Host Versus Nonhost Resistance: Distinct Wars with Similar Arsenals

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ABSTRACT

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Plants face several challenges by bacterial, fungal, oomycete, and viral pathogens during their life cycle. In order to defend against these biotic stresses, plants possess a dynamic, innate, natural immune system that efficiently detects potential pathogens and initiates a resistance response in the form of basal resistance and/or resistance (*R*)-gene-mediated defense, which is often associated with a hypersensitive response. Depending upon the nature of plant–pathogen interactions, plants generally have two main defense mechanisms, host resistance and nonhost resistance. Host resistance is generally controlled by single *R* genes and less durable compared with nonhost resistance. In contrast, nonhost resistance is believed to be a multi-gene trait and more durable. In this review, we describe the mechanisms of host and nonhost resistance against fungal and bacterial plant pathogens. In addition, we also attempt to compare host and nonhost resistance responses to identify similarities and differences, and their practical applications in crop improvement.

Additional keywords: gene-for-gene resistance, plant disease resistance, *R* gene resistance.

Plants are important components of any food chain. During their life cycle, plants are often challenged by numerous abiotic and biotic stresses. Among biotic stresses, diseases caused by fungi, oomycete, bacteria, and viruses have significant economic significance. Fungal and oomycete diseases such as wheat stem rust (caused by *Puccinia graminis*), Asian soybean rust (caused by *Phakopsora pachyrhizi*), potato blight (caused by *Phytophthora infestans*), banana black sigatoka (caused by *Mycosphaerella fijiensis*), and rice blast (caused by *Magnaporthe oryzae*) are considered major threats to world food security (Pennisi 2010). In general, plants are resistant to most microorganisms, and there are only a few plant pathogens that have the ability to cause disease (Lipka et al. 2008). In response to pathogen infection, plants have a dynamic immune system comprised of several mechanisms to defend against plant pathogens as previously explained in a four-phased zig-zag model (Jones and Dangl 2006).

Depending upon the nature of the plant–pathogen interactions, plants generally have two types of disease resistance—host resistance and nonhost resistance. Host resistance is mostly cultivar- or accession-specific and less durable (Mysore and Ryu 2004). So far, most of the breeding efforts have focused on host resistance where a single or multiple resistance (*R*) genes were

introduced into susceptible cultivars. Unfortunately, resistance imparted by most *R* genes is less durable because of monocultures, which puts tremendous selection pressure on pathogens to lose or mutate their corresponding effectors to evade detection by the host (Dangl et al. 2013). However, there are some core effectors that contribute toward pathogen virulence (Dangl et al. 2013). Loss/mutation of such effectors sometimes has negative implications on pathogen virulence and results in improved durability of corresponding host *R* genes (Vera Cruz et al. 2000). Another form of resistance is nonhost resistance; unlike host resistance, nonhost resistance can act against all races of a particular pathogen and can occur in all cultivars of a host plant species (Heath 2000). Thus, nonhost resistance is more durable and is the common form of plant defense mechanism exhibited by plants toward a vast majority of potential pathogens (Heath 2000; Mysore and Ryu 2004; Niks and Marcel 2009; Senthil-Kumar and Mysore 2013). For a long time, nonhost resistance has been considered to protect crops from many potential pathogens because of its durability (Niks and Marcel 2009). Complete understanding of nonhost resistance mechanisms is imperative to develop cultivars by the transfer of genes involved in nonhost resistance across species (Ayliffe and Lagudah 2004; Zhao et al. 2005). Moreover, nonhost resistance is usually more complicated due to the involvement of multiple pathways.

In this review, we briefly describe the mechanisms of host and nonhost resistance against fungal, oomycete, and bacterial plant pathogens. In addition, we compare host and nonhost resistance

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mechanisms, and highlight the similarities and differences between them. We also compare host and nonhost resistance in terms of their practical application in crop improvement.

MECHANISMS OF HOST AND NONHOST RESISTANCE

Host resistance and nonhost resistance are most commonly differentiated based on pathogen adaptation to a particular species (host) and lack of adaptation to other species (nonhost). Both host and nonhost resistances are the outcomes of the plant immune response. Plant innate immunity has been well described in previous reviews (Chisholm et al. 2006; Cohn et al. 2001; Dangl and Jones 2001; Dodds and Rathjen 2010; Jones and Dangl 2006). Among several components of the plant immune response, basal defense is the first line of defense and is initiated during the early phases of pathogen detection. Basal defense in plants is initiated with the perception of evolutionarily conserved microbial- or pathogen-associated molecular patterns (MAMPs or PAMPs) such as flagellin and EF-Tu by plant extracellular pathogen recognition receptors (PRRs) such as leucine-rich repeat kinases (Dangl et al. 2013; Zipfel 2008). Such responses are referred to as PAMP-triggered immunity (PTI). There are also some overlaps between basal defense and nonhost resistance because it is possible that both host and nonhost plants may recognize similar factors to initiate a defense response. Initiation of plant defense responses and the counter attack of pathogen are well explained by the widely accepted zig-zag model proposed by Jones and Dangl (2006). According to this model, there are numerous PRRs in plants to recognize PAMPs and to initiate basal defense responses, but some well-adapted pathogens secrete effectors to evade recognition by plant PRRs and to promote pathogen growth and virulence (Bent and Mackay 2007; Dangl et al. 2013; Zipfel 2008). Suppression of PTI by pathogen effectors leads to effector-triggered susceptibility (ETS). In turn, plants have evolved to recognize these effectors or avirulence (Avr) proteins with the help of R proteins (Nimchuk et al. 2003). Therefore, in response to ETS, host plants trigger R proteins to interact directly or indirectly with pathogen effectors and induce a stronger defense response, referred to as effector-triggered immunity (ETI). There are several examples of direct recognition of pathogen Avr proteins by plant R proteins (Dodds et al. 2006), but in some cases indirect recognition is also possible in which plant decoy proteins interact with Avr proteins and subsequent activation of R proteins (van der Hoorn and Kamoun 2008). This mechanism is also referred to as guard hypothesis (Dangl and Jones 2001; van der Biezen and Jones 1998). Direct and indirect recognition of Avr proteins by R proteins is followed by a strong defense signaling response that is associated with localized programmed cell death, called hypersensitive response (HR), to limit the pathogen growth.

Both pathogen and host undergo natural selection to diversify effectors and R proteins to achieve superiority in this molecular arms race (Boller and He 2009). ETI, which is determined by the recognition of a pathogen's effector or Avr protein by corresponding plant R protein, is also the basis of classical gene-for-gene resistance (Flor 1971). Most R proteins contain a nucleotide-binding site and leucine rich repeats (NBS-LRRs), and are involved, upon recognition of Avr protein, in the development of HR through the generation of reactive oxygen species (ROS). The well-studied host resistance is often considered gene-for-gene resistance and is usually very specific to a particular plant genotype or cultivar and against a particular race of the pathogen (Flor 1971). In contrast, nonhost resistance is not pathogen-race-specific and is a broad spectrum resistance exhibited by the whole plant species against a particular pathogen (Heath 2000). Nonhost resistance is often multi-tiered, with several obstacles depending upon a particular host to stop the colonization by a potential pathogen (Thordal-Christensen 2003). These obstacles include, but are not limited to, the presence/absence of signals from plants, such as surface

topology features that are required to initiate pathogen growth; preformed barriers such as cell wall, cuticle, phytoanticipins, etc.; and induced defense responses such as lignin accumulation, production of antimicrobials like phytoalexins, HR response, induction of pathogenesis-related (PR) proteins, etc. (Senthil-Kumar and Mysore 2013; Thordal-Christensen 2003). Depending upon the presence or absence of visual symptoms, nonhost resistance is again divided into type I and type II nonhost resistance (Mysore and Ryu 2004). Type I nonhost resistance does not produce any visual symptoms, whereas type II nonhost resistance is associated with visual necrosis/cell death due to HR (Mysore and Ryu 2004). Type I nonhost resistance typically involves passive or preformed barriers and/or active defense mechanisms that are induced in response to general elicitors of pathogens such as PAMPs (Mysore and Ryu 2004; Thordal-Christensen 2003). Type I nonhost resistance resembles PTI, whereas type II nonhost resistance involves HR and is triggered in response to pathogen elicitor/effector recognition and is similar to ETI (Senthil-Kumar and Mysore 2013). For example, recognition of pathogen effectors by nonhost plant species has been reported previously when *AvrA* and *AvrD* from *Pseudomonas syringae* pv. *tomato* were recognized by *R* genes *Rpg2* and *Rpg4*, respectively, of the nonhost plant soybean (Ashfield et al. 1995; Keen et al. 1991). In addition, *AvrRxo1* from *Xanthomonas oryzae* pv. *oryzae* was recognized by the *R* gene *Rxo1* of the nonhost plant maize (Zhao et al. 2004). Despite the fact that there are some overlaps between host and nonhost resistance, nonhost resistance is more complex and the mechanism of resistance may vary, depending upon the nature of pathogen (virus, bacteria, and fungi) and the plant species.

HOST VERSUS NONHOST RESISTANCE AGAINST FUNGAL AND OOMYCETE PATHOGENS IN PLANTS

Although nonhost resistance is considered to be a different type than host resistance, there are significant overlaps between them. Fungal pathogens recognize specific plant cues in the form of surface topology or composition of plant waxes (Hoch et al. 1987). Preformed barriers such as surface waxes have been shown to be important for growth and differentiation of nonhost fungal pathogens such as *Blumeria graminis* f. sp. *hordei* on cabbage and tobacco, and *Phakopsora pachyrhizi* on *Medicago truncatula* (Tsuba et al. 2002; Uppalapati et al. 2012). A mutation in the *IRG1* (*INHIBITOR OF RUST GERM TUBE DIFFERENTIATION 1*) gene in *M. truncatula* that causes loss of epicuticular wax accumulation on the abaxial side of the leaf was found to inhibit growth and development of germ tubes of both host and nonhost pathogens (Uppalapati et al. 2012). In contrast, epicuticular waxes were shown to be important for host resistance in cocoa against black pod disease caused by *Phytophthora palmivora* and *Phytophthora megakarya* (Nyadanu et al. 2012). In addition, a role of waxes in host resistance was also reported in *Lolium* spp. against powdery mildew pathogen, *Erysiphe graminis* (Carver et al. 1990). In both cases, epicuticular wax was directly correlated with resistance, suggesting a positive role of epicuticular waxes in host resistance.

Actin microfilaments are part of the plant cytoskeleton, and the role of actin microfilaments in plant defense is well established (Day et al. 2011). Involvement of *ACTIN DEPOLYMERIZATION FACTORS* (*Adf3* and *TaAdf7*, a *Triticum aestivum* homolog of *Adf7*) in host resistance against rust pathogens has been shown (Fu et al. 2014; Moscou et al. 2011; Wang et al. 2013). Apart from host resistance, nonhost resistance against several nonhost plant-pathogen combinations was compromised when actin polymerization was disrupted with specific inhibitors, indicating the importance of actin microfilaments in nonhost resistance as well (Kobayashi et al. 1997).

Another level of resistance against nonhost pathogens is triggered at the time of pathogen penetration through the plasma membrane. Three *PENETRATION* genes, *PEN1*, *PEN2*, and *PEN3*,

have been identified in Arabidopsis and are involved in penetration resistance against the nonhost powdery mildew pathogen *Blumeria graminis* f. sp. *hordei* and Asian soybean rust pathogen *Phakopsora pachyrhizi* (Collins et al. 2003; Lipka et al. 2005; Loehrer et al. 2008; Stein et al. 2006). In Arabidopsis, *PEN1* encodes a membrane-associated syntaxin containing a SNARE (soluble N-ethylmaleimide sensitive factor attachment protein receptor) domain which forms a complex with SNAP33 (soluble N-ethylmaleimide-sensitive factor adaptor protein 33) and VAMP721/VAMP722 (vesicle-associated membrane proteins), and is involved in vesicle transport to cell periphery in response to nonhost pathogen *B. graminis* f. sp. *hordei* (Assaad et al. 2004; Collins et al. 2003; Kwon et al. 2008). Similarly, *Required for mlo-specific resistance 1* (*Ror1*) and *Ror2*, an ortholog of *PEN1*, genes are also involved in penetration resistance in barley against nonhost rust pathogen *Phakopsora pachyrhizi* (Hoeftle et al. 2009). *Ror2* is also involved in pre-invasive resistance against host pathogen *B. graminis* f. sp. *hordei* (Collins et al. 2003). In Arabidopsis, *PEN2*, *ARABIDOPSIS G PROTEIN BETA SUBUNIT 1* (*AGB1*), *POWDERY MILDEW RESISTANT 5* (*PMR5*), and *MILDEW RESISTANCE LOCUS O* (*MLO2*) genes are involved in both pre- and postinvasive nonhost resistance against *B. graminis* f. sp. *hordei* (Nakao et al. 2011). *PMR5* restricts fungal hyphae elongation whereas *AGB1* and *MLO2* restrict both hyphae elongation and branching of nonhost pathogen *B. graminis* f. sp. *hordei* (Nakao et al. 2011). The *Mlo* family gene was first identified in barley, but unlike Arabidopsis *MLO2*, mutation in the *Mlo* locus of barley conferred durable resistance against biotrophic host pathogen *B. graminis* f. sp. *hordei* and hyper-susceptibility against hemi-biotrophic nonhost pathogen *Magnaporthe oryzae*, indicating the involvement of yet another gene in both host and nonhost resistance, even though the outcome was antagonistic (Buschges et al. 1997; Jarosch et al. 1999). However, the *Mlo* gene product is considered to act as a negative regulator of cell death due to the association of a mutation in *Mlo* with resistance against biotrophic fungal pathogens and susceptibility against necrotrophic fungal pathogens (Király et al. 2002). Barley *mlo* alleles cause enhanced susceptibility against host pathogens *Bipolaris sorokiniana*, a necrotroph, and *Ramularia collo-cygni*, which lives in host as an endophyte but later changes to necrotrophic mode (Kumar et al. 2001; McGrann et al. 2014).

Fungal pathogens that successfully overcome penetration or pre-invasion resistance produce infection hyphae and/or haustoria to absorb nutrients from plant cells. At this point, pathogens encounter postinvasion resistance from plants. Plant genes such as *ENHANCED DISEASE SUSCEPTIBILITY 1* (*EDS1*), *PHYTOALEXIN DEFICIENT 4* (*PAD4*), and *SENESCENCE ASSOCIATED GENE 101* (*SAG101*), which are also involved in basal defense during host-pathogen interactions, are also implicated in postinvasion defense (Lipka et al. 2005; Stein et al. 2006). Individual mutations in these genes have an effect on postinvasion defense in Arabidopsis against nonhost pathogen *B. graminis* f. sp. *hordei*. In addition, a triple mutant of *pen2/pad4/eds1* completely broke down the nonhost resistance barrier against *B. graminis* f. sp. *hordei* and pea powdery mildew pathogen *Erysiphe pisi* (Lipka et al. 2005). *EDS1* was initially identified in Arabidopsis as a component of basal defense against host pathogen *Hyaloperonospora parasitica* (Parker et al. 1996). *EDS1* and *PAD4* are also required for several Arabidopsis *R* genes belonging to TIR-NB-LRR class-mediated resistance (Wiermer et al. 2005). Apart from a few plant genes that are commonly required for host and nonhost resistance, some effectors are also commonly recognized by host and nonhost plant species. For example, *Avr3a* of *Phytophthora infestans* and *Avr1b-1*, a homolog of *Avr3a* in *Phytophthora sojae*, are recognized by their corresponding host *R* genes, *R3a* of potato and *Rps1b* of soybean, respectively (Armstrong et al. 2005; Shan et al. 2004). In addition, *PcAvr3a1* of *Phytophthora capsici*, which is also a homolog of *Avr3a* of *Phytophthora infestans*, is recognized by a dominant *R* gene of nonhost *Nicotiana* species,

indicating parallel mechanisms among host and nonhost resistance (Vega-Arreguín et al. 2014).

Additionally, there are several examples where potential *R* genes were identified in nonhost plant species, and after transferring to host plant species, those *R* genes have successfully conferred resistance against host pathogens (Sumit 2013; Zhao et al. 2005). Examples of successful transgenic deployment of *R* genes between plant species have been reviewed previously (Wulff et al. 2011). These studies indicate a conserved mechanism involved downstream of recognition among various plant species, irrespective of their classification as host or nonhost (Stam et al. 2014).

At the cellular level, both nonhost and host resistance are associated with similar cellular responses such as cytoplasmic aggregation involving relocation of organelles, production of ROS, and HR (Hückelhoven et al. 2001; Hückelhoven and Kogel 2003; Takemoto et al. 2003; Vleeshouwers et al. 2000). However, apart from overlaps or similarities in host and nonhost resistance mechanisms, there is evidence that also suggests distinct or independent mechanisms. Distinct cellular processes and timing of HR have also been reported among host and nonhost interactions against penetration of rust and powdery mildew fungi in cowpea and French beans (Christopher-Kozjan and Heath 2003). In nonhost interactions, the cell death process was rapid (less than one hour) and the plant cell nucleus was seen associated with fungal haustorium. During host resistance in contrast to nonhost resistance, the cell death response took longer (two or more hours) and no consistent association of plant cell nucleus with the intracellular fungi was found (Christopher-Kozjan and Heath 2003). Nonetheless, no differences were observed in cellular signaling during HR, such as influx of calcium and protein kinase activity between host and nonhost resistance (Christopher-Kozjan and Heath 2003). However, there are also few examples where plant nucleus has been shown to be associated with the pathogen structures, such as haustoria, during host resistance (Griffis et al. 2014). For example, during host resistance of a potato cultivar (*Solanum tuberosum* L. cv. Datura) against oomycete pathogen *Phytophthora infestans* (race 4) the plant cell nucleus conglomerate around the intracellular oomycete haustorium which is followed by cell death response (Freytag et al. 1994). Based on our current understanding, host and nonhost mechanisms against fungal and oomycete pathogens have some similarities and overlaps by the involvement of common genes in both types of resistance but are yet distinct in recognition and initiation of defense response.

HOST VERSUS NONHOST RESISTANCE AGAINST BACTERIAL PATHOGENS IN PLANTS

Similar to the way plants have evolved to combat infections by fungal and oomycete pathogens, plants have also evolved defense mechanisms to prevent attacks from bacterial pathogens. Most bacterial pathogens get access to the plant milieu through natural openings (hydathodes and stomata) and wounds (Hirano and Upper, 1983). The most studied plant pathogenic bacteria belong to the genus *Pseudomonas* (type III secretion), *Xanthomonas* (type III secretion), *Erwinia* (type II secretion), *Ralstonia* (type III secretion), and *Agrobacterium* (type IV secretion). Species within these genera of bacterial pathogens use different types of secretion systems to secrete effector proteins into a host cell for the suppression of plant defense systems. Many gram-negative plant bacterial pathogens employ a type III secretion system (T3SS) to colonize host plants by suppressing plant defense (Buttner and He 2009). For example, *AvrPto* from *Pseudomonas syringae* pv. *tomato* blocks callose deposition in tomato plants (Hauck et al. 2003) and suppresses HR induced in nonhost plants (Kang et al. 2004). In Arabidopsis, *AvrRpm1* (from *Pseudomonas syringae* pv. *maculicola*) and *AvrRpt2* (from *Pseudomonas syringae* pv. *tomato*) effectors

inhibit PAMP-mediated defense signaling pathways (Kim et al. 2009). Plants, on the other hand, have evolved to express R proteins that can detect the presence of T3SS effectors inside the plant cell and initiate defense responses such as HR, ROS production, and expression of *PR* genes. As described above, this phenomenon is also referred to as ETI. In contrast to R protein-mediated host resistance, early recognition of bacterial PAMPs is also important for initiating the downstream signaling pathway for nonhost resistance. PRRs recognize bacterial PAMPs, induce defense signaling and defend against nonadapted bacterial pathogens. In *Arabidopsis*, flagellin (a PAMP)-induced defense plays an important role in nonhost resistance against bacterial pathogens (Li et al. 2005). The flg22 peptide of flagellin from *Pseudomonas* bacteria is perceived by FLS2, a receptor-like kinase that activates downstream events. It has been reported that ROS and defense phytohormones, such as salicylic acid (SA), jasmonic acid (JA), and abscisic acid (ABA), play a role in the defense signaling pathway for nonhost resistance (Li et al. 2012; Mishina and Zeier 2007; van Wees and Glazebrook 2003). Since SA, JA, and ABA are the major hormones for plant defense and development, genes involved in their signaling pathway are not only involved in nonhost resistance but also closely associated with plant growth and development.

Several plant genes and proteins have been identified that play a role in both host and nonhost resistance. For example, in *Nicotiana benthamiana*, the suppressor of the G2 allele of S-phase kinase-associated protein 1 (SGT1) has been known for the production of ROS and HR cell death against nonhost bacterial pathogens (Shibata et al. 2011; Wang et al. 2010). Also, SGT1 together with Rar1 (Required for Mla12 Resistance 1) is required for resistance responses mediated by NBS-LRR and other R proteins (Azevedo et al. 2002; Peart et al. 2002). *GLYCOLATE OXIDASE* (*GOX*) and *NONHOST 1* (*NHO1*) genes have also been demonstrated to be required for both host and nonhost resistance in *Arabidopsis* (Lu et al. 2001; Rojas et al. 2012). Another important gene for the SA signaling pathway, *EDS1*, also contributes to host, nonhost, and basal resistance against bacterial pathogens (Aarts et al. 1998; Glazebrook 2001; Moreau et al. 2012). Apart from plant genes, several pathogen genes also determine host/nonhost status of a plant. In *Pseudomonas*, several *survival in Arabidopsis extracts* (*sax*) genes in host bacterial strains are implicated in overcoming *Arabidopsis* defense. Depending upon the presence or absence of *sax* genes, *Arabidopsis* host or nonhost status against certain bacterial pathogens is decided (Fan et al. 2011).

EVOLUTIONARY PERSPECTIVE OF HOST AND NONHOST RESISTANCE

The concept of host and nonhost resistance is derived from the fact that not all pathogens can infect all plant species. Host and nonhost interactions between plants and pathogens are dynamic and greatly influenced by evolution. At the molecular level, depending upon the genetic distance from the host species, host resistance is predominantly regulated by ETI, whereas nonhost resistance is regulated by PTI and/or ETI (Schulze-Lefert and Panstruga 2011; Senthil-Kumar and Mysore 2013) (Fig. 1). Within host species, the variation of resistance among cultivars and accessions is mainly defined by a large repertoire of *R* genes that continuously evolve due to gene duplication/deletion, recombination, mutations, and selection pressure for resistance against pathogens (Ellis et al. 2000). On the other hand, pathogens also evolve their effector proteins to maintain virulence on host species. Co-evolution of host and pathogen is also the basis of the zig-zag model that has been developed for plant immunity against pathogens (Jones and Dangl 2006). In some instances, the host plant evolves and acquires a nonhost status by one-sided evolution of the plant while the pathogen is specialized to a particular host and does not counter evolve (Antonovics et al. 2013). Generally, durability of nonhost resistance increases against a specialized pathogen when the nonhost species is evolutionarily divergent from the source host species (Fig. 1). On the contrary, highly evolving pathogens have the potential to overcome the defense exhibited by nonhost species evolutionarily divergent from their source host (Fig. 1). In general, an increase in genetic distance of nonhost from adapted host increases the durability of nonhost resistance because of the presence of several mechanisms to block the pathogen infection (Antonovics et al. 2013). Additionally, pathogens which keep evolving generally have a large host range. Several factors which influence genetic structure and evolutionary trajectory of a pathogen population include the host range, mode of reproduction, transmission and dispersal, life-cycle complexity and epidemiology, and host longevity (Barrett et al. 2008). A good example of a pathogen with a large host range, long-distance transmission, sexual and asexual modes of reproduction, and a complex life cycle including an alternate host is *Puccinia* spp. The *Puccinia* spp. cause rust diseases in monocots and cause economically significant damage on several crop plants in the United States (Roelfs 1978). The host range of *Puccinia graminis* alone is very large and covers 365 species in 54 genera (Anikster 1984). Another example is *Puccinia*

FIGURE 1

Evolution of host and nonhost resistance. **A**, Host resistance is primarily controlled by R-AVR recognition. A micro-evolution creates diversity within host species for resistance/susceptibility and also within pathogen to develop new races with diverse suite of effectors. Red, yellow, and green indicate host variations for susceptibility, partial resistance/susceptibility, and resistance, respectively. **B**, Outcomes of nonhost interactions vary with genetic distance from host species and the pathogen's ability to evolve. A rapidly evolving pathogen due to co-speciation, host shift, and host jump has better capability to adapt to new nonhost species by breaking the nonhost barriers. Durability of nonhost resistance with respect to genetic distance is depicted as a gradient from red to green, where red is less durable and green is more durable. The contribution of PAMP-triggered immunity and effector-triggered immunity also increases and decreases, respectively, with the increase in genetic distance from host to nonhost (based on information from Schulze-Lefert and Panstruga 2011).

coronata var. *hordei*, also has a broad host range and infects *Hordeum*, *Bromus*, *Agropyron*, *Aegilops*, *Phalaris*, and *Secale* genera (Jin and Steffenson 1999). It can be presumed that such pathogens have a large repertoire of effectors compared to a specialized pathogen (Niks and Marcel 2009). Recently, a new race (Ug99) of *Puccinia graminis* f. sp. *tritici* emerged in Uganda in 1998 which is virulent on most wheat cultivars grown all over the world (Pretorius et al. 2000; Singh et al. 2011). Sexual reproduction and long distance dispersal of windborne spores are the major contributing factors for emergence of new races and rust epidemics. Intercontinental long-distance dispersal of *Puccinia graminis* f. sp. *tritici* has been reported previously (Watson 1981). *Puccinia graminis* f. sp. *tritici* overwinters and completes its sexual cycle on the alternate host barberry (*Berberis vulgaris*), and the presence of barberries increases genetic diversity and infectivity of rust (Burdon and Roelfs 1985). Therefore, a barberry eradication program was conducted from 1918 to 1980 in the United States to reduce wheat stem rust epidemics (Roelfs 1982).

Apart from co-evolution, which largely determines host–pathogen interactions, co-speciation, host-shift speciation, and host jump play a role in the adaptation of pathogens to new plant species (Fig. 1) (Schulze-Lefert and Panstruga 2011; de Vienne et al. 2013). Co-speciation happens when both host and pathogen undergo speciation simultaneously to maintain their interactions. The presence of co-speciation has been experimentally proven by comparing phylogenetic trees of rodents and their ectoparasites, which showed a high degree of concordance (Hafner and Nadler 1988). Host-shift happens when pathogens usually shift from their natural host to related nonhost species. For example, *Blumeria graminis* that causes powdery mildew disease on barley underwent host-shift from barley to the related nonhost species, wheat (Inuma et al. 2007). Similarly, rice blast pathogen *Magnaporthe oryzae* also shifted host to cause wheat blast in the mid-1980s (Couch et al. 2005). On the other hand, host jump involves adaption of the pathogen to a distantly related plant species from their source host or sometimes even across kingdom (Raffaele et al. 2010; van Baarlen et al. 2007). For example, many plant bacterial and fungal pathogens such as *Pseudomonas aeruginosa*, *Agrobacterium radiobacter*, *Alternaria* spp., and *Fusarium* spp. have a wide plant host range but are also capable of infecting mammalian hosts indicating a cross kingdom jump in the past (van Baarlen et al. 2007). A very good example of host jump is related to *Phytophthora infestans* that was responsible for the famous 19th century Irish potato famine. *Phytophthora infestans* that infect several *Solanum* species evolved through host jump from *Phytophthora mirabilis* that infect the four o'clock plant (*Mirabilis jalapa*) (Grünwald and Flier 2005; Raffaele et al. 2010). Recent findings suggest that the host specialization followed by host jump is dependent on reciprocal amino acid changes in effector proteins such as a single amino acid change in one of the effector protein that binds and inhibits a plant's protease defense (Dong et al. 2014; Raffaele et al. 2010). Horizontal gene transfer of pathogenicity genes between pathogen species beyond reproductive barriers also helps bacterial and fungal pathogens to shift their hosts and infect nonhosts (de la Cruz and Davies 2000; Rosewich and Kistler 2000). Interspecific horizontal gene transfer has been reported for the *ToxA* gene that was transferred from *Phaeosphaeria nodorum* to *Pyrenophora tritici-repentis*, which causes tan spot disease of wheat (Friesen et al. 2006).

Based on the current understanding, plant pathogen interactions are highly influenced by evolutionary forces that act on both plants and pathogens. Host and nonhost status is decided by both plant and pathogen, which is again affected by speciation, biology of plant, and pathogen, including mode of reproduction, geographical proximity, epidemiology, and host range of the pathogen.

HOST VERSUS NONHOST RESISTANCE: PRACTICAL APPLICATION FOR CROP IMPROVEMENT

Compared with host resistance, nonhost resistance is considered more durable; but at the same time, nonhost resistance is more complicated and difficult to apply in crop breeding. Availability of both susceptible and resistant individuals in host populations against a particular pathogen makes it easier to identify underlying genetic factors responsible for resistance by employing genetic and quantitative trait loci mapping. Contrarily, a nonhost plant population generally lacks susceptible individuals, especially if the nonhost is distantly related to the susceptible host. Under these circumstances, inheritance of nonhost resistance can be achieved by employing three different strategies: crossing host × nonhost where cross species hybridization is possible; crossing nonhost × nonhost if there are variations in resistance; and crossing rare susceptible and common resistant individuals in marginal host species (Niks and Marcel 2009). Marginal host species are those which are mostly nonhost to a pathogen species, but rarely individuals with lower susceptibility than host species still exist (Niks and Marcel 2009). Lack of natural variation for resistance in host and nonhost species can be overcome by generating variations using mutagenesis and gene silencing. Several genes involved in nonhost resistance of *M. truncatula* against *Phakopsora pachyrhizi* were identified by screening a large *Tnt1* insertion mutagenized population of *M. truncatula* (Tadege et al. 2008; Uppalapati et al. 2012). In addition, *PEN* genes were identified and characterized in nonhost *Arabidopsis* by screening a mutant population upon infection with *Blumeria graminis* f. sp. *hordei* (Collins et al. 2003; Lipka et al. 2005; Stein et al. 2006). In another approach, virus-induced gene silencing (VIGS)-based forward genetics screening was utilized to identify the role of genes such as *SQUALENE SYNTHASE* (*SQS*), *GOX*, *ORNITHINE DELTA-AMINOTRANSFERASE* (*δOAT*), and *PROLINE DEHYDROGENASE* (*ProDH*) in nonhost resistance of *N. benthamiana* against several bacterial pathogens (Rojas et al. 2012; Senthil-Kumar and Mysore 2012; Wang et al. 2012).

The next step after identification of genes involved in nonhost resistance is to successfully transfer them to susceptible host species. Genes involved in nonhost resistance are often difficult to transfer compared with host resistance genes, since they need either wide hybridization or transgenic approaches. Wide hybridization has been successfully employed in the past to transfer sources of resistance against multiple diseases in wheat by transferring individual rye chromosomes to wheat (Riley and Macer 1966). More recently, a barley leaf rust resistance gene, *Rph22*, was successfully transferred from nonhost species *Hordeum bulbosum* to *Hordeum vulgare* (cultivated barley) (Johnston et al. 2013). Similarly, a transgenic approach has also been implemented successfully in the past in which a nonhost resistance gene, *Rxo1*, from maize was transferred to rice and imparted resistance against the bacterial streak pathogen *Xanthomonas oryzae* pv. *oryzicola* (Zhao et al. 2005). Recently, another *Arabidopsis* gene involved in nonhost resistance, *PHYTOPHTHORA SOJAE SUSCEPTIBLE 1* (*PSSI*), was identified in the *Arabidopsis pen1-1* mutant background which is required for both pre- and post-penetration nonhost resistance against the hemibiotrophic oomycete fungal pathogen *Phytophthora sojae* and necrotrophic fungal pathogen *Fusarium virguliforme* (Sumit et al. 2012). *PSSI* encodes a glycine-rich protein (GRP), and expression of *AtGRP1* in soybean cultivar Williams-82 led to enhanced resistance against *Phytophthora sojae* and *F. virguliforme* (Sumit 2013).

CONCLUDING REMARKS

Host resistance has been studied extensively, but nonhost resistance is only beginning to be understood. Host resistance is mainly controlled by gene-for-gene resistance, whereas nonhost

resistance is usually more complicated due to the involvement of multiple pathways. Due to the durability of nonhost resistance over host resistance, nonhost resistance holds great promise for agriculture. Based on the available information on host and nonhost resistance, we compared these two forms of resistance. Despite their classification into two classes, host and nonhost resistance share more similarities than differences in their mechanisms and resistance process. Due to similarities in downstream mechanisms, genes involved in nonhost resistance have been successfully transferred from nonhost to host species (Johnston et al. 2013; Sumit 2013; Zhao et al. 2005). But identification and utilization of sources of nonhost resistance in crop improvement are still challenging. We speculate that with the aid of the latest molecular biology and genomics tools, such as improved transformation methods, advanced tissue culture techniques, mutagenesis, genome editing, VIGS, and genome sequencing, more novel sources of nonhost resistance will be identified and effectively utilized in future plant breeding.

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