

Review

Host Pathogen Interaction at the Plant Cell Wall

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Plants produce various defense compounds as a response to pathogen infection. Pathogen also produces many enzymes to establish itself in the host cell. The result is an interaction between the host and the pathogen at the host cell wall, a highly dynamic structure. The host defense responses includes structural as well as biochemical responses, the details of which have been reviewed here.

Keywords: Plant defense response, cell wall appositions, defense barrier; reactive oxygen species

INTRODUCTION

Plants are ubiquitous green factories on earth. Unlike mammals they lack mobile defender cells and a somatic adaptive immune system. Instead, they rely on the innate immunity of each cell and on systemic signals emanating from infection sites (Jens and Christina, 2009; Amil-Ruiz et al., 2011). Plant pathogens adopt diverse life strategies and can be broadly divided into those that kill the host and feed on the contents (necrotrophs) and those that require a living host to complete their life cycle (biotrophs). Microbial necrotrophy is often accompanied by production of toxins (AbuQamar et al., 2006). Pathogenic bacteria proliferate in intercellular spaces (apoplast) after entering through gas (stomata) or water (hydathodes) or gain access via wounds (Melotto et al., 2008). Nematodes and aphids feed by inserting a stylet directly into a plant cell (Bos et al., 2010) whereas fungi directly enters epidermal cells or extend hyphae on top of, between or through plant cells. Pathogenic and symbiotic fungi have haustoria. These diverse pathogen classes all deliver effector molecules (virulence factors) into the plant cell to enhance microbial fitness (Dangl and Jones, 2001; Craig et al., 2009; Amil-Ruiz et al., 2011).

Plant cell wall is a highly dynamic structure that besides providing mechanical support needs to respond to various environmental and developmental cues and fulfils important functions in signaling events, the defence against biotic and abiotic stresses and growth

(Bosch et al., 2011). It also constitutes a reservoir of antimicrobial compounds and is a source of signaling molecules (Carpita and McCann, 2000; Hernández-Blanco et al., 2007; Almagro et al., 2009).

Plant cell walls are divided into two categories: primary walls, that surround growing cells and secondary walls that are thickened structures containing lignin and surrounding specialised cells (Keegstera, 2010). Structurally three layers may be found in plant cell walls- Middle lamella, Primary cell wall and Secondary cell wall (Buchanan et al., 2000). The main components of the primary cell wall of dicots are a cellulose-xyloglucan network which is the main load-bearing structure that is embedded in a matrix of pectic polysaccharides (Eckardt, 2004). The pectic matrix has three major components- homogalactouronan, RG I and RG II. In addition to effect on wall strength and cell adhesion, pectins also control wall porosity (Baron-Epel et al., 1988, Liberman et al., 1999; Diet et al., 2006; Cosgrove, 2005), which in turn regulates the mobility of cell wall modifying proteins and thus, cell wall expansion (Willats et al., 2001; McCartney et al., 2003).

Virulence exerted by pathogens

To be successful in attacking a host cell, a pathogen must pass the outer barrier of a cell. A simple but major pathogenic mechanism in plants involve cell wall degradation by a battery of polysaccharidases secreted by pathogens. Most of the degradative enzymes are glycoside hydrolases, which degrade the cellulose and pectate matrices by the addition of water to break the

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glycosidic bonds. The plant cell wall is composed of two types of polysaccharide matrices: the pectate network and the cellulose network (Herron et al., 2000). The pectate network consists of the smooth region composed of homogalacturonans and the hairy region composed of highly branched rhamnogalacturonans.

Enzymes, which degrade the pectate network, belong to two classifications: glycoside hydrolases and polysaccharide lyases. Glycoside hydrolases incorporate a water molecule via a general acid catalysis during the cleavage of the glycosidic bond between the two saccharide units. In contrast, polysaccharide lyases cleave the glycosidic bond via a β -elimination reaction that removes a proton. The final product contains an unsaturated bond between C-4 and C-5 of the saccharide unit at the non-reducing end. Enzymes, which degrade the cellulose network, all function as glycoside hydrolases. Generally, hydrolases have acidic pH optima, using aspartic and glutamic acid groups during catalysis, whereas lyases have basic pH optima, using catalytic amino acids that are still under active investigation (Herron et al., 2000).

In certain pathogens, such as *Erwinia chrysanthemi*, the genetic organization and regulation of many secretory saccharidases have been elucidated (Reverchon et al., 1997). One finding is that many pathogenic organisms secrete multiple isozymes of the same enzyme but the transcription of the genes is often independently regulated (Herron et al., 2000).

Pathogen induced local responses

Hypersensitive response (HR) is one of the most powerful weapons in a plant's arsenal against pathogen attack and is characterized by rapid, localised cell death at the site of infection (Hammond-Kosack and Jones, 1996). This cell death response likely benefits the plant by depriving pathogens of access to further nutrient sources and limiting pathogen proliferation (Kumudini et al., 2001). The HR cell death is often preceded by changes in ion fluxes, oxidative burst and cross-linking of cell wall proteins. Most of the HR is usually accompanied by an increase in salicylic acid (SA) biosynthesis, transcriptional activation of various pathogenesis-related (PR) genes and the establishment of a long-lasting systemic response known as systemic acquired resistance (SAR) (Dangl et al., 1996; Hammond-Kosack and Jones, 1996; Devadas and Raina, 2002; Boyle et al., 2009; Durrant and Dong, 2004). Production of reactive oxygen species (ROS) is associated with HR and is one of the earliest responses of plants to microbial pathogens (Cohn et al., 2001; Torres et al., 2006; de León, 2011).

Evidence indicates hypersensitive cell death is a form of programmed cell death that resembles apoptotic cell death in other organisms (Morel and Dangl, 1997; Tsujimoto and Shimizu, 2005; Mishra et al., 2011).

Morphologically, a key difference between programmed

cell death of plant cells and apoptosis in animals is the absence of engulfment by neighbouring cells in plants (Lam, 2004). Experiments on several *Arabidopsis* mutants with spontaneous cell death that mimic pathogen-induced cell death support the idea that hypersensitive cell death may be controlled by plant's own genetic mechanisms (Greenberg, 1997; Glazebrook, 1999; Greenberg and Yao, 2004; Hofius et al., 2011).

Reactive Oxygen Species (ROS)

Production of ROS is one of the earliest cellular responses following successful pathogen recognition via consumption of oxygen in a so-called oxidative burst (Ashry and Mohamed, 2011). The oxidative burst has been known for more than 30 years in mammals (Wojtaszek, 1997). However, in plants the phenomenon was demonstrated much later (Doke, 1983). ROS molecules have an important role in some physiological processes like plant growth and development (Mendoza, 2011). Apoplastic generation of superoxide (O_2^-), or its dismutation byproduct hydrogen peroxide (H_2O_2), singlet oxygen (O_2) and hydroxyl radical (OH^\cdot) has been documented following recognition of a variety of pathogens (Torres et al., 2006; Mendoza, 2011). Although the primary oxidative burst following pathogen recognition occurs in the apoplast, ROS produced in other cellular compartments may also have functions in defense. High levels of ROS can be produced inside the plant cell as by-products of metabolic processes, especially, light-driven production of ROS as a by-product of photosynthesis (Karpinski et al., 2003; Apel and Hirt, 2004; Gill and Tuteja, 2010).

The different ROS includes H_2O_2 , can act as a local signal for cell death and also as a diffusible signal for the induction of defensive genes in adjacent cells (Alvarez et al., 1998; Torres et al., 2006). O_2^- in living cells exists in equilibrium with its protonated form, the hydroperoxyl radical (O_2H^\cdot). At the physiological level, pH is not very reactive against major macromolecular components of the cell (Michalak, 2006). OH^\cdot is the most reactive species responsible for the irreversible modifications of cellular macromolecules and damage of organelles (Wojtaszek, 1997; Elesak et al., 2007; Galaris et al., 2008; Torres et al., 2006). ROS metabolism during the pathogen attack is followed by assistance of various antioxidant enzymes such as peroxidase (POX), superoxide dismutase (SOD), catalase (CAT) and ascorbate peroxidase (APX). POX is also produced as a defence response stimulated in plants in response to pathogen infection like *Fusarium oxysporum* (Morkunas and Gemerek, 2007; Ashry and Mohamed, 2011).

POX is among the major oxido-reductive enzymes that participate in the wall-building processes such as oxidation of phenols, suberization and lignifications of host plant cells during the defense reaction

against pathogenic agents (Chittoor and Leach, 1999). One of the important physiological roles of POXs is the synthesis of cell-wall polymers (lignin and suberin), which constitute physical barriers for both biotic and abiotic stresses (Cosgrove, 1997; Quiroga et al., 2000; Cai et al., 2009) which might confer the plant with high rigidity. Recent pharmacological experiments indicate that nitric oxide (NO) -a signal found in the immune, nervous, and vascular system of vertebrates also- plays an important role in plant disease resistance. Generation of NO augments the induction of HR cell death by H₂O₂ in soybean (*Glycine max*) suspension cultures (Delledonne et al., 1998; 2001). Likewise, inhibitors of NO synthesis as well as NO scavengers are able to block the HR induced by avirulent *Pseudomonas syringae* in soybean cell cultures and in *Arabidopsis* plants. Compared to ROS, NO induces a complementary set of plant defense genes, including two key enzymes of the phenylpropanoid pathway, namely Phenyl alanine ammonia lyase (PAL) and chalcone synthase (CHS) (Zeier et al., 2004; Ferrer et al., 2008).

Recognizing pathogens

Plants have evolved two strategies to detect pathogens (Chisholm et al., 2006; Jones and Dangl, 2006). On the external face of the host cell, plants are equipped to sense evolutionarily conserved microbial molecular signatures, collectively called pathogen-associated molecular patterns (PAMPs) or microbe-associated molecular patterns (MAMPs), are recognized by receptor proteins called pattern recognition receptors (PRRs) (Boller and Felix, 2009). PAMPs are typically essential components of whole classes of pathogens, such as bacterial flagellin or fungal chitin. Plants also respond to endogenous molecules released by pathogen invasion, such as cell wall or cuticular fragments called danger-associated molecular patterns (DAMPs). Stimulation of PRRs leads to PAMP-triggered immunity, an ancient form of innate immunity (Chisholm et al., 2006; Jones and Dangl, 2006).

The second class of perception involves recognition by intracellular receptors of pathogen virulence molecules called effectors; this recognition induces effector-triggered immunity (ETI). This mode of recognition leads to co-evolutionary dynamics between the plant and pathogen that are quite different from PTI in contrast to PAMPs, effectors are characteristically variable and dispensable. Generally, PTI and ETI give rise to similar responses, although ETI is qualitatively stronger and faster and involves HR (Dodds and Rathjen, 2010). PAMPs are detected by pattern recognition receptors (PRRs), typically cell surface-localized receptor kinases or LRR-RLP proteins (Zhang and Zhou, 2010).

Deposition of papillae

Following germination of pathogen on the leaf surface forms a specialized infection structure called appressorium. A penetration peg emerges from the appressorium and it penetrates the host leaf epidermal cell directly (approximately 12–20 h). If penetration succeeds and the host cell remains alive, a feeding structure develops called haustorium, which extracts nutrients to supply the development of superficial hyphae that ramify over the leaf surface and form a colony (Vanacker et al., 2000). Host cells respond to attempted penetration by depositing wall appositions, papillae, directly beneath appressoria. Papillae have been found to contain callose, phenolic compounds, lignin, ROS, and proteins and are thought to act as a physical barrier to halt penetration by the fungal penetration pegs (Aist, 1976; McLusky et al., 1999; Lyngkjaer and Carver, 1999; Underwood and Somerville, 2008). Their deposition involves generation of NO (Prats et al., 2005) and H₂O₂ (Vanacker et al., 2000), cytoskeletal rearrangement (Kobayashi et al., 1997; Opalski et al., 2005) and redirected cytoplasmic streaming and aggregation (Zeyen et al., 2002; Ridout, 2009).

These events direct vesicles containing papilla components to the site of attempted penetration. Vesicle targeting involves SNARE proteins and the general membrane trafficking factor SNAP (Assaad et al., 2004), suggesting that papilla formation is mediated by processes akin to membrane/vesicle trafficking in animal systems (Pelham, 2001; Böhlenius et al., 2010). Effective papilla defence also enhances the ability of cells adjacent to the attacked cell to form papillae in response to subsequent attacks (Lyngkjær and Carver, 2000; Prats et al., 2006), indicating that intercellular communication is a consequence of the response.

Cuticular layer as a defensive barrier

Cuticle is considered to constitute a physical barrier to microbial invaders through which cutinase-producing pathogens can penetrate. In addition to its role as a barrier, the cuticle is likely to be a source of signals used by invading pathogens to prepare and adjust for the colonization of their host. Production of cutinase in *Fusarium solani* f. sp. *pisi* is induced by cutin monomers present in the surrounding medium (Woloshuk et al., 1986). A model was proposed whereby fungi sense the presence of cutin monomers on the plant surface and induce high levels of cutinase required for invasion (Kolattukudy, 1985). Cuticular components can also regulate developmental processes in pathogenic fungi. For instance, cutin monomers induce germination and appressorium in *Magnaporthe grisea* (Gilbert et al., 1996; Skamnioti and Gur, 2007) and formation of the

appressorial tube in *Erysiphe graminis* (Francis et al., 1996). Screening mechanism of cell wall intactness in hostile environment is not known. Plants can sense a variety of molecules released during interaction with pathogens (Bais et al., 2004). In particular, breakdown products of the plant cell wall are known to act as elicitors of defences (Boller, 1995).

Callose deposition and cell wall appositions (CWA)

Callose is a linear homopolymer made up of β -1,3-linked glucose residue with some β -1,6-branches, is widespread in higher plants, in which it is a component of specialized cell walls or cell wall-associated structures at particular stages of growth and differentiation (Stone and Clarke, 1992). Callose has many functions in plant development, as involved at multiple stages of pollen development (Stone and Clarke 1992; McCormick, 1993; Backues et al., 2010), deposited at cell plates during cytokinesis (Samuels et al., 1995; Hong et al., 2001), deposited at plasmodesmata to regulate the cell-to-cell movement of molecules by controlling the size exclusion limit of plasmodesmata (Iglesias and Meins, 2000). Preinvasive basal defense against many pathogenic fungi is manifested at the stage of penetration by the formation of a local CWA called papilla (Böhlenius et al., 2010). To prevent pathogen penetration, plant cells respond by local reinforcement of the cell wall beneath the site of the penetration attempt by forming a papilla. This process involves deposition of the callose matrix together with the accumulation of components such as H_2O_2 , phenolics and various proteins and glycoproteins with hydrolytic and antifungal properties (Flors et al., 2005). Pathogen-induced callose could negatively regulate the SA signaling pathway of plants which results in increased resistance to pathogen (Chen and Kim, 2009). Formation of CWA is achieved by rapid reorganisation of actin microfilaments, actin-dependent transport of secretory products to the infection site and local activation of callose synthesis. Qualitative cytochemical experiments shown that callose was widely distributed in the underlying matrix of wall appositions (Kumudini and Shetty, 2002). Callose is less permeable to small molecules than other cell wall components and may there for restrict the passage of nutrients to the fungus and consequently to slow fungal growth, so that the other defence can act further to restrict the progress of infection (Silva et al., 2006). Wound callose is formed rapidly, mostly within minutes of wound initiation and is deposited between the plasma membrane and the cell wall (Nakashima et al., 2003).

Role of lignin in plant defence

Lignin is the second most abundant polymer found in nature (Jung and Weiting 1998) is a polymeric material

composed of phenylpropanoid units derived from three cinnamyl alcohols (monolignols): *p*-coumaryl, coniferyl, and sinapyl alcohols (Hatfield and Vermerris, 2001). From a functional point of view, lignins impart strength to cell walls, facilitate water transport, and impede the degradation of wall polysaccharides, thus acting as a major line of defense against pathogens, insects, and other herbivores (Hatfield and Vermerris, 2001). It retards the enzymatic digestion of the host cell wall by pathogens. Following their release, activation of enzymes may lead to oxidative linkage of phenolics on the plant cell wall, even without major transcriptional activation of biosynthetic pathways (Kumudini, 2005). Lignification is a mechanism for disease resistant in plants, and it renders the cell wall more resistant to mechanical pressure applied during penetration by fungal appressoria as well as more water resistant and thus less accessible to cell wall-degrading enzymes (Vance et al., 1980). Lignin formation occurs through a series of steps including many enzymes starting with phenylalanine ammonia lyase catalyzed reaction. Terminating reaction requires H_2O_2 and cell wall bound POX that polymerises the C6-C3 units into lignin (Marjamaa et al., 2009). As lignin polymerizes, it forms covalent cross-links with carbohydrate and protein and renders cell walls highly resistant to mechanical and enzymatic disruption (Lattanzio et al., 2006).

Phenolic compounds

Phenolic compounds are natural constituents of all plants and antibiotic phenols have been implicated in plant defense mechanisms (Baker et al., 2005). Among them, some occur constitutively and function as preformed inhibitors associated with non-host resistance while others are formed in response to pathogen ingress as part of an active defense response (Bahadur et al., 2007). Accumulation of autofluorescent phenolic compounds at the site of penetration is one of the readily observed host defence response. Plants need phenolic compounds for pigmentation, growth, reproduction, resistance to pathogens and for many other functions. Studies have shown that plant defence against pathogens, nematodes, phytophagous insects is based on the synthesis, release and accumulation of various phenolic compounds (Makoi and Ndakidemi, 2007). Defense gene products include polyphenol oxidase, peroxidase (POD) that catalyzes the formation of lignin, and phenylalanine ammonia-lyase (PAL) that is involved in phenolics synthesis (Raju et al., 2008).

Phenolic compounds delivered along the phenylpropanoid pathway play an important role in defense to pathogen infection either as preformed or postinfectious defense factors. They have been assigned to various important biological functions in defense such as cell wall reinforcement and antimicrobial activity as modulators of plant hormones in defense signaling or as scavengers of reactive oxygen

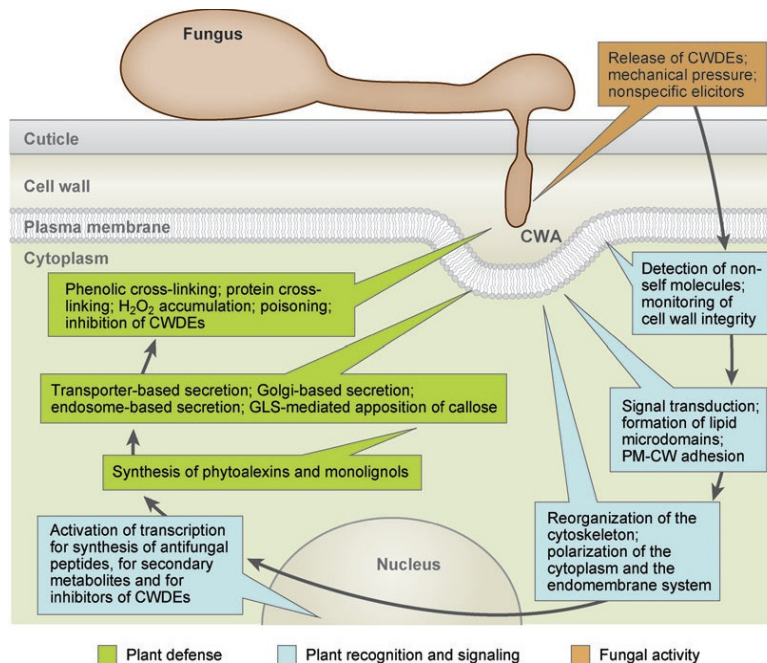


Figure 1. Biochemical and molecular mechanisms for cell wall-associated defense (Huckelhoven, 2007)

species (Tuncel and Nergiz, 1993). Particularly the phenolic polymer lignin is an important principal structural component of secondary vascular tissue and fibers in higher plants (Chen et al., 2009).

Putative guanidine compounds.

These are guanidine containing compounds located in papillae and HR cells, with high pKa value can also polarize the membranes and are able to adversely affect the pathogenic fungal growth can be demonstrated by Sakaguchi reaction. Some of the important compounds containing guanidine include arginine, agmatine and hordatine. Arginine is found in plant chromosomes, agmatine occurs in phenyl propanoid dimers, which are components of lignin and hordatine is an antifungal compound. It has been speculated that guanidine containing compound can act as an inhibitory substance to prevent the pathogen (Wei et al., 1994)

Hydroxyproline- rich glycoproteins (HRGPs)

HRGPs are abundant structural proteins in the plant cell wall. This generic term includes molecules rich in hydroxyproline/ proline: extensin, arabinogalactan-proteins, proline/ hydroxyproline-rich proteins and solanaceous lectin (Sommer-Knudsen et al., 1998). These proteins are known to be involved in plant defence, both in dicots (Esquerré-Tugayé et al., 1979; Mazau and Esquerré-Tugayé, 1986) and in monocots

(Kang and Buchenauer, 2003; Shailasree et al., 2004). The involvement of HRGPs in plant defence is likely because of early and massive accumulation in the cell wall together with the relative transcripts (Templeton et al., 1990) and in tissues immediately adjacent to the inoculation site in incompatible combinations (Benhamou et al., 1990); their accumulation is highly localized at sites where bacterial and fungal growth is arrested (O'Connell et al., 1990); artificial induction of HRGP increases resistance, whereas inhibition decreases it (Toppan et al., 1982).

HRGP accumulation and cross-linking processes in response to pathogen attacks has been noted (Bradley et al., 1992; Brisson et al., 1994; Brady and Fry, 1997; Shailasree et al., 2004) and the HRGP gene-encoding sequence has been studied (García-Muniz et al., 1998). HRGP mRNA accumulation has been induced by application of elicitors isolated from fungi and accumulation of the transcripts has also been induced by exogenous SA administration to cultured parsley cells (Thulke and Conrath, 1998), but the relationships between SA or acibenzolar-S-methyl level and HRGP accumulation are still largely unknown (Raggi, 2007; Huckelhoven, 2007).

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