack is Arabidopsis plant. A mutant Arabidopsis plant in FLS2 is more susceptible to infections with the pathogenic bacterium, Pseudomonas syringae –pv. tomato DC3000 (Pto DC3000), when surface-inoculated (Zhang et al., 2010; Zipfel et al., 2004).

Mechanisms of PAMP triggered immunity (PTI) and the response of host plants to PAMPs recognition

Flagellin perception is the most characterized in plants. It is recognized by a leucine-rich repeat receptor like kinase known as flagellin sensitive 2 (FLS2) localized on the plasma membrane of the host plant (Boyd et al., 2018). The binding of bacterial flagellin to the extracellular domain of FLS2 leads to activation of signaling cascades that result in the activation of a defence response in the host plant (Pieterse et al., 2009). FLS2 activation involves its association with other proteins including BR11 associated kinase 1 (BAK1) and localization to less mobilized areas of the cytosol through the plasma membrane in a ligand-dependent manner to activate PTI (Ali and Reddy, 2008). The defense responses that occur during PTI include molecular, morphological and physiological changes. Early changes occurring within seconds to minutes include ion-flux across the plasma membrane (Jabs et al., 1997), an oxidative burst (activation of a cluster of reactive oxygen species, ROS, largely produced by the activity of the membrane-localized NADPH oxidases), mitogen activated protein (MAP) kinase activation and protein phosphorylation (Shen et al., 2017). This is followed by transcriptional reprogramming of some genes most especially the defence-related genes including the pathogenesis-related genes and the signal transduction genes that leads to defence-related protein accumulation and stomatal closure (Schwessinger, and Zipfel, 2008). Stomata provide a major entry point for many plant pathogens and A. thaliana stomata has been shown to close within an hour in response to PAMP (Melotto et al., 2006). During PAMP-triggered immunity (PTI), mitogen activated protein kinase (MAPK) activation leads to the phosphorylation of the WRKY transcription factor, DREB2A, Arabidopsis (Bhalerao and Somssich, 2009). This phosphorylation leads to the activation of the WRKY transcription factor, thus leading to increase in the expression of the associated genes.

The ability of the host plant to induce stomatal closure following PAMP perception is an essential response to the pathogen, since it decreases the water potential of the guard cells thereby increasing the water potential (Melotto et al., 2006). This leads to the flaccidity of the guard cells, thus leading to stomatal closure. Stomatal closure following PAMP perception is mediated by ABA signaling to the guard cells (Melotto et al., 2006).

Pathogen attack: Evolution of secretion systems and effectors to suppress PAMP-triggered immunity

As the “arms race” continued, successful pathogens have evolved secretion systems and effectors proteins to suppress PTI, thus leading to effector-triggered susceptibility in the host plant (Henry et al., 2012). Examples of phytopathogens that use this strategy to infect the host plant include Pseudomonas syringae pv lycopersici and Agrobacterium tumefaciens. There are four basic types of secretion pathways in plant pathogenic bacteria, Type I, II, III, and IV. The type I secretion system (TTSS) is used by phytopathogenic bacteria to deliver effectors to the host extracellular space, whereas type III and IV pathways can deliver effectors directly into host cell (Bhat and Shahnaz, 2014). With the aid of the latter two pathways, phytopathogens are able to deliver all the aforementioned biochemical weapons into the host plant to cause a disease (Bhat and Shahnaz, 2014). The type III secretion system is encoded by the hrp genes (hypersensitive response and pathogenicity genes) and it is the most studied because of its importance in pathogenicity (Wei and Colliner, 2017). The secretion via this pathway is a one step process with no intermediary in the periplasm. Examples of TTSS effectors include HopA1 and HopG1 secreted by Pseudomonas syringae (Bhat and Shahnaz, 2014). The Vir D2/T-DNA nucleoprotein complex from A. tumefaciens is transported directly into the host cell through the type IV pathway and it is the only pathway that is known to translocate both proteins and nucleic acids (Bhat and Shahnaz, 2014).

Pathogens secrete molecules that manipulate host cell structure and function when they infect the host plant. Some of these molecules are referred to as effectors (Bai et al., 2016). These effectors are derived from the expression of the avr genes. Effectors are secreted into the host plants from pathogen secretion systems and they could be apoplastic or cytoplasmic, depending on whether they are secreted to the host extracellular space or cytoplasm, respectively (Bhat and Shahnaz, 2014). When effectors enter the host plant cell, they can either act as toxins or elicitors (Bhat and Shahnaz, 2014). They may tryp the wire by acting as elicitors if the host plant has a cognate resistance gene that encodes a resistance protein, thus activating a strong hypersensitive reaction that follows the gene-for-gene concept (Flor, 1955 and Jones and Dangl, 2006).

Mechanisms of effector-triggered susceptibility

Effectors enhance the virulence of the pathogen by suppressing the host defence response and also increasing the availability of nutrients to the pathogen. They may act by carrying out enzymatic activity or binding to other proteins to modify their function. Effector traffic to different cell compartments upon entering the host cell and they may have more than one target in the host plant. AvrPtt2 is a TTSS effector with proteolytic activity against at least five Arabidopsis proteins (Takemoto and Jones, 2005). Some effectors proteins such as Avr2, Avr4, and ECP6 secreted by the tomato fungal pathogen Cladosporium fulvum act in the extracellular space where they interfere with apoplastic plant defences (Kamoun, 2006). Phytopathogens must first overcome the apoplastic immunity before a successful colonization of the host plant to cause a disease condition. The apoplast therefore serves as a battle ground in plant-pathogen interaction (Gupta et al., 2015). Some cytoplasmic effectors such as Xanthomonad transcription activator-like (TAL) effectors, Phytoplasma SAP11, and Phytophthora Cinklers (CRNs) are capable of being localized in the nucleus after entering the host plant and the help of the nuclear localization signals that they possess, thus altering the transcription of defence-related genes during infection (Bai et al., 2009; Mak et al., 2013; Schornack et al., 2010 and Van den et al., 1996). The type-III effector, HopG1, secreted by P. syringae targets plant mitochondria, whereas HopH1 is secreted by P. syringae and HopH2 targets plant mitochondria (Bai et al., 2010 and Jelenska et al., 2007). HopG1 targets mitochondria; disrupt plant development and suppresses plant innate immunity (Block et al., 2010). HopZ1a disorders microtubules network, thereby interfering with the plant secretory pathway and suppressing plant defence brought about by the cell wall. (Bhat and Shahnaz, 2014). TSSS effectors of the plant pathogenic bacteria Pseudomonas syringae and Xanthomonas campestris have been reported to target secretory pathways, which indicates that protein trafficking plays a significant role in plant innate immunity (Wang et al., 2016).
Protein trafficking helps to transport the necessary molecules (arms) needed to protect the host plant following pathogen perception (Thordal-Christensen, 2009). Therefore, one of the virulence strategies of an invading phytopathogen is to interfere with protein trafficking. _Pseudomonas syringae_ secretes HopM1 which is restricted to the trans-PLASMA POLAR BODY (PPOB) pathway. Death in Arabidopsis and thereby facilitates bacterial entry into the host plant (Melotto et al., 2006). This suggests that the stomata play an important function in plant innate immunity against bacterial invasion. _Xanthomonas_ effectors of AvrBs3 family are known to induce cellular division and enlargement in susceptible host plants (Boch and Bonas, 2010). Other morphological changes include galls and witches broom induced by _Agrobacterium_ spp. and other bacteria such as _phytoplasma_ respectively (Christie, 2004 and Hoshi et al., 2009). _Pseudomonas syringae_ secretes effectors such as HopU1, AvrRpt2, AvrB, HopAO1, HopE1, HopAM1, AvrPm1, AvrPtoB and HopXls which are capable of inhibiting PAMP-induced cell death and it may also negatively alter defence gene expression (Cui et al., 2009).

### Plant counter attack: Development of effector-triggered immunity

Continuing the arms race, the plants never surrender to the attempted devastating effect of the pathogens. Some successful and well-adapted plants have evolved another set of receptors known as intracellular resistance proteins encoded by the _R_ genes to recognize pathogen effectors (Cui et al., 2015). An example of a plant that uses this strategy to defend itself against pathogen attack is _Arabidopsis_ (Zhang et al., 2010). These resistance proteins are immune-receptors characterized by two domains; a nucleotide binding site (NBS) and leucine-rich repeats (LRR). The NBS domain located approximately in the middle of the R protein comprises several conserved amino acid motifs that are believed to function in ATP hydrolysis (Tameling et al., 2002). The LRR domain comprises a core of about 26 amino acid repeats found at the C-terminal end of the protein and it is predicted to modulate direct or indirect interactions between the _R_ protein and its corresponding effector molecule (Pieterse et al., 2006). Pathogen effectors are recognized in a specific manner by intracellular resistance proteins which could be direct or indirect. The direct recognition follows the ligand receptor model, where the _R_ gene products act as receptors that directly interact with the _avir_ gene products (effectors) (Pieterse et al., 2009). This interaction activates a resistant reaction that follows the gene-for-gene concept. Indirect recognition of effector proteins could follow either the guard model or the decoy model. According to the guard model, the effector target is monitored by the _R_ protein and these results in the change of the target, therefore, activating the resistance proteins to trigger a hypersensitive reaction in the host plant as observed in _Pseudomonas syringae_ (Dang and Jones, 2001). The perception of AvrPto effector protein produced by _Pseudomonas syringae_ by the tomato proteins, Prp and Prf is in accordance with the guard model (Tang et al., 1996). The decoy model is similar to the guard model, however, the manipulation of the guarded effector target by the effector facilitates pathogen fitness in the absence of the corresponding _R_ gene (Van Der Hoorn and Kamoun, 2008). The recognition of the effector protein by the cognate resistance gene prevents the blockage of PAMP signaling, thus activating effector-triggered immunity (ETI) in the host plant, and hence turning the table on the pathogen by making the effectors liabilities (Pieterse et al., 2009). Therefore, the presence of effectors in phytopathogens could either be an advantage or disadvantage to the pathogen depending on the absence or presence of a cognate resistance protein that recognizes the effector protein. Pathogenesis caused by pathogen effectors can be overcome by the activation of ETI as explained using the gene-for-gene concept (Cui et al., 2015; Flor, 1955). ETI is a stronger form of immunity compared to PTI. ETI may be accompanied by the induction of a hypersensitive response (HR), which is a form of programmed cell death and this is a direct recognition of effectors against biotrophic phytopathogens (Hammond-Kosack and Jones, 1996). The HR causes cell death, which is programmed death, and therefore mediates the defence mechanisms that destroy healthy tissues which it utilizes as a nutritional source and also prevents the further spread of the pathogen (Greenberg, and Yao, 2004). HR also triggers a wide variety of defence responses, which include systemic acquired resistance (SAR), which serves as a warning throughout the plant of the invasion by the pathogen and the initiation of long-distance signalling molecules such as salicylic acid and ethylene (Fu and Dong, 2013). The gene-for-gene concept

Genetic analysis of the interactions between flax (_Linum usitatissimum_) and flax rust (_Melampora lini_) led Herold H Flor to the formulation of a gene-for-gene concept (Flor, 1955). He found that the resistance of flax to specific flax rust strain could be inherited monogenically by the next generation. The gene-for-gene concept proposes that the _avir_ gene products are specifically recognized by the cognate resistance gene product of the host plant to activate a strong defence response known as effector-triggered immunity, thereby making the host plant resistant to the avirulent strain of the pathogen (Nobuta and Meyers, 2005). This type of resistance is also known as cultivar-specific resistance (Agrios, 2005). In rice, the LRR-RR, Xa21 confers resistance to _Xanthomonas oryzae pv oryzae_ strains carrying the _avir_ gene, AvrXa21 (Song et al., 1995). According to the gene-for-gene hypothesis, pathogens may be virulent for several reasons, (a) the pathogen does not encode an avirulent protein, (b) the plant lacks a factor, for example, a resistance protein that would enable it to detect the avirulent protein, and (c) the pathogen and plant respectively lack both the avirulent and the corresponding resistance protein (Nobuta and Meyers, 2005).

### Pathogen attack: Development of mechanisms to suppress ETI

At present, some well-adapted pathogens have developed mechanisms to suppress effector-triggered immunity. One of these mechanisms is the silencing of effector genes by endogenous pathogen _sRNA_ to escape _R_ protein recognition (Wang et al., 2015). In this case, recognition of effector proteins by the cognate resistance proteins activates effector-triggered immunity, thereby making the effectors a liability to the pathogen. Silencing of the pathogen effector gene is a mechanism to escape recognition by resistance proteins, thereby hindering the activation of any immune response and thus making the host plant susceptible. The silencing is sRNA-mediated in a phenomenon known as RNA interference (RNAi) (Das et al., 2014). Some effector genes of _Pseudomonas syringae_ Phytophthora are usually located in the transposable element (TE) rich regions that give rise to sRNAs (Ventukuri et al., 2012; Whisson et al., 2012). An example of a pathogen that uses this mechanism to infect the host plant is _Phytophthora sojae_. Qutob et al. (2013) observed sRNA mediated silencing of an effector gene _PsAvr3a_ in a virulent strain of _Phytophthora sojae_. When infecting plants carrying the _Rps5a_ resistance gene; but this silencing was absent in the avirulent strain, _P7076_. Another attack strategy developed by pathogens to silence host immune genes is by sRNA effectors (cross-kingdom RNAi) (Wang et al., 2015). Some phytopathogens have evolved mechanisms for silencing of the host immune genes in order to enhance infection. They achieve this by producing sRNA effectors, which they secrete into the host plants to silence their defence-related genes (Wang et al., 2015). The sRNA effectors are small interfering RNA molecules secreted by the pathogen to silence the immune genes of the host plant in a phenomenon known as RNA interference (RNAi). This type of RNAi that describes a phenomenon in which non-coding RNA molecules to produce an RNA trigger that moves into a recipient organism of different kingdom to cause gene silencing is known as cross-kingdom RNA interference (Wang et al., 2015). Cross-kingdom RNAi indicates that gene silencing signal can travel extracellularly over long distance, even across the cell wall in the case of plant-pathogen interaction. _Botrytis cinerea_ is a very virulent pathogen that produces _sRNA effector_ to silence the host immune gene (Weiberg et al., 2013). Cross-kingdom RNAi has also been observed in the interaction between _Verticillium dahlia_ and the model plant _Arabidopsis thaliana_ (Wang et al., 2015).

### CONCLUSION

The \"arms race\" between plants and phytopathogens is an ongoing process that has been in existence over evolutionary periods. The plants seem to be winning in some plant-pathosystems, while in others, the pathogens are winning. Research efforts in the field of phytopathology, such as screening for resistance gene and disease tolerant plants, should therefore, be geared towards assisting the susceptible plants to overcome the deleterious effects of phytopathogens in order to ensure food security.

### REFERENCES


