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Papain-like cysteine proteases as hubs in plant immunity

Author for correspondence:
 Gunther Doehlemann
 Tel: +49 2214701647
 Email: g.doehlemann@uni-koeln.de

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Johana C. Misas-Villamil¹, Renier A. L. van der Hoorn² and Gunther Doehlemann¹

¹Botanical Institute and Center of Excellence on Plant Sciences (CEPLAS), University of Cologne, BioCenter, Zuelpicher Str. 47a, D-50674, Cologne, Germany; ²The Plant Chemetics Laboratory, Department of Plant Sciences, University of Oxford, South Parks Lane Road, Oxford, OX1 3RB, UK

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Summary

Plants deploy a sophisticated immune system to cope with different microbial pathogens and other invaders. Recent research provides an increasing body of evidence for papain-like cysteine proteases (PLCPs) being central hubs in plant immunity. PLCPs are required for full resistance of plants to various pathogens. At the same time, PLCPs are targeted by secreted pathogen effectors to suppress immune responses. Consequently, they are subject to a co-evolutionary host–pathogen arms race. When activated, PLCPs induce a broad spectrum of defense responses including plant cell death. While the important role of PLCPs in plant immunity has become more evident, it remains largely elusive how these enzymes are activated and which signaling pathways are triggered to orchestrate different downstream responses.

I. Introduction

Plants are continuously challenged by microbes and have developed different mechanisms to defeat pathogens and other invaders. The first contact with microbes usually takes place in extracellular compartments, namely on the epidermal surface and in the apoplast, including cell walls. Processes in this extracellular battleground determine the primary outcome in the majority of plant–microbe interactions. After this first contact, different signaling pathways in the cell are activated to orchestrate downstream responses such as modulation of various enzymatic activities. In this article, we will emphasize the role of papain-like cysteine proteases (PLCPs), which control key processes at different

levels of plant defense. PLCPs are prominent enzymes in the plant apoplast and belong to MEROPS (<https://merops.sanger.ac.uk/>) protease family C1A of clan CA, of which papain is the type member. In animals PLCPs are often called cathepsins and PLCPs in plants fall into nine subfamilies (Richau *et al.*, 2012). PLCPs are produced as pre-proteases, containing an N-terminal signal peptide for secretion and an auto-inhibitory pro-domain that needs to be removed for protein activation, releasing a mature 25–35 kDa active protease. The protease domain contains the catalytic triad formed by the amino acids Cys, His and Asn. Some PLCPs also carry a C-terminal granulin domain with unknown function. In plants, nine PLCP subfamilies can be found (Fig. 1; Richau *et al.*, 2012). Based on recent research, we present here five observations

demonstrating that PLCPs are essential and central hubs of plant immunity:

II. Depletion of PLCPs hampers plant immunity

Many cases of protease depletion (e.g. by knockout or RNAi) indicate important roles for PLCPs in plant immunity. Arabidopsis null mutants for the PLCP RD21 are more susceptible to the necrotrophic fungal pathogen *Botrytis cinerea* (Shindo *et al.*, 2012), although these lines were more resistant for the same pathogen in detached leaf assays (Lampl *et al.*, 2013). Silencing of *Nicotiana benthamiana* C14 leads to increased susceptibility for the oomycete pathogen *Phytophthora infestans* (Kaschani *et al.*, 2010; Bozkurt *et al.*, 2011). Likewise, tomato *rcr3* null mutants have lost resistance based on the *Cf-2* resistance gene against both the fungus *Cladosporium fulvum* and the nematode *Globodera rostochiensis* (Dixon *et al.*, 2000; Lozano-Torres *et al.*, 2012). The *rcr3* null mutants are also more susceptible for *P. infestans* (Song *et al.*, 2009), even in the absence of *Cf-2* (Ilyas *et al.*, 2015). Antisense lines depleted for the Pip1 protease of tomato are hypersusceptible to *C. fulvum*, *Pseudomonas syringae* and *P. infestans* (Ilyas *et al.*, 2015). Interestingly, silencing *NbPip1* in *N. benthamiana* blocks Avr4/Cf-4 induced hypersensitive response (HR) (Xu *et al.*, 2012), whereas silencing *NbCYP1* or *NbCYP2* in *N. benthamiana* increases susceptibility to the necrotrophic fungal pathogen *Colletotrichum destructivum* (Hao *et al.*, 2006). Furthermore, Arabidopsis *rd19* null mutants are impaired in resistance to the bacterial pathogen *Ralstonia solanacearum* (Bernoux *et al.*, 2008). Resistance to herbivore attack is also tightly linked to protease expression. Most prominent example is papain from Papaya, which is present in wound-exuding latex and is activated during wounding (El Moussaoui *et al.*, 2001; Azarkan *et al.*, 2006). Papain is also

responsible for the strong toxicity of papaya leaves to insects (Konno *et al.*, 2004). In maize leaves, Mir1 accumulates at wounding sites and confers enhanced resistance against caterpillars by degrading the peritrophic matrix of the insect gut (Pechan *et al.*, 2000, 2002). Accumulation of Mir1 also enhances resistance to root-feeding herbivores (Gill *et al.*, 2011) and Mir1 itself acts as an ethylene-dependent, long-distance transport signal that confers resistance to corn leaf aphids (Louis *et al.*, 2015). In summary, PLCPs are found to be required for plant defense to various kinds of biotic stresses in unrelated species.

III. PLCPs are common targets of pathogen effectors

PLCPs representing different subfamilies are targeted by a variety of unrelated pathogen-derived effectors (Table 1). C14 of tomato and potato is inhibited by the cystatin-like effectors EpiC1 and EpiC2B, which are secreted by *P. infestans* (Kaschani *et al.*, 2010). The C14 protease of tomato is also targeted by the *P. infestans* effector AvrBb2, which prevents C14 secretion into the apoplast presumably by blocking its function in defense (Bozkurt *et al.*, 2011). Closely related to C14 are maize proteases CP1A and CP1B, which are inhibited by the Pit2 effector from the fungal pathogen *Ustilago maydis* (Mueller *et al.*, 2013). Pit2 also suppresses the activity of maize proteases XCP2 and CP2, respectively (Mueller *et al.*, 2013). Likewise, tomato CYP1, is targeted and inhibited by the RNA-silencing suppressor V2 from the tomato yellow leaf curl geminivirus (Bar-Ziv *et al.*, 2012, 2015). A striking example for a PLCP being targeted by unrelated plant pathogens is tomato Rcr3. At first, it was found to be required for fungal resistance (Krüger *et al.*, 2002). The fungal pathogen *C. fulvum* secretes the effector Avr2, which inhibits Rcr3 (Rooney *et al.*, 2005). In addition, Rcr3 is inhibited by EpiC1 and EpiC2B from *P. infestans* (Song *et al.*, 2009) as well as by Gr-VAP1, an allergen-like effector secreted by the nematode *G. rostochiensis* (Lozano-Torres *et al.*, 2012). Notably, Avr2, EpiC1/2B and Gr-VAP1, although all inhibiting Rcr3, are unrelated proteins. A PLCP closely related to Rcr3 is tomato Pip1, which is also inhibited by EpiC2B (Tian *et al.*, 2007) and Avr2 (Shabab *et al.*, 2008). Another example is Arabidopsis RD19, which is re-localized to the host cell nucleus by the bacterial type III effector PopP2 from *R. solanacearum* (Bernoux *et al.*, 2008). In summary, a growing body of literature demonstrates that evolutionarily unrelated plant pathogens including fungi, oomycete, nematodes, bacteria and viruses actively interfere with the activity and subcellular location of plant PLCPs.

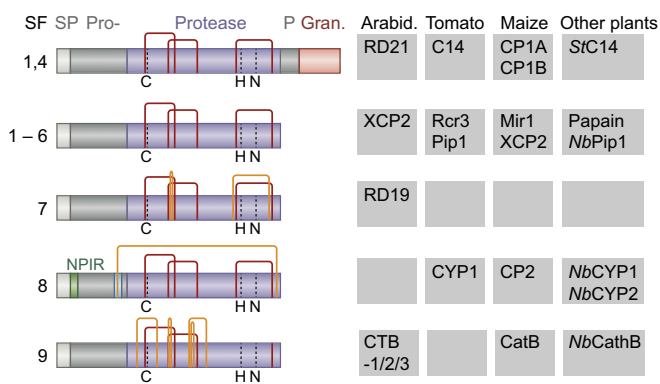


Fig. 1 Schematic representation of papain-like cysteine proteases (PLCPs) found in different plants. In general, PLCPs contain a signal peptide (SP, light grey), an auto-inhibitory pro-domain (Pro-, grey) and a protease domain (purple). The mature protease domain holds the catalytic triad Cys-His-Asn. Some members of subfamily 1 and subfamily 4 also have at the C-terminus a proline rich domain (P, grey) and a granulin domain (Gran., pink). Subfamily 8 proteases have at the N-terminus a vacuolar targeting signal (NP1R, green) and a minichain that remains after cleavage of the pro-domain (light blue). Subfamily 9 proteases contain the C-terminus motif ECGIE (red). Disulphide bridges common to most PLCPs (red thin lines) and, subfamily specific disulphide bridges (orange thin lines) are indicated. SF, subfamily classification; Arabid., Arabidopsis. Examples of known and characterized PLCPs described in plants (right, grey boxes).

IV. PLCPs induce defense responses and cell death

One of the first indications that apoplastic cysteine proteases may act in immune signalling was the finding that E-64, a well-known inhibitor of cysteine proteases, can delay hypersensitive response in the cowpea–cowpea rust fungus system (D’Silva *et al.*, 1998). Later on, it was discovered that *N. benthamiana* Cathepsin B (*NbCathB*) is required for the hypersensitive response and disease resistance induced by nonhost bacterial pathogens (Gilroy *et al.*, 2007; McLellan *et al.*, 2009). Furthermore, Arabidopsis Cathepsin B

Table 1 Plant papain-like cysteine proteases (PLCPs) involved in biotic interactions

PLCP	Species	SF	Function/phenotype	References
RD21	Arabidopsis	1	Knockout (KO)-lines susceptible to <i>Botrytis cinerea</i> KO-lines resistant to <i>B. cinerea</i> in detached leaves and <i>Sclerotinia sclerotiorum</i> . Inhibited by AtSerp1	Shindo <i>et al.</i> (2012) Lampl <i>et al.</i> (2013)
Mir1	Maize	1	Accumulates at wounding sites Enhanced resistance against caterpillars/root-feeding herbivores Acts as ethylene signal conferring resistance to aphids	Pechan <i>et al.</i> (2000, 2002) Gill <i>et al.</i> (2011) Louis <i>et al.</i> (2015)
C14	Potato	1	Inhibited by <i>Phytophthora infestans</i> effectors EPIC1 and EPIC2B. Protease under diversifying selection.	Kaschani <i>et al.</i> (2010); Kaschani & Van der Hoorn (2011)
Papain	Tomato Papaya	3	Targeted by <i>P. infestans</i> effectors EPIC1, EPIC2B and AvrB1b2 Activated during wounding Involved in defense against polyphagous pests	Kaschani <i>et al.</i> (2010); Bozkurt <i>et al.</i> (2011) Azarkan <i>et al.</i> (2006) Konno <i>et al.</i> (2004)
XCP2	Arabidopsis Maize	3	Increases susceptibility to <i>Ralstonia solanacearum</i> Inhibited by <i>Ustilago maydis</i> effector Pit2 and maize cystatin CC9	Zhang <i>et al.</i> (2014) Mueller <i>et al.</i> (2013); Van der Linde <i>et al.</i> (2012a,b)
C14	<i>Nicotiana benthamiana</i>	4	Silenced plants resistant to <i>P. infestans</i>	Kaschani <i>et al.</i> (2010); Bozkurt <i>et al.</i> (2011)
CP1A/ CP1B	Maize	4	Inhibited by <i>U. maydis</i> effector Pit2 and maize cystatin CC9	Mueller <i>et al.</i> (2013); Van der Linde <i>et al.</i> (2012a,b)
Rcr3	Tomato	6	Resistance to <i>Cladosporium fulvum</i> , <i>Globodera rostochiensis</i> and <i>P. infestans</i> Required for the function of Cf2 conferring fungal resistance Inhibited by effectors Avr2, EPIC1, EPIC2B and GrVAP1	Dixon <i>et al.</i> (2000); Lozano-Torres <i>et al.</i> (2012); Song <i>et al.</i> (2009) Krüger <i>et al.</i> (2002) Rooney <i>et al.</i> (2005); Song <i>et al.</i> (2009); Lozano-Torres <i>et al.</i> (2012)
Pip1	Tomato	6	Mutants are hypersusceptible to <i>C. fulvum</i> , <i>P. infestans</i> and <i>Pseudomonas syringae</i> Inhibited by <i>P. infestans</i> EPIC2B and <i>C. fulvum</i> Avr2	Ilyas <i>et al.</i> (2015) Tian <i>et al.</i> (2007); Shabab <i>et al.</i> (2008) Xu <i>et al.</i> (2012)
RD19	<i>N. benthamiana</i> Arabidopsis	7	Silencing blocks HR induced by Avr4/Cf4 recognition Mutants are impaired in resistance to <i>R. solanacearum</i> Targeted by PopP2 from <i>R. solanacearum</i>	Bernoux <i>et al.</i> (2008) Bernoux <i>et al.</i> (2008) Hao <i>et al.</i> (2006)
CYP1/ CYP2	<i>N. benthamiana</i>	8	Silencing enhanced susceptibility to <i>Colletotrichum destructivum</i>	Hao <i>et al.</i> (2006)
CYP1	Tomato	8	Inhibited by V2 from tomato yellow leaf curl geminivirus	Bar-Ziv <i>et al.</i> (2012, 2015)
CP2	Maize	8	Inhibited by <i>U. maydis</i> effector Pit2 and maize cystatin CC9	Mueller <i>et al.</i> (2013); Van der Linde <i>et al.</i> (2012a,b)
CathB	Arabidopsis	9	Required for hypersensitive response (HR) induced by nonhost bacterial pathogens Mutants show reduced programmed cell death during abiotic stress	Gilroy <i>et al.</i> (2007); McLellan <i>et al.</i> (2009) Ge <i>et al.</i> (2016)

SF, phylogenetic classification of PLCPs into subfamilies according to Richau *et al.* (2012).

(*ctb*) mutants show reduced programmed cell death (PCD) induced by abiotic stresses (Ge *et al.*, 2016). Arabidopsis RD21 has been identified as a 'pro-death' signal activated during elicitation of cell death. The serpin protease inhibitor, AtSerp1, exhibits a pro-survival function by covalently inhibiting RD21 and causing a change in compartmentalization (Lampl *et al.*, 2013). Gene expression analyses on barley have shown upregulation of PLCPs during senescence, a form of PCD, for almost all members of different subfamilies (Diaz-Mendoza *et al.*, 2014) but a role during disease resistance still remains to be elucidated.

Besides the contribution of PLCPs in PCD, direct evidence for the importance of apoplastic cysteine proteases during defence responses came from the finding that salicylic acid (SA) treatment activates PLCPs in maize, and that PLCPs themselves activate SA-related gene expression (Van der Linde *et al.*, 2012a,b). Remarkably, inhibition of maize apoplastic cysteine proteases by the endogenous cystatin CC9 is essential to suppress host immunity during infection with the biotrophic pathogen *U. maydis* (Van der Linde *et al.*, 2012a,b). Furthermore, Arabidopsis PIRIN2, a

member of the cupin protein subfamily, stabilizes the protease XCP2 and increases susceptibility to the vascular pathogen *R. solanacearum* (Zhang *et al.*, 2014). Recently, a 9-lipoxygenase-derived cyclopentanone in maize, 10-oxo-11-phytoenoic acid (10-OPEA), was found to act as a potent cell death signal in multiple organs present during biotic stresses and developmental conditions (Christensen *et al.*, 2015, 2016). The cell death inducing activity of 10-OPEA was characterized by ion leakage and apoptotic-like DNA fragmentation in maize treated leaves (Christensen *et al.*, 2015). Interestingly, the cell-death inducing activity of 10-OPEA requires induction of PLCPs. Consequently, maize plants overexpressing the cystatin CC9 were partially insensitive to 10-OPEA providing further evidence for the importance of PLCPs during immunity.

V. PLCPs can act as co-receptors

Tomato Rcr3 is required for the function of the receptor-like protein Cf-2, which confers resistance against *C. fulvum* secreting

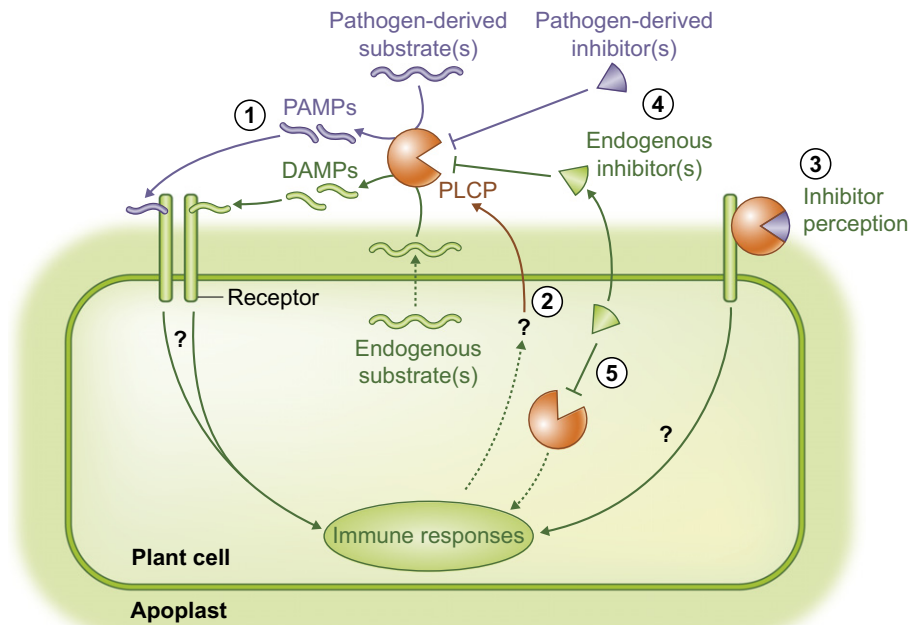


Fig. 2 Tentative model summarizing known and hypothetical functions of papain-like cysteine proteases (PLCPs) during plant immune-signaling. (1) PLCPs might release damage associated molecular patterns (DAMPs) or pathogen associated molecular patterns (PAMPs) that are recognized by receptors activating signaling cascades and consequently immune responses. (2) Likewise, induction of defense responses, for example by salicylic acid (SA) signaling, may lead to an activation of PLCPs, establishing a feedback loop. (3) PLCPs act as co-receptors and 'decoys' that evolve during an evolutionary arms race to avoid pathogen colonization. (4) To overcome immunity, pathogens produce effector molecules inhibiting PLCP activity. Because PLCPs are mainly activated by post-transcriptional processing, endogenous inhibitors such as cystatins or serpins may control the outcome in different signaling pathways leading to activation or deactivation of immune responses including programmed cell death (PCD) (5).

Avr2 (Krüger *et al.*, 2002). Avr2 binds to and inhibits Rcr3 and this complex is sensed by Cf-2, consistent with the Guard and Decoy Models (Rooney *et al.*, 2005; Van der Hoorn & Kamoun, 2008). Remarkably, Rcr3 is also required for the perception of nematode effector Gr-VAP1, which also inhibits Rcr3 and triggers immune responses in the presence of Cf-2 (Lozano-Torres *et al.*, 2012). Interestingly, VAP proteins from different nematodes can suppress PCD mediated by surface-localized immune receptors in *Arabidopsis* (Lozano-Torres *et al.*, 2014). The molecular mechanism of Avr2/Gr-VAP1 perception is not yet understood fully, but one emerging hypothesis is that Rcr3 is constitutively bound to Cf-2 protein, acting as a co-receptor to perceive the presence of protease inhibitors (Ilyas *et al.*, 2015). Rcr3 of cultivated tomato (Rcr3^{lyc}) triggers auto-necrosis in combination with Cf-2, which originates from *S. pimpinellifolium* (Krüger *et al.*, 2002). However, the allelic Rcr3^{pim} protein suppresses this necrotic response in the Rcr3^{pim}/Rcr3^{lyc} hybrid, suggesting that Rcr3^{pim} protein can outcompete Rcr3^{lyc} and consistent with the pre-existing co-receptor model (Ilyas *et al.*, 2015). These data illustrate that PLCPs can operate as co-receptors, sensing perturbations of receptor proteins thus activating defense responses.

VI. Natural variation in PLCPs is caused by arms races and host adaptation

Antagonistic protease-inhibitor interactions cause an arms race that has left its traces in the natural variation of proteases. This was first observed for Rcr3 and Pip1 (Shabab *et al.*, 2008). Natural variation

of Rcr3 in wild tomato species resides on the surface of Rcr3, surrounding the active site, and likely represents the footprints of pathogen-derived inhibitors. Indeed, the variant N194D residue in Rcr3 locates close the catalytic Cys and reduces its interaction with Avr2 (Shabab *et al.*, 2008). Interestingly, N194D is also the only variant residue that exclusively prevents inhibition by Avr2 in natural Rcr3 variants (Hörger *et al.*, 2012). The N194D mutation also abolished HR-inducing activity in plants carrying *Cf-2* resistance genes. Other variant residues affect the strength of the HR response, presumably because of the interaction of Rcr3 with Cf-2 (Hörger *et al.*, 2012). Natural variation within Rcr3 also affects its interaction with Gr-VAP1 of the nematode *G. rostochiensis*, which interacts with Rcr3^{pim} but not Rcr3^{lyc}, even though these proteases only differ in a few amino acids (Lozano-Torres *et al.*, 2012). The other apoplastic proteases of tomato do not accumulate many variant residues on the surface, consistent with not being targeted by pathogen-derived inhibitors (Shabab *et al.*, 2008). This includes C14 of wild tomato, which is inhibited by cystatin-like EpiC of *P. infestans*. However, *P. infestans* has coevolved with wild potato, and C14 in wild potato carries variant residues at its surface, illustrating that traces of arms races can be found only in coevolving host-pathogen interactions (Kaschani & Van der Hoorn, 2011). Interestingly, the cystatin-like *PmEpiC* inhibitor of *P. mirabilis*, which has jumped onto a different host plant only recently, carries an adaptation that facilitates inhibition of the proteases of the new host, but causes reduced affinity to the proteases of the presumed former host (Dong *et al.*, 2014). Taken together,

PLCP inhibitor arms races strengthen the notion that PLCPs are an important part of extracellular defense.

VII. Conclusion: how do PLCPs activate immunity?

In light of the increasing evidence of papain-like cysteine proteases (PLCPs) being crucial components of plant immunity, one of the most intriguing questions is how their activity actually results in defense stimulation (Fig. 2). Interestingly, their capability to induce immune responses is not restricted to plants, which may suggest activation of highly conserved pathways in the innate immune system. Known plant-derived allergens are cysteine proteases, such as the ragweed (*Ambrosia artemisiifolia*) allergen Amba11 (Bouley *et al.*, 2015), papain or bromelain (Stewart & Thompson, 1996). For Papain it has been found that its proteolytic activity is required for triggering immune responses including MAPK signaling in human cells (Rosenstein *et al.*, 2014). Besides the well-known mechanism that proteases break down the barrier in lungs against allergens, a recently discovered mechanism of PLCPs to induce immune responses is the activation of protease-activated G-protein coupled receptors (Reddy *et al.*, 2015). Interestingly, not only endogenous Cathepsin S, but also the plant-derived proteases papain and mucunin (from tropical bean) were found to induce protease-activated receptors in mammals (Reddy *et al.*, 2015). Controlled proteolysis of receptor proteins, also referred to as ectodomain shedding, is well known in animal systems but little known in plants. First evidence for this mechanism comes from the *Arabidopsis thaliana* chitin receptor CERK1, yet the protease involved in this process remains elusive (Petutschnig *et al.*, 2014). Besides activation of receptors, proteases can release small peptides that are perceived as DAMPs to induce immunity. A fascinating mechanism was found for a soybean subtilisin-like protease, which releases an embedded cryptic 12-aa signal that triggers defense gene activation (Pearce *et al.*, 2010). However, for PLCPs this kind of mechanism has not been identified so far. It is challenging to deepen our understanding of the involvement of PLCPs in plant immunity because many open questions still have to be addressed. For example, to which extent is proteolytic activity of PLCPs required for triggering plant immunity? How is activation of PLCPs orchestrated? Salicylic acid treatment in maize triggers activation of PLCPs but there is still the possibility that it acts as a feedback loop because PLCPs themselves induce *PR*-gene expression (Van der Linde *et al.*, 2012a). Additionally, the substrates of PLCPs are still unknown. Plants contain a plethora of PLCPs localized in different compartments, but how is specificity achieved? Interestingly, E-64d has been used extensively to suppress autophagy but also apoplastic cysteine proteases. Is it a strategy that pathogens like *P. infestans* deploy to prevent secretion of PLCPs into the apoplast by AvrB1b2 (Bozkurt *et al.*, 2011), or to antagonize host autophagy cargo receptors to counteract host defenses (Dagdas *et al.*, 2016)? Furthermore, activation of PLCPs in the cell might induce a massive proteolytic activity provoking clearance of cell contents and cell death. In this case PLCPs may need little specificity whilst still releasing signaling molecules. In light of all

the different immune responses involving PLCP activity, it will be a striking challenge to elucidate how target-specificity of PLCPs is regulated and how they discriminate between pathogen and host proteins.

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See also the Commentary on this article by Ökmen & Doehlemann, 212: 799–801.