

Minireview

# Molecular Mechanisms of Generation for Nitric Oxide and Reactive Oxygen Species, and Role of the Radical Burst in Plant Immunity

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Rapid production of nitric oxide (NO) and reactive oxygen species (ROS) has been implicated in the regulation of innate immunity in plants. A potato calcium-dependent protein kinase (StCDPK5) activates an NADPH oxidase StRBOHA to D by direct phosphorylation of N-terminal regions, and heterologous expression of StCDPK5 and StRBOHs in *Nicotiana benthamiana* results in oxidative burst. The transgenic potato plants that carry a constitutively active StCDPK5 driven by a pathogen-inducible promoter of the potato showed high resistance to late blight pathogen *Phytophthora infestans* accompanied by HR-like cell death and H<sub>2</sub>O<sub>2</sub> accumulation in the attacked cells. In contrast, these plants showed high susceptibility to early blight necrotrophic pathogen *Alternaria solani*, suggesting that oxidative burst confers high resistance to biotrophic pathogen, but high susceptibility to necrotrophic pathogen. NO and ROS synergistically function in defense responses. Two MAPK cascades, MEK2-SIPK and cytokinesis-related MEK1-NTF6, are involved in the induction of *NbRBOHB* gene in *N. benthamiana*. On the other hand, NO burst is regulated by the MEK2-SIPK cascade. Conditional activation of SIPK in potato plants induces oxidative and NO bursts, and confers resistance to both biotrophic and necrotrophic pathogens, indicating the plants may have obtained during evolution the signaling pathway which regulates both NO and ROS production to adapt to wide-spectrum pathogens.

## INTRODUCTION

Rapid production of nitric oxide (NO) and reactive oxygen species (ROS), called NO burst and oxidative burst, respectively, have been implicated in diverse physiological processes, such as resistance to biotic and abiotic stress, hormonal signaling and development in plants (Doke, 1983; Hong et al., 2008; Torres et al., 2006; Wendehenne et al., 2004). Recently, NO has attracted attention as a radical that participates in plant innate immunity. NO activates the mitogen-activated protein kinase (MAPK) cascade (Clarke et al., 2000) and increases the

expression of defense genes, such as those coding for phenylalanine ammonia-lyase (PAL) and pathogenesis-related proteins (Durner et al., 1998). In animals, NO is produced by NO synthase (NOS). The sources of NO synthesis in plants include reduction of nitrite by nitrate reductase (NR), oxidation of arginine to citrulline by NOS. Although evidences for arginine-dependent NO synthesis in plants have accumulated, no gene or protein that has a sequence similar to known mammalian-type NOS has been found in plants (Butt et al., 2003; Garcia-Mata and Lamattina, 2003). Guo et al. (2003) identified a NOS-like enzyme from Arabidopsis (*Arabidopsis thaliana*) (AtNOS1) with a sequence similar to a protein that has been implicated in NO synthesis in the snail *Helix pomatia*. The AtNOS1 protein has no NOS activity (Zemojtel et al., 2006), and therefore the AtNOS1 was renamed AtNOA1 for NO ASSOCIATED1 (Crawford et al., 2006). Recent studies showed that AtNOA1 has circularly permuted GTPase activity (Moreau et al., 2008). The function of AtNOA1 remains to be resolved. However, the Arabidopsis mutant *noa1* is still useful for its phenotype, which shows reduced levels of NO in plant growth, fertility, hormonal signaling, salt tolerance and plant-pathogen responses (Guo et al., 2003; He et al., 2004; Kato et al., 2008; Zeidler et al., 2004; Zhao et al., 2007). Knocking out or down the *NOA1* provides a powerful tool to analyze the NO function.

The activation mechanism of NADPH oxidase has been well investigated for mammals. NADPH oxidases have Nox/Duox (NADPH oxidase/dual oxidase) as a catalytic subunit. In phagocytes, gp91<sup>phox</sup>, known as Nox2, forms a multi-protein complex with p22<sup>phox</sup>, p67<sup>phox</sup>, p47<sup>phox</sup>, p40<sup>phox</sup> and Rac2 (Sumimoto, 2008). Nox organizer 1 (Noxo1) and Nox activator 1 (Noxa1) are homologs of p47<sup>phox</sup> and p67<sup>phox</sup>, respectively, and are required for Nox1 activation (Takeya et al., 2003). Nox5, Duox1, and Duox2 have N-terminal extensions, including EF-hand motifs, and are likely regulated by Ca<sup>2+</sup> directly (Bánfi et al., 2004; Dupuy et al., 1999). *Respiratory burst oxidase homolog (RBOH)* is a plant homolog of Nox5 in mammalian NADPH oxidase and found in several plant genomes, such as Arabidopsis, rice (*Oryza sativa*), tomato (*Solanum lycopersicum*), potato (*Solanum tuberosum*), tobacco (*Nicotiana tabacum*), and *Nicotiana benthamiana* (Amicucci et al., 1999; Groom et al., 1996; Keller et al.,

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1998; Simon-Plas et al., 2002; Torres et al., 1998; Yoshie et al., 2005; Yoshioka et al., 2001; 2003). Several lines of evidence indicate that RBOH has a pivotal role in ROS-mediated signaling, such as defense responses, plant development and cell elongation. *AtRBOHD* and *AtRBOHF* function in ROS production during pathogen signals (Torres et al., 2002) and abscisic acid-induced stomatal closure in guard cells (Kwak et al., 2003). Virus-induced gene silencing (VIGS) of *NbRBOHA* and *NbRBOHB* in *N. benthamiana* attenuates ROS production and resistance to *Phytophthora infestans* (Asai et al., 2008; Yoshioka et al., 2003). Loss-of-function of tomato *RBOHs* by an antisense technique reduces ROS production in leaves and induces morphological abnormality (Sagi et al., 2004). In root hair development, ROS production by *AtRBOHC/RHD2* controls cell expansion through the activation of  $\text{Ca}^{2+}$  channels (Foreman et al., 2003). Except for RBOH and Rac, the homologs of other subunits of phagocyte NADPH oxidase are not found by Arabidopsis genome sequencing (Arabidopsis Genome Initiative, 2000). RBOH protein has been shown to localize on the plasma membrane (Kobayashi et al., 2006). The N-terminal extension includes two  $\text{Ca}^{2+}$  binding EF-hand motifs and suggests participation of  $\text{Ca}^{2+}$  signaling in the activation process (Keller et al., 1998). Sagi and Fluhr (2001) showed that  $\text{Ca}^{2+}$  directly activates an RBOH-like enzyme in tomato and tobacco plasma membranes by using denaturing gel assay and then by regeneration. Rac GTPase is also implicated to regulate RBOH by means of N-terminal extension. Wong et al. (2007) indicated direct interaction between Rac and the N-terminal of RBOH and the interaction may activate NADPH oxidase activity in plants. They also suggested that cytosolic  $\text{Ca}^{2+}$  concentration might modulate NADPH oxidase activity by regulating the interaction between Rac and RBOH. Furthermore, it was reported that a calcium-dependent protein kinase (CDPK) activates NADPH oxidase by the direct phosphorylation of its N-terminal region (Kobayashi et al., 2007). The conditional expression of an active CDPK in transgenic potato plants induce oxidative burst and confers resistance to virulent *P. infestans*. However, the transgenic potato plants are more susceptible than wild-type plants to infection by necrotrophic pathogen *Alternaria solani*.

NO and ROS together, but not individually, are required to induce cell death (Delledonne et al., 1998), and balanced production of NO and  $\text{H}_2\text{O}_2$  is important to induce hypersensitive response (HR) cell death (Delledonne et al., 2001). However, little is known how these molecules are coordinately regulated, and functions in plant immune responses. Recently, we found that MAPKs regulate production of NOA1-associated NO and NADPH oxidase-dependent ROS (Asai et al., 2008). In this review, we discuss the molecular mechanisms of the regulation of NO and ROS production and roles of radical bursts in resistance to pathogens.

### MAPKs regulate NADPH oxidase genes

The timely recognition of invading microbes and the rapid induction of defense responses are essential for plant disease resistance. At least two recognition systems are used by plants (Jones and Dangl, 2006). Plant defenses are often initiated by a gene-for-gene interaction between a dominant plant resistance (R) gene and a pathogen avirulence (Avr) gene, which provides race-specific resistance that is easily overcome by pathogen mutations. Plants also use a much less specific recognition system that identifies pathogen-associated molecular patterns (PAMPs), such as flagellin (Zipfel et al., 2004) and EF-Tu (Zipfel et al., 2006), so-called general elicitors. Both animals and plants can recognize invariant PAMPs that are characteris-

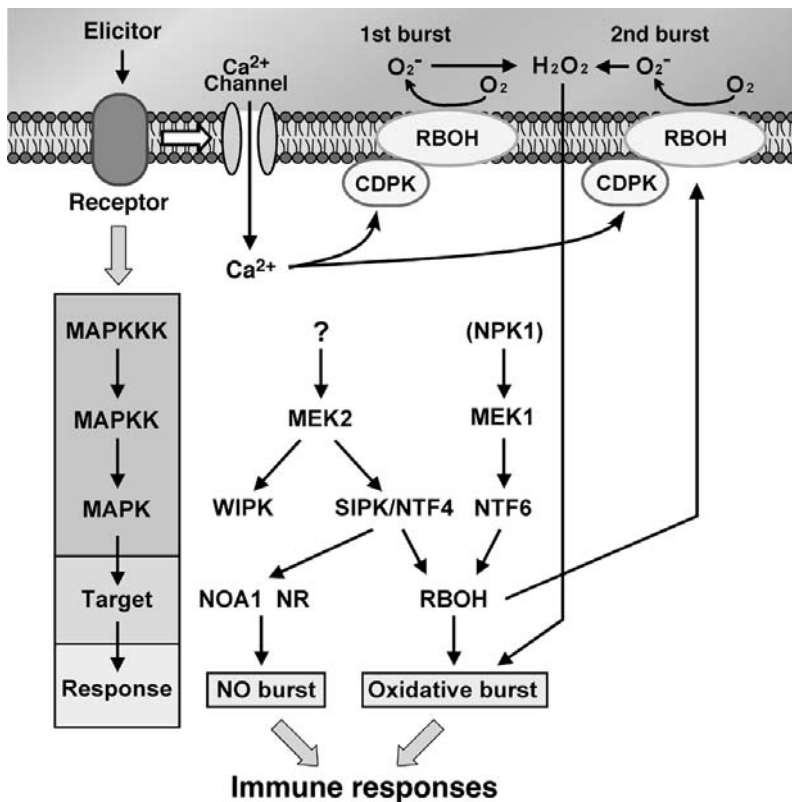
tic of pathogenic microorganisms by corresponding pattern recognition receptors.

The MAPK cascade is a major evolutionarily conserved signaling pathway used to transduce extracellular stimuli into intracellular responses among eukaryotes (MAPK Group, 2002; Pitzschke et al., 2009). In the MAPK signal transduction cascade, a MAPK is activated by a MAPK kinase (MAPKK), which itself is activated by a MAPKK kinase (MAPKKK). Many studies have extensively characterized plant MAPKs, including tobacco wound-induced protein kinase (WIPK) (Seo et al., 1999) and salicylic acid (SA)-induced protein kinase (SIPK) (Zhang and Klessig, 1997) and their orthologs in other plant species (Katou et al., 2005; Lee et al., 2004; Pedley and Martin, 2005). WIPK and SIPK participate either in R gene-dependent resistance to tobacco mosaic virus (TMV) (Jin et al., 2003), to *Cladosporium fulvum*-derived effector Avr9 (Romeis et al., 1999) in a gene-for-gene-specific way or in PAMPs-responsive resistance in *Colletotrichum orbiculare*-*N. benthamiana* interactions (Tanaka et al., 2009). NtMEK2, a tobacco MAPKK, is upstream of both WIPK and SIPK (Yang et al., 2001). Expression of NtMEK2<sup>DD</sup>, a constitutively active mutant of NtMEK2, induces HR-like cell death, defense gene expression, and generation of ROS, all of which are preceded by activation of endogenous WIPK and SIPK (Ren et al., 2002; Yang et al., 2001). NPK1-MEK1/NQK1-NTF6/NRK1 is a pivotal MAPK cascade in the regulation of cytokinesis (Sasabe et al., 2006). Like WIPK or SIPK, silencing *NbNPK1*, *NbMEK1* or *NbNTF6* attenuates N- and Pto-mediated resistance against TMV (Jin et al., 2002; Liu et al., 2004) and *Pseudomonas syringae* AvrPto, respectively (Ekengren et al., 2003). These studies indicated that MAPK cascades MEK2-WIPK/SIPK and NPK1-MEK1-NTF6 participate in disease resistance in plants.

The potato ortholog of tobacco NtMEK2, StMEK2 (formerly described as StMEK1) was also cloned (Katou et al., 2003). Transient expression of StMEK2<sup>DD</sup> induced HR-like cell death and ROS production in *N. benthamiana* leaves (Katou et al., 2003; 2005). We found that StMEK2<sup>DD</sup> induces accumulation of *NbRBOHB* mRNA (Yoshioka et al., 2003), suggesting that the transcriptional activation of *RBOH* is one of the functions of the MAPK cascade in ROS production. We also showed that silencing *NbRBOHA* and *NbRBOHB* in *N. benthamiana* plants leads to less ROS production and reduced resistance to *P. infestans* (Yoshioka et al., 2003). NTF4 is a tobacco MAPK that reveals high homology with SIPK (93.6% in identity) and a similar expression pattern and activation profile of SIPK (Ren et al., 2006). The conditional expression of *NTF4* induces autophosphorylation and HR-like cell death (Ren et al., 2006). It was shown that NbNTF4, like NbSIPK, also regulates the radical bursts (Asai et al., 2008). NTF4 may play a similar role to SIPK in the signaling of basal defense. INF1-induced expression of *NbRBOHB* was compromised in *SIPK/NTF4/NTF6*-silenced leaves, but not in *WIPK*-silenced leaves (Asai et al., 2008). Furthermore, conditional expression of *NbMEK1<sup>DD</sup>* induced expression of *NbRBOHB*. These results indicated that INF1 regulates *NbRBOHB*-dependent ROS generation through MEK2-SIPK/NTF4 and MEK1-NTF6 cascades. Fig. 1 summarizes mechanisms of radical burst regulated by MAPK cascades.

### CDPK activates NADPH oxidase by direct phosphorylation of its N-terminal region

Transient influx of  $\text{Ca}^{2+}$  into cytoplasm after perception of pathogen signals constitutes an early element of signaling cascades triggering oxidative burst and HR cell death (Blume et al., 2000; Grant et al., 2000; Lecourieux et al., 2006). CDPKs are



**Fig. 1.** Scheme of proposed model for signaling pathway leading to radical burst. Elicitor induces  $\text{Ca}^{2+}$  influx. Increase of intracellular  $\text{Ca}^{2+}$  concentration provokes  $\text{Ca}^{2+}$  binding to EF-hand motifs of CDPK and RBOH N-terminal region. Phosphorylation of RBOH by the CDPK results in the phase I (1st) and phase II (2nd) bursts. The elicitor induces NOA1- and NR-mediated NO burst by means of MEK2-SIPK/NTF4 cascade. MEK2-SIPK/NTF4 and (NPK1)-MEK1-NTF6 cascades up-regulate inducible form of *RBOH* gene. Question mark indicates unidentified MAPKKK.

Ser/Thr protein kinases that include a  $\text{Ca}^{2+}$  binding calmodulin-like domain and are the best-characterized calcium sensors in plants. CDPKs are encoded by a large multigene family with possible redundancy or diversity or both in their functions (Freymark et al., 2007; Harmon et al., 2001). Accumulating evidence indicates that CDPKs regulate many aspects of plant growth and development (Bachmann et al., 1996; Yoon et al., 2006), hormonal responses (Gargantini et al., 2009; McCubbin et al., 2004; Mori et al., 2006) and adaptation to biotic and abiotic stresses (Chico et al., 2002; Freymark et al., 2007; Ivashuta et al., 2005; Ludwig et al., 2005; Romeis et al., 2001; Saijo et al., 2000). Some CDPK genes are induced transcriptionally by pathogen signals (Chico et al., 2002; Murillo et al., 2001; Romeis et al., 2001; Yoon et al., 1999). CDPKs have been suggested to function upstream of ROS production (Kobayashi et al., 2007; Ludwig et al., 2004). Ectopic expression of Arabidopsis *AK1* (*AtCPK1*) increases NADPH oxidase activity and ROS production in tomato protoplasts (Xing et al., 2001). Functional analysis using artificially activated CDPK has shown that CDPK consists of four domains: an N-terminal variable domain (V), a Ser/Thr protein kinase domain (K), an autoinhibitory junction domain, and a C-terminal calmodulin-like domain including four EF-hand motifs (Harper et al., 2004). A junction domain between the kinase and calmodulin-like domains is a pseudo-substrate in the absence of  $\text{Ca}^{2+}$  and keeps a low activity state (Harmon et al., 1994). A truncated VK form, with the junction and calmodulin-like domains removed, shows constitutive-activity in the absence of  $\text{Ca}^{2+}$  (Harper et al., 1994). Ludwig et al. (2005) showed that transient expression of NtCDPK2VK stimulates ROS production and HR-like cell death by abiotic hypo-osmotic and wound stresses, and that NtCDPK2VK increases the level of jasmonic acid, 12-oxo-phytodienoic acid and ethylene under abiotic stress stimuli and has a cross-talk

with MAPKs in ethylene signaling.

Pathogen infection or elicitor treatment causes immediate phase I oxidative burst, and then massive phase II oxidative burst in potato leaves and tubers (Chai and Doke, 1987; Yoshioka et al., 2001). We previously isolated *StRBOHA* to *D* from potato plants (Yamamizo et al., 2006; Yoshioka et al., 2001). In potato tubers, *StRBOHA* is constitutively expressed at a low level, and *StRBOHB* is induced by treatment with cell wall elicitor from *P. infestans* (Yoshioka et al., 2001). In leaves, *StRBOHA*, *StRBOHB* and *StRBOHD* are expressed at a low level, but *StRBOHC* is markedly induced in response to *P. infestans* (Yamamizo et al., 2006). The promoter analysis of *StRBOHC* demonstrated that MEK2 regulates the gene activation at the transcriptional level (unpublished results). NADPH oxidase inhibitor diphenylene iodonium (DPI) blocked both bursts, whilst pretreatment of tuber with the protein synthesis inhibitor cycloheximide abolished only the second burst. These data suggest that *StRBOHA* and *StRBOHB* plus C contribute to phase I and phase II bursts, respectively (Yamamizo et al., 2006; Yoshioka et al., 2001). We found that both bursts are also inhibited by a protein kinase inhibitor or a calcium inhibitor (Miura et al., 1995). These findings led us to investigate the direct phosphorylation of the N-terminal region of the *StRBOH* protein by certain protein kinases for the activation of the enzymes. We identified Ser82 and Ser97 in the N-terminus of potato *StRBOHB* as potential phosphorylation sites by in-gel kinase assays using the mutated N-terminal proteins of *StRBOHB* (Kobayashi et al., 2007). Moreover, an anti-phosphopeptide (pSer82) antibody indicated that the Ser82 was phosphorylated by pathogen signals in plants. We cloned *StCDPK5* by cDNA expression screening using the anti-pSer82 antibody and cells expressing an N-terminus of *StRBOHB*, and

mass spectrometry analyses showed that the CDPK phosphorylated only Ser82 and Ser97 in the N-terminus in a calcium-dependent manner. Ectopic expression of the constitutively active mutant of StCDPK5, StCDPK5VK, provoked ROS production in *N. benthamiana* leaves. The CDPK-mediated ROS production was disrupted by knockdown of *NbRBOHB* in tobacco. The loss-of-function was complemented by heterologous expression of wild-type potato StRBOHB, but not by a mutant (S82A/S97A). Furthermore, the heterologous expression of StCDPK5VK phosphorylated Ser82 of StRBOHB in tobacco. Comparing the differences in predicted amino acid sequences of the four StRBOHBs, StRBOHA, StRBOHC and StRBOHD also have presumable phosphorylation motifs corresponding to those of StRBOHB, and the recombinant N-terminal peptides of the four StRBOHBs are phosphorylated by StCDPK5 *in vitro* (Kobayashi et al., 2007). Phosphoproteomics analyses of elicitor signaling in Arabidopsis indicate that the N-terminal region of AtRBOHD is phosphorylated *in vivo* when treated with flg22 and xylanase, and mutagenesis in some of the phosphorylation sites decreases flg22-triggered oxidative bursts (Benschop et al., 2007; Nühse et al., 2007). AtRBOHD is synergistically activated by  $\text{Ca}^{2+}$  binding and phosphorylation in a heterologous expression system using a mammalian cell line (Ogasawara et al., 2008). AtRBOHC/RHD2, which is required for root hair elongation, activates ROS production through calcium-dependent protein phosphorylation (Takeda et al., 2008). These results suggest that N-terminal phosphorylation is a conserved process in RBOH activation. Mammalian NOX5, which carries an N-terminal extension including EF-hand motifs, is regulated by direct phosphorylation (Jagnandan et al., 2007; Serrander et al., 2007).

Furthermore, analyses by the BiFC (bimolecular fluorescence complementation) method indicated that StRBOHB and StCDPK5 interact on the plasma membrane and mutations of *N*-myristoylation and palmitoylation sites of the StCDPK5, which are responsible for localization on the membrane, eliminate these interactions (unpublished results). These lines of evidence suggest that the StCDPK5 induces phosphorylation of RBOHBs and regulates the oxidative burst. Figure 1 indicates mechanisms of oxidative burst regulated by CDPK.

#### CDPK-triggered oxidative burst confers resistance to late blight but increases susceptibility to early blight pathogen in potato

The importance of RBOH-dependent ROS production has been shown by using *RBOH* mutants or knock-down techniques (Asai et al., 2008; Foreman et al., 2003; Kwak et al., 2003; Sagi et al., 2004; Simon-Plas et al., 2002; Torres et al., 2002; 2005; Yoshie et al., 2005; Yoshioka et al., 2003). However, gain-of-function analysis of NADPH oxidase has not been reported. StCDPK5 phosphorylates the N-terminus of StRBOHBs calcium dependently, and induces oxidative burst. These data suggest that StCDPK5VK is a useful tool for gain-of-function analysis of NADPH oxidase in defense responses during plant-pathogen interactions, because overexpression of the *RBOH* gene does not induce ROS production (Torres et al., 2005). Substitution of phosphorylated Ser by Asp of AtRBOHD does not produce a gain-of-function mutant (Nühse et al., 2007). We also failed to produce a constitutively active mutant of StRBOHB by double mutation of S82D/S97D in the N-terminal, even though double mutation of S82A/S97A lost ROS productivity by StCDPK5VK (Kobayashi et al., 2007). We generated transgenic potato plants containing constitutively active StCDPK5VK and investigated the role of RBOH-

dependent ROS production in resistance to biotrophic and necrotrophic pathogens and defense response (Kobayashi et al., 2009).

Late blight, caused by the notorious oomycete pathogen *P. infestans*, is a devastating disease of potato and tomato. During the 1840s it caused the Irish potato famine and over one million fatalities. Although *P. infestans* is often considered a hemi-biotrophic pathogen (i.e., pathogens that live part of their lives as biotrophs, and the other part, often associated with later stages of infection, as necrotrophs or saprophytes; Agrios, 2005), the means by which it is a near-obligate pathogen under natural and agricultural conditions suggest that it is better considered a potential biotrophic pathogen (Fry, 2008). We generated transgenic potato plants containing *StCDPK5VK* under control of a pathogen-inducible promoter *PVS3* (Yamamoto et al., 2006). ROS production was induced by inoculation with virulent *P. infestans* and *A. solani* at the infection sites in the transgenic plants. Transgenic potato plants containing *PVS3::StCDPK5VK* indicated resistance to biotrophic pathogen *P. infestans* after inoculation, but increased susceptibility to necrotrophic pathogen *A. solani*. These results provide evidence that StCDPK5VK-mediated ROS production confers resistance to biotrophic pathogens, but increases susceptibility to necrotrophic pathogens (Kobayashi et al., 2009). This suggests that StCDPK5-mediated ROS production has a pivotal role in defense signaling, and that necrotrophic pathogens hijacks the host cell death signaling to invade host cells together with host-specific toxins as a pathogenicity factor (Gilchrist, 1998; Glazebrook, 2005; Greenberg, 1997). Arabidopsis mutants with delayed or reduced cell death response are generally more resistant to necrotrophic pathogen *Botrytis cinerea* that causes gray mold disease, but mutants in which cell death is accelerated are more susceptible (van Baaren et al., 2007). Growth of *B. cinerea* and necrotrophic fungal pathogen *Sclerotinia sclerotiorum* is suppressed in the HR-deficient Arabidopsis mutant *dnd1* and is increased by pretreatment with glucose and glucose oxidase (GO), which generate  $\text{H}_2\text{O}_2$  (Govrin and Levine, 2000). Arabidopsis mutants lacking DELLAs increases RBOH-dependent ROS accumulation in biotic and abiotic responses and shows substantially strong disease symptoms caused by *B. cinerea* and *Alternaria brassicicola*, and resistance to hemi-biotrophic bacterial pathogen *P. syringae* pv. *tomato* DC3000 (Achard et al., 2008; Navarro et al., 2008). Loss-of-function analyses using inhibitors and VIGS have investigated the role of the radical burst in pathogenesis. ROS function has a negative role in resistance or has a positive role in expansion of disease lesions during *B. cinerea* and *N. benthamiana* interaction (Asai and Yoshioka, 2009). Taking these results together, phenotypes of *PVS3::StCDPK5VK* plants seem to reflect roles of ROS produced by RBOHBs in infected cells.

HR-like cell death was observed by cells expressing *StCDPK5VK* in response to *P. infestans*, which is surprising because Agrobacterium-mediated transient expression of *StCDPK5VK* did not induce visible cell death in *N. benthamiana* leaves. This suggests that ROS activate cell death by cooperation with other signals induced by virulent *P. infestans* infection. One of the best-characterized signals as a counterpart of ROS in cell death is NO (Zaninotto et al., 2006). NO is generated in plant-pathogen interactions by putative NOS or NR (Delledonne et al., 1998; Yamamoto et al., 2003). NO and ROS together, but not individually, are required to induce cell death (Delledonne et al., 1998), and balanced production of NO and  $\text{H}_2\text{O}_2$  is important to induce HR cell death (Delledonne et al., 2001). Catalase-deficient tobacco leaves, which accumulate sublethal levels of  $\text{H}_2\text{O}_2$  under moderate high light condition, show cell death with

NO treatment but not leaves of wild-type plants (Zago et al., 2006). Genome-wide cDNA-amplified fragment length polymorphism analysis has shown that many genes are specifically induced by combined action of NO and H<sub>2</sub>O<sub>2</sub> (Zago et al., 2006). Peroxynitrite (ONOO<sup>-</sup>) generated from the reaction of NO and O<sub>2</sub><sup>-</sup> is also related to plant-pathogen interactions. Urate, a natural peroxynitrite scavenger, reduces HR cell death caused by avirulent *P. syringae* in Arabidopsis (Alamillo and García-Olmedo, 2001). Taking these results together, we speculate that increased ROS production causes cell death by coordinated and balanced production of NO in response to virulent pathogens.

Studies have shown that the effects of the ROS and NO production on defense response appear to be diverse in plant-pathogen interactions. Arabidopsis lacking the NO ASSOCIATED1 (AtNOA1) mutant that reduces NO production shows an increase in susceptibility to virulent *P. syringae* (Zeidler et al., 2004), indicating that NO participates in basal defense during compatible hemi-biotrophic bacterial pathogen and Arabidopsis interaction. In *N. benthamiana*, *NbRBOHB* silencing has a strong effect on resistance to the potential pathogen *P. infestans* (Yoshioka et al., 2003) but not to *B. cinerea*, and *NbNOA1* silencing induces high susceptibility to *B. cinerea* but not to *P. infestans* (Asai and Yoshioka, 2009; Asai et al., 2008). We indicated that transgenic potato plants expressing *StCDPK5VK* fused to a pathogen-inducible promoter show high resistance to *P. infestans* but high susceptibility to the necrotrophic pathogen *A. solani*. *StCDPK5VK* induces production of ROS, but not of NO. The results support the conclusion that ROS may have a negative role in disease resistance to necrotrophic pathogens or a positive role in expansion of disease lesions. Transgenic potato plants expressing a constitutively active form of MAPKK, *StMEK2* (*StMEK2<sup>DD</sup>*) controlled by the same pathogen-inducible promoter as for *StCDPK5VK*, are resistant to both *P. infestans* and *A. solani* (Yamamizo et al., 2006). *MEK2<sup>DD</sup>* activates SIPK, which induces both RBOH-dependent ROS and NOA1-mediated NO production in *N. benthamiana* (Asai et al., 2008). These results support the idea that NO contributes to disease resistance against necrotrophic pathogens *A. solani* and *B. cinerea*, but synergistically works with ROS to induce cell death providing an advantage for these necrotrophic pathogens. NO may have diverse functions as a counterpart of ROS to contribute to cell death or resistance to a wide spectrum of pathogens, or both, leaving open the question how NO and ROS direct the cellular phenotype. One possible explanation for the diverse effect is that changes in redox balance correspond to a shift toward host cell death or defense response. ROS production does not always result in increased susceptibility, which depends on the timing and the intensity of ROS (Asselbergh et al., 2007). *B. cinerea* endo-polygalacturonase 1 (BcPG1), first known as a virulence factor (ten Have et al., 1998), elicits cell death and several defense responses, including production of NO and ROS and activation of MAPKs (Kars et al., 2005; Poinssot et al., 2003; Vandelle et al., 2006). However, mutants overproducing BcPG1 indicate decreased pathogenicity in grape and bean, triggering intense oxidative bursts (Kunz et al., 2006). Loss-of-function analysis indicates that ROS produced by AtRBOHD acts as a negative regulator of the runaway cell death in Arabidopsis *Isd1* mutant (Torres et al., 2005).

Transgenic potato plants expressing a fungal GO increase levels of H<sub>2</sub>O<sub>2</sub> and show resistance to a broad range of plant pathogens, including *A. solani* and *P. infestans* (Wu et al., 1995; 1997). These conflicting responses with *PVS3::StCDPK5VK* plants may be attributed to temporal and quantitative differences in ROS

production. *PVS3::StCDPK5VK* plants induced ROS production only in pathogen interactions, but GO-transgenic plants have constitutively higher levels of ROS and increased defense-related gene expression, SA accumulation, and lignin content (Wu et al., 1997). Pathogen infection or elicitor treatment causes immediate phase I oxidative burst, and then massive phase II oxidative burst. A protein synthesis inhibitor abolishes only phase II oxidative burst in potato leaves and tubers (Chai and Doke, 1987; Yoshioka et al., 2001), suggesting that *StCDPK5VK*-induced ROS production in transgenic potato increases phase II oxidative burst. We think the increased massive second oxidative burst may cause cell death in pathogen-attacked cells expressing *StCDPK5VK*. Thus, several arguments exist about the role of ROS during plant and pathogen interactions. Gain-of-function analysis of NADPH oxidase at least shows that ROS has a positive effect on disease resistance to biotrophic pathogens and a negative effect on disease resistance to necrotrophic pathogens.

## Conclusions and perspectives

ROS and NO are believed to play important roles independently or coordinately in plant innate immunity. ROS generated on the plasma membrane are released to the apoplast where they activate the Ca<sup>2+</sup> channel to increase the level of cytosolic Ca<sup>2+</sup> (Lecourieux et al., 2002). Ca<sup>2+</sup> may function not only as an inducer of the oxidative burst, but also as a signaling molecule downstream of the oxidative burst and causes various cellular responses, including defense (Asai and Yoshioka, 2008). However, NO signaling includes various messenger molecules, such as cGMP, cADP ribose and Ca<sup>2+</sup> (Durner et al., 1998; Romero-Puertas et al., 2004; Wendehenne et al., 2001), which both directly and indirectly modulate the expression of specific genes (Parani et al., 2004; Polverari et al., 2003). NO signaling pathways often include post-translational modification of target proteins, such as NO-dependent Cys S-nitrosylation that can modulate the activity and function of different proteins (Feechan et al., 2005; Lindermayr et al., 2005; Romero-Puertas et al., 2004; Sokolovski and Blatt, 2004). NO can also react with O<sub>2</sub><sup>-</sup> to form the reactive molecule ONOO<sup>-</sup>, which leads to formation of NO<sub>2</sub> and the effective oxidant hydroxyl radical. ONOO<sup>-</sup> is also responsible for Tyr nitration (Saito et al., 2006), which is the major toxic reactive nitrogen species in animal cells (Stamler et al., 1992). ONOO<sup>-</sup> is relevant to HR and defense gene expression (Alamillo and García-Olmedo, 2001). One study emphasized that the combination of NO and H<sub>2</sub>O<sub>2</sub>, but not ONOO<sup>-</sup>, takes part in the induction of defense responses (Delledonne et al., 2001). Recent studies indicate that these redox changes regulate MAPK activity by attenuating a protein Tyr phosphatase activity (Gupta and Luan, 2003) and the conformation of NPR1, a master regulator of SA-mediated defense genes (Tada et al., 2008). Thus, identification of sensor and effector proteins for radicals will be most important in dissecting the complexities of defense-related redox signaling.

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