GRIM REAPER peptide binds to receptor kinase PRK5 to trigger cell death in *Arabidopsis*

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Abstract

Recognition of extracellular peptides by plasma membrane-localized receptor proteins is commonly used in signal transduction. In plants, very little is known about how extracellular peptides are processed and activated in order to allow recognition by receptors. Here, we show that induction of cell death *in planta* by a secreted plant protein GRIM REAPER (GRI) is dependent on the activity of the type II metacaspase METACASPASE-9. GRI is cleaved by METACASPASE-9 *in vitro* resulting in the release of an 11 amino acid peptide. This peptide bound *in vivo* to the extracellular domain of the plasma membrane-localized, atypical leucine-rich repeat receptor-like kinase POLLEN-SPECIFIC RECEPTOR-LIKE KINASE 5 (PRK5) and was sufficient to induce oxidative stress/ROS-dependent cell death. This shows a signaling pathway in plants from processing and activation of an extracellular protein to recognition by its receptor.

Keywords ligand; protease; receptor-like kinase; secreted protein

Subject Categories Plant Biology; Signal Transduction

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Introduction

Recognition of extracellular signals is central for plant development and survival. Plant-encoded extracellular peptides and proteins are important components for developmental and stress response regulators (Boller & Felix, 2009; Butenko et al, 2009). In the immune response, plants also recognize pathogen-associated molecular patterns (PAMPs) of microbial origin (Boller & Felix, 2009). The *Arabidopsis thaliana* genome encodes several hundred secreted proteins (Butenko et al, 2009; Murphy et al, 2012) and more than 400 membrane-spanning receptor-like protein kinases (RLKs) (Shiu & Bleecker, 2003). This suggests a large number of potential ligand–receptor interactions providing a complex network of extracellular signaling modules in plants (Boller & Felix, 2009). Nonetheless, only a few peptide–receptor interactions have so far been identified (Butenko et al, 2009). For the known plant extracellular ligand–receptor systems, the peptide ligands are either small (e.g. systemin, PEP1, CLAVATA) or only a short stretch of amino acids (aa) within the proteins (e.g. fig22, elf18) is recognized by their receptor (Altenbach & Robatzek, 2007; Boller & Felix, 2009). In animals, a number of secreted proteins are processed by proteolytic cleavage to release the active signaling peptide (Pimenta & Lebrun, 2007), and in plants, similar mechanisms are involved in peptide activation (Murphy et al, 2012).

Almost 700 proteases (Tsiatsiani et al, 2012; Rawlings et al, 2014) encoded in the *Arabidopsis* genome have diverse functions and specificities ranging from the processing of signal peptides required for subcellular targeting to degradation of proteins (van der Hoorn, 2008). However, plant protease substrates remain largely unexplored (Tsiatsiani et al, 2012). Metacaspases, distant relatives of animal caspases (Vercammen et al, 2007; Tsiatsiani et al, 2011), are a class of cysteine-dependent proteases in plants, fungi and
Metacaspases are important regulators of biotic and abiotic stress responses, development and cell death in plants (Hoeberichts et al., 2003; Vercammen et al., 2007; He et al., 2008; Coll et al., 2010; Tsiatsiani et al., 2011; Watanabe & Lam, 2011). To date, several substrates have been identified for plant metacaspases (Tsiatsiani et al., 2011)—a Tudor staphylococcal nuclease (Sundström et al., 2009) in Picea abies and a number of substrates for A. thaliana METACASPASE-9 (AtMC9; Tsiatsiani et al., 2013; Vercammen et al., 2006). However, there are no instances reported for plants where a protease processes a secreted (pre)protein, thereby producing a ligand for a known receptor in a specific biological process.

We have previously described an ozone (O₃)-sensitive Arabidopsis mutant named grim reaper (gri; Wrzaczek et al., 2009b). The cause for the O₃ sensitivity of the mutant was the presence of a truncated fragment of GRI in the gri insertion mutant. A 66-aa fragment of the secreted GRI protein, that is present in the mutant, induced cell death, as measured by elevated ion leakage, upon infiltration into plant leaves. Cell death induction by GRI-peptide was dependent on the plant hormone salicylic acid but also on production of extracellular superoxide. The gri mutant displayed enhanced resistance to a virulent bacterial pathogen.

Here, we show that a subfragment of Arabidopsis GRI contains sufficient information to induce elevated ion leakage. A metacaspase, AtMC9 (Bollhöfer et al., 2013), is required in vivo for the activation of GRI in the extracellular space and is able to directly cleave GRI in vitro. AtMC9-processed peptide-mediated signaling is dependent upon binding to POLLEN-SPECIFIC RECEPTOR-LIKE KINASE 5 (PRK5), an atypical, enzymatically inactive RLK, which serves as a receptor for the peptide. Our results are an important step in understanding the processing of extracellular peptide ligands and their recognition through receptors.

Results

A 20-aa GRI-peptide contains information sufficient to induce elevated ion leakage

The extracellular Arabidopsis protein GRIM REAPER (GRI) is involved in reactive oxygen species (ROS)-mediated cell death (Wrzaczek et al., 2009b). Under superoxide-producing conditions infiltration of a 66-aa part of GRI, GRIp31–96, that is, present in the gri mutant, into Arabidopsis leaves induced cell death, as measured by elevated ion leakage (Fig 1A). Background ion leakage in the control infiltration (with GST) is caused by the wounding due to mechanical stress of infiltration (Fig 1A). When testing four shorter and overlapping peptides (Supplementary Fig S1A) in the leaf infiltration assay, only the 20-aa peptide GRIp65–84 induced ion leakage similarly to bacterially produced GST-GRIp31–96 and biochemically pure GRIp31–96 (Fig 1A; Supplementary Fig S1B) shows dead cells with elevated ion leakage.

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**Figure 1.** The LRR RLK PRKS is required for GRI-peptide-induced ion leakage.


B) Infiltration of increasing concentrations of GRIp31–84 into Col-0 leaves, electrolyte leakage was measured after 12 h. Background (red line) shows ion leakage from infiltration of leaves with increasing concentrations of (inactive) GRIp31–96.

C) Infiltration of leaves with 37 nM GRIp31–96 induced elevated ion leakage in Col-0 and prk4, but not in prk5-1 or prk5-2. Infiltration with GST caused the same background effect for all lines.

D) Genomic complementation of prk5 rescues the insensitivity to induction of elevated ion leakage by GRIp31–96.

E) Enzymatic superoxide production from xanthine/xanthine oxidase (XXO) induced more electrolyte leakage in gri compared to Col-0 or prk5-1, prk5-2 and prk4 after infiltration into leaves. Infiltration with xanthine buffer (X) was used as a control.

Data information: All panels show average ± standard deviation (SD) of four replicates consisting of four leaf disks each. Asterisks indicate statistically significant differences from GST infiltration (A, C, D, from infiltration with (inactive) GRIp80–96 (B) or from Col-0 (E) according to Sidak’s test (P < 0.05). All experiments were repeated at least four times with similar results.
visualized by Trypan blue staining). The three other peptides were inactive. Notably, the 20-aa-long peptide GRIp65–84 induced elevated ion leakage in a dose-responsive manner (Fig 1B).

A leucine-rich repeat RLK mediates GRI-peptide-induced ion leakage

GRI is related to the Solanaceae stigma-specific protein STIG1 (Goldman et al, 1994). Tomato LeSTIG1 interacted in vitro with the ectodomains of two RLKs, the pollen receptor kinases LePRK1 and LePRK2 (Tang et al, 2004; Löcke et al, 2010; Huang et al, 2014). Therefore, we tested the potential interaction of GRI with RLKs.

Leaves from Arabidopsis T-DNA insertion lines for leucine-rich repeat (LRR) RLKs homologous to the two tomato RLKs were infiltrated with the 66-aa GRIp31–96 and 20-aa GRIp65–84 peptides and scored for cell death. Two T-DNA insertion alleles in At1g50610 (SALK_016815 and SALK_101260) in the last exon and in the S′ UTR region, respectively, displayed reduced ion leakage levels in response to peptide infiltration (Fig 1C). This gene has recently been named PRK5 (Chang et al, 2013). Thus, the mutants are referred to as prk5-1 (SALK_016815; Chang et al, 2013) and prk5-2 (SALK_101260), respectively. Complementation of prk5 with a genomic clone consisting of a 1,500 base pair promoter region and the coding region of PRK5 restored the wild-type phenotype (Fig 1D). PRK5 has previously been described as a pollen-specific RLK (Chang et al, 2013), but RT-PCR analysis demonstrated the presence of low levels of PRK5 transcript in leaves (Supplementary Fig S2). While PRK5 transcript levels are low in plant organs other than pollen tubes under normal growth conditions (Supplementary Fig S3), analysis of publicly available expression data suggests that transcript abundance is increased in response to biotic and abiotic stresses (Supplementary Figs S4, S5, S6, S7 and S8). Similarly, GRI transcript abundance is lower in leaves than in flowers (Wrzaczek et al, 2009b). Our previous results suggested that GRI-induced cell death as evidenced by increased ion leakage was dependent on superoxide production. Therefore, we used infiltration of an enzymatic system, xanthine with xanthine oxidase (XXO), to produce superoxide in the extracellular space and analyze the response of prk5. Compared to wild-type plants, the loss-of-function mutants prk5 and prk4 showed slightly less, statistically not significant (but reproducible), ion leakage as induced by extracellular superoxide while the gain-of-function mutant gri (Wrzaczek et al, 2009b) exhibited increased sensitivity (Fig 1E). This indicates that in leaves, PRK5 could act as a downstream element for ROS-dependent cell death induced by GRI or a smaller subdomain of it.

PRK5 is a plasma membrane-localized, enzymatically atypical protein kinase

PRK5 belongs to the LRR RLK subtype III (Shiu & Bleecker, 2003) and consists of 686 aa (calculated MW: 76.86 kDa; pl 7.84). A transmembrane domain separates the extracellular region with a signal peptide from the intracellular kinase domain, which contains a Y-based sorting/endocytosis motif in the C-terminus (Fig 2A). Structural prediction suggests that the extracellular domain (Supplementary Fig S9A) is similar to other LRR RLKs and the intracellular domain (Supplementary Fig S9B) has the overall typical sequence and structural conservation of protein kinases. The few known plant receptors for extracellular proteins are plasma membrane-localized (Aker & de Vries, 2008). We analyzed the subcellular localization of PRK5 tagged with cyan fluorescent protein (PRK5-CFP; Fig 2B) using transient expression in Arabidopsis mesophyll protoplasts. PRK5-CFP co-localization with the plasma membrane marker CAAX-yellow fluorescent protein (CAAX-YFP; Kwaaitaal et al, 2011) (Fig 2C–F) was markedly distinct from the cytoplasmic YFP (Supplementary Fig S10A). PRK5-YFP also localized to the cell periphery in Nicotiana benthamiana epidermal cells (Supplementary Fig S10B–G). After plasmolysis, Hechtian strands (Vahisalu et al, 2008), which connect the plasma membrane to the cell wall, were visible verifying that PRK5-YFP was localized to the plasma membrane.

While the overall kinase domain structure is preserved in PRK5, critical amino acids in the kinase subdomains VIb and VII (Stone & Walker, 1995) are not conserved in PRK5 (Fig 2G, Supplementary Fig S11A and B). The aspartic acid (D) residue, which is conserved in active RLKs (e.g. in FLS2, EFR, BRI1, CRK7) is altered to histidine (H) in PRK5. In the inactive RLKs STRUBBELIG (SUB; Vaddepalli et al, 2011) and BAK1-INTERACTING RECEPTOR-LIKE KINASE 2 (BIR2; Halter et al, 2014b), this residue is changed to asparagine (N). This suggested that PRK5 could be enzymatically inactive and accordingly, recombinant GLUTATHIONE-S-TRANSFERASE (GST)-tagged PRK5 (GST-PRK5) did not have kinase activity toward the artificial substrate myelin-basic protein. Intriguingly, mutations restoring the consensus kinase sequence in the catalytic core (H500D A520G; Supplementary Fig S11C) turned GST-PRK5 into an active kinase in the presence of MnCl2 (Fig 2H) and MgCl2 (Supplementary Fig S11D). Taken together, PRK5 closely resembles an active kinase based on sequence and modeling, but, at least in vitro, is enzymatically inactive.

PRK5 binds GRIp31–96 in vitro

Since PRK5 was required for cell death induction by GRIp31–96 and GRIp65–84, we investigated the interaction between GRI and the ectodomain of PRK5 in vitro. Recombinant full-length GRI (minus signal peptide; GRI31–96) or GRI31–96 fused to GST was incubated with 35S-methionine-labeled in vitro-produced extracellular domains of PRK540–281 or PRK440–279. GRI31–96 interacted directly with PRK540–281, while GRI31–168 showed slightly weaker interaction (Fig 3A; Supplementary Fig S12 shows Western analysis with α-GST, α-GRI and α-GRI-peptide antibodies). Binding of GRI31–96 and GRI31–168 to the PRK4 extracellular domain was weaker compared to binding of GRI31–96 to PRK540–281 (Fig 3A). Given the high sequence similarity of PRK4 and PRK5 (70.15% sequence identity; 77.76% sequence similarity; Supplementary Fig S12E), it is not surprising that GRI31–96 and GRI31–168 were still able to interact at least to some extent with both receptors. No interaction was, however, detected with the ectodomain of a different RLK, FLAGELLIN-SENSITIVE 2 (FLS2; Supplementary Fig S12F). These results suggest that GRI and the 66-aa peptide GRI31–96 can directly interact with the extracellular domains of receptors, preferentially with the ectodomain of PRK5.

Native PRK5 binds GRIp65–84

GRIp65–84 is a subfragment of GRIp31–96 sufficient to induce elevated ion leakage upon infiltration into Arabidopsis leaves. To investigate whether the interaction of GRI and PRK5 can take place in vitro, an
additional tyrosine (Y) was added to the N-terminus of GRIp$_{65-84}$ to allow radiolabeling with iodine$^{125}$ (125I). The Y-GRIp$_{65-84}$ peptide showed similar activity in inducing elevated ion leakage compared to GRIp$_{65-84}$ and GRIp$_{31-96}$ (Fig 3B). In radioligand binding assays, 125I-Y-GRIp$_{65-84}$ bound to membrane fractions from wild-type plants, whereas binding was strongly reduced in prk5-2 extracts, and excess of 10$\mu$M non-radiolabeled Y-GRIp$_{65-84}$ reduced binding to background levels (Fig 3C). 

125I-Y-GRIp$_{65-84}$ bound to microsomal fractions of protoplasts overexpressing PRK5-c-myc and also, albeit with lower affinity, PRK4-c-myc (Fig 3D and E). Specific binding of 125I-Y-GRIp$_{65-84}$ was competed out by non-radioactive Y-GRIp$_{65-84}$ with an IC$_{50}$ of 25.2 nM (Fig 3F). Of the four short peptides, only GRIp$_{65-84}$ competed for binding (Fig 3G). Interestingly, the 66-aa-long GRIp$_{31-96}$ did not compete for binding of 125I-Y-GRIp$_{65-84}$ (Fig 3G), indicating that, even though it interacted with the ectodomain of PRK5 in vitro, binding activity to membrane fractions would require further processing. Reasons might be that the receptor used in the in vitro assay was without co-receptors or other interacting proteins which in vivo might set additional constraints for ligand binding. In addition, as shown in other similar systems (Löcke et al., 2010), other extracellular proteins interacting with GRI might add further constraints for the ligand–receptor interaction in vivo. Together, the results suggest that the extracellular domain of PRK5 serves as a sensor for peptides derived from GRI through direct protein–protein interaction.

A metacaspase is required for activation of GRI-peptide

Although infiltration of both the 66-aa GRIp$_{31-96}$ and the 20-aa GRIp$_{65-84}$ induced cell death in planta (Fig 1A), the 66-aa peptide...
Proteolytic GRI cleavage and receptor interaction

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AtMC9 preference for basic residues at substrate positions P3 and P1 (K and R; Versammen et al., 2006, 2004).

In accordance with this, recombinant AtMC9 (rAtMC9; Versammen et al., 2004) directly cleaved bacterially produced maltose-binding protein (MBP)-GRI fusion protein in vitro (Fig 4A).

The inactive mutant rAtMC9mut (Belenghi et al., 2007) showed no proteolytic activity toward MBP-GRI (Fig 4A). The shift in the molecular weight of MBP-GRI25–168 in Western blot analysis with α-MBP antibody suggested cleavage of GRI at the SKTR motif, which is located at the N-terminus of GRI52–84. The position of the AtMC9 cleavage site(s) in the MBP-GRI25–168 protein was determined by LC-MS/MS following in-solution labeling with a trideutero-acetyl group (AcD3) of primary alpha-amines of newly formed N-termini generated by AtMC9 cleavage. Analysis led to the identification of the peptides <AcD3>-440-LYK96, and <AcD3>-68-460-TSKR84, thus showing that in vitro AtMC9 cleaves MBP-GRI25–168 not only after arginine 67 (R67 of the SKTR motif) but also after lysine 97 (K97, the second K of the KANK sequence; Supplementary Fig S1A–C). To assess the in vivo relevance of GRI-peptide cleavage by AtMC9, we used the atm9 mutant (Bollhöner et al., 2013). The short 20-aa peptide GRI52–84 was able to induce cell death in atm9 (Fig 4B) but not the longer 66-aa GRI51–96. In addition, atm9 displayed slight, statistically not significant but reproducible, reduction in the ion leakage induced by XCO compared to wild-type plants (Supplementary Fig S1A). This suggests that AtMC9 activity is required to modify the 66-aa GRI51–96 for the induction of elevated ion leakage.

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To investigate the cleavage of GRI in more detail, we analyzed the fragments generated by incubation of GRIp31–96 (the 66-aa subfragment of GRI, which is produced in the gri mutant; Wrzaczek et al., 2009b) with rAtMC9. Reverse-phase-HPLC and mass spectrometric analysis revealed cleavage of the peptide after lysine 65 (K65) and arginine 67 (R67) in the SKTR motif and an additional site after lysine 78 (K78) in the KKKK pattern (Fig 4C; Supplementary Fig S16A). GRIp68–78 induced elevated ion leakage in cell death induction compared to the other GRI-derived peptides.

Excess of non-radioactive Y-GRIp68–78, Y-GRIp68–78, Y-GRIp68–78, and GRIp68–78 showed similar activity in cell death induction compared to the other GRI-derived peptides. Excess of non-radioactive Y-GRIp68–78 (10 μM) reduced binding to background levels (dark gray bars; all bars show the average of four samples, triangles show individual data points).

The affinity of 125I-Y-GRIp68–78 to the receptor (Kd = 1.9 nM) was calculated by non-linear regression analysis. Scatchard plot is shown in Supplementary Fig S17.

Data information: Data in (B) and (D) are shown as average ± SD of four replicates consisting of four leaf disks each. Asterisks in (B) and (D) mark statistically significant differences from infiltration with background levels (dark gray bars; all bars show the average of four samples, triangles show individual data points).

Source data are available online for this figure.

To address the relevance of this cleavage for GRI-peptide activity, we tested an 11-aa peptide GRIp68–78 (Fig 4C). GRIp68–78 induced cell death in Col-0 but not in prk5-1 (Fig 4B) or prk5-2 (Supplementary Fig S16A). GRIp68–78 but not GRIp31–96 induced ion leakage in atmc9-1 (Fig 4B). As cell death induction by GRI-peptide is dependent on salicylic acid and extracellular superoxide (Wrzaczek et al., 2009b), we tested induction of elevated ion leakage by GRIp68–78 in mutants deficient in salicylic acid (salicylic acid deficient 2 [sid2]) and extracellular superoxide production (respiratory burst oxidase homolog D [rbohD]). Neither GRIp31–96 nor GRIp68–78 induced...
elevated ion leakage in sid2 and rbohD (Supplementary Fig S16B). These results suggest that salicylic acid and extracellular superoxide are still required for cell death induction by the processed GRIp68–78. A tyrosine-labeled version of the 11-aa peptide, Y-GRIp68–78, also induced elevated ion leakage (Fig 4D) and 125I-labeled Y-GRIp68–78 bound to membrane extracts from wild-type plants (Fig 4E). However, binding was reduced to background levels in prk5-1 and prk5-2 (Fig 4E). Binding of 125I-Y-GRIp68–78 was competed out by addition of non-radioactive GRIp68–78 and GRIp65–84 but not by other peptides (Fig 4F). The high binding background could result from anionic interactions be due to the strong basic nature of the 11-aa peptide (Fig 4G, Supplementary Fig S17), which may affect calculation of the dissociation constant (Kd) of 1.9 nM for GRIp68–78. The results suggest that an 11-aa peptide derived from GRI based on identified AtMC9-cleavage sites is sufficient to induce cell death in Arabidopsis leaves and binds with high specificity to the extracellular domain of the receptor PRK5. The gri mutant has previously been found to be more resistant to the virulent bacterial pathogen Pseudomonas syringae pv. tomato DC3000 (Wrzaczek et al., 2009b). However, prk5 and atmc9 did not display altered pathogen resistance (Supplementary Fig S18). A reason for this might be that the infiltration with the pathogen into gri—where a ‘pre-activated’ GRI-derived peptide could already be present—leads to a number of cells undergoing cell death, which would lead to the initiation of a hyper-sensitive response (HR). In the prk5 and atmc9 mutants this pre-activated GRI-derived peptide is not recognized (in prk5) or produced (in atmc9). Thus, prk5 and atmc9 did not exhibit altered sensitivity to the virulent pathogen. However, more detailed analysis of this aspect will be required in the future using prk5 gri and atmc9 gri double mutants as well as overexpression of prk5. Also, a complete loss-of-function allele for gri will be crucial for further dissection of the roles of GRI and derived peptides.

Our hypothesis that GRI is an in vivo target of AtMC9 is supported by the fact that both proteins have been reported to be present in the extracellular space (Vercammen et al., 2006; Wrzaczek et al., 2009b). Additional lines of evidence suggest that proteolytic processing is required for the biological activity of GRI. The 66-aa GRIp31–96 was unable to compete out the binding of radioactively labeled 125I-Y-GRIp68–84 in plant membrane fractions (Figs 3G and 4F) and was unable to induce elevated ion leakage in the atmc9 mutant. While metacaspases are involved in stress adaptation and cell death regulation in plants (Tsiatsiani et al., 2011; Lam & Zhang, 2012), the role of AtMC9 in these processes has previously been unknown. Our results show that AtMC9 directly cleaves GRI and is thus involved in the processing and activation of the extracellular peptide.

Discussion

In this study, we describe how the secreted protein GRI is cleaved by a protease and a resulting peptide is subsequently recognized by a transmembrane receptor. GRI is a secreted Arabidopsis protein with similarity to STIG1 from tobacco and tomato. A 66-aa N-terminal fragment of GRI, which is produced in the gain-of-function mutant gri, was previously shown to induce cell death when infiltrated into Arabidopsis leaves (Wrzaczek et al., 2009b). We show that recombinant GRI and GRIp31–96 were cleaved by the metacaspase AtMC9 in vitro, releasing an 11-aa peptide (Fig 4) that was sufficient for the induction of cell death as inferred from ion leakage measurements. Physiological evidence indicated that this metacaspase-dependent processing of GRI was required for cell death induction in planta.

We identified PRK5, a receptor-like kinase, as the receptor for GRI-derived peptides generated through cleavage by AtMC9. PRK5 is required for cell death induction by GRI. PRK5 is present in leaves at low levels similar to GRI itself. While STIG1 and PRK5 have been described to function in floral organs (Goldman et al., 1994; Chang et al., 2013), our results show that GRI and its receptor also have functions in leaves. Involvement of a signaling component in several different processes is common for plant signaling. For example, BRII-ASSOCIATED KINASE (BAK1) has originally been described to function in brassinosteroid signaling but also has important roles in PAMP and DAMP signaling (Lieber et al., 2014).

Our in silico and in vitro analyses suggest that PRK5 is enzymatically inactive (Fig 2G and H). Estimates indicate that 10 to 20% of all RLKs in Arabidopsis might be catalytically inactive (Castells & Casacuberta, 2007; Blum et al., 2014). Only a few—to our knowledge—have been linked to a biological process based on mutant analysis; examples include BIR2 (Halter et al., 2014b), SUB (Vaddepalli et al., 2011) and SHORT SUSPENSOR (SSR; Bayer et al., 2009). While SUB has been suggested to bind a ligand (Vaddepalli et al., 2011), no ligands have so far been identified for SSR. BIR2 is suggested to control BAK1-receptor complex assembly in the absence of peptide ligands and thus might not recognize a ligand either (Halter et al., 2014a,b). PRK5 is the first atypical, kinase-inactive, plant RLK that acts as a primary receptor for a peptide ligand.

We have previously shown that cell death induction by a 66-aa GRI-peptide occurs under conditions that lead to superoxide production (Wrzaczek et al., 2009b), for example, through mechanical stress and wounding caused by infiltration of the peptide into Arabidopsis leaves. Removal of superoxide production, either by coinfiltration of the peptide with superoxide dismutase or by peptide infiltration into a mutant deficient in the NADPH oxidase RBOHD, reduced cell death to background levels. Extracellular superoxide was still required for cell death induction by GRIp68–78 (Supplementary Fig S16B). Wounding induces ROS production and is one of the signals that have been shown to initiate the so-called ‘ROS wave’ (Mittler et al., 2011). Our results suggest that ROS can act as a parallel signal, perhaps together with other wound-induced cues, to sensitize cells to cell death induction by GRI-derived peptides (Supplementary Fig S19).

It is currently unknown how extracellular ROS are sensed by cells. Accurate ROS sensing most likely relies on a broad range of independent mechanisms (Wrzaczek et al., 2013), and it is unlikely that ROS participate in classical ligand-receptor interactions. ROS might rather react with extracellular components including cell walls, lipids and also proteins/peptides. While ROS may act as a cue in parallel to GRIp68–78, the full-length GRI itself could be subject to redox regulation (Supplementary Fig S19) through two cysteine motifs (C-9X-C-2X-C) in its C-terminal region. The cysteine motifs in GRI are similar to the pattern found in DUF26 (domain of unknown function 26) proteins, C-8X-C-2X-C (Wrzaczek et al., 2010). In both cases, the cysteine motifs are suggested to be a target for redox regulation. The C-2X-C part of DUF26 and GRI also is a classical target for thioredoxins (Zhang et al., 2011). Recently, an extracellular
thioredoxin has been shown to regulate stress responses through ROS (Zhang et al., 2011). Thereby, GRI could be involved in the apoplastic redox sensory mechanisms regulated through interaction with thioredoxins and reorganization of thiol bonds. This regulation could affect cleavage of GRI by modulation of the three-dimensional structure of the protein and changing accessibility of the AtMC9 cleavage sites through redox regulation of thiol bonds. Thus, GRI may be controlled dually by conformational change and proteolytic cleavage (Wrzaczek et al., 2009a). GRI was not identified in a recent analysis of the AtMC9 degradome (Tsatsianis et al., 2013). However, that study was performed on young seedlings as compared to the older plants used in the work described here. It is interesting to note that AtMC9 activity can be regulated through S-nitrosylation (Belenghi et al., 2007). Evidence suggests that there is a significant cross talk between reactive nitrogen species (RNS) and ROS, but the clear relationship between the two remains elusive (Wang et al., 2013). The functional unit of GRI and metacaspase could be regulated by ROS/RNS on multiple levels and be part of the apoplastic redox sensing machinery in plants.

GRI is a member of a small protein family with six members in Arabidopsis. The C-terminus of GRI containing the cysteine repeats is highly similar to STIG1 and the Arabidopsis orthologs, but the N-terminal part after the signal peptide, which contains the cell death-inducing peptide motif, shows strikingly lower levels of conservation. Future research should address the question whether the conservation of the C-terminus of GRI is linked to cell death regulation or whether it is involved in other processes. No functions have been described for any of the GRI orthologs in Arabidopsis, but the conservation of the C-terminal cysteine motifs might point toward a common mode of regulation among GRI, STIG1 and related proteins. Interestingly, for CLAVATAS3/ESR-RELATED 18 (CLE18), two different peptides derived from the precursor protein have been shown to have individual and possibly antagonistic functions (Murphy et al., 2012). This suggests that more than one biologically active peptide could be generated from a single precursor. It remains to be determined whether this also applies to GRI and related proteins. It also remains to be seen whether GRI interacts with other extracellular proteins as has been shown for tomato LeSTIG1 (Locke et al., 2010).

The combination of GRI, AtMC9 and PRK5 provides a functional unit comprising secreted protein, protease and the receptor for the cleavage product. This scheme is likely to be employed in the regulation of many other ligand–receptor interactions in plants. Future research on the functions of GRI, AtMC9 and PRK5 in plant development including stigma–pollen interactions and cell death regulation, and the roles of the other proteins similar to GRI will increase our understanding of extracellular signaling in plants.

Materials and Methods

Plant material and growth conditions

Arabidopsis thaliana ecotype Columbia-0 (Col-0) was used as wild-type. The grr (Wrzaczek et al., 2009b) and atmc9 (Bollhöfer et al., 2013) lines were previously described. The prk5-1, prk5-2 and prk4 T-DNA insertion lines were obtained from the European Arabidopsis Stock Centre (http://www.arabidopsis.info).

Seeds were sown on 1:1 peat–vermiculite mixture, stratified for 2 days and grown under controlled conditions (Vahisalu et al., 2008) under 12-h/12-h day/night cycle (temperature 23/18°C, relative humidity 70/90%). For in vivo radio-ligand binding assays, A. thaliana seedlings were grown on agar plates at 12-h/12-h day/night cycle, temperature 23/18°C for 7 days.

Peptide and XXO infiltration experiments as well as pathogen infection assays were performed as previously described (Wrzaczek et al., 2009b). Protoplast preparation, transfection and extracts for ligand binding assays and Western analysis were prepared as described (Lee et al., 2011). For transient gene expression studies, Arabidopsis protoplasts were transfected with PRK5-CFP, PRK4-CFP, or controls (cytoplasmic YFP, plasma membrane-localized CAAX-YFP (Kwaaitaal et al., 2011) under the control of 35S promoter and incubated for 48 h at room temperature in darkness prior to confocal microscopy.

Plasmid constructs

Constructs were created by PCR, and restriction or Gateway sites were introduced via the PCR primers. For expression of GRI as a MBP fusion, the coding sequence of GRI minus the signal peptide was cloned EcoRI/PstI into the pMAL-c2x vector (New England Biolabs). For expression of GRI as a GST-fusion protein, the coding sequence of GRI or GRIp31 (66 minus the signal peptide was cloned EcoRI/NotI or EcoRI/Sall, respectively, into the pGEX-4T-1 vector (GE Healthcare Life Science). The kinase domains of PRK5 and PRK4 were cloned EcoRI/NotI into pGEX-4T-1. For coupled in vitro transcription and translation, the ectodomains of PRK5, PRK4 and FLS2 were cloned into pZeRO-2.1 (Invitrogen). For genomic complementation lines, the coding region of PRK5 including 1,500-bp promoter region was amplified by PCR and cloned into pGreenII0179 (Hellens et al., 2000). Plants were transformed by Agrobacterium tumefaciens-mediated gene transfer. Homozygous single-insert plants carrying the transgene were selected based on antibiotic resistance. The coding regions of PRK5 and PRK4 were cloned PacI/EcoRI into a modified version of the pGW88 (Rozhon et al., 2010) vector containing a 6x c-myc or YFP tag under the control of the UBQ10 promoter. For confocal microscopy of protoplasts, the coding regions of PRK5 and PRK4 were Gateway-cloned into the CZN575 vector containing the sCFP3a tag.

Trypan blue staining

Trypan blue staining was performed as described (Dat et al, 2003).

GRI-derived peptides and radiiodine-labeling

Peptides were synthesized and purified to > 95% purity on a reverse-phase high-pressure liquid chromatography by GenScript (USA), Proteogenix (France; Y-GRI65–84 and Y-fig22) or in house on an Applied Biosystems 433A Peptide Synthesizer at VIB Ghent (GRIp68–78). Peptides were dissolved in H2O (stock solution 10 mg/ml) and diluted to the required concentrations just before experiments. GRIp65–68 and Y-GRI68–78 were radiolabeled with [125I] iodine using chloramine-T to yield 125I-Y-GRI65–84 and Y-GRI68–78, respectively, with a specific radioactivity > 2,000 Ci/mmol by BIOTREND Chemikalien (Germany).
Radio-ligand binding assays

Binding assays were performed as described (Bauer et al., 2001) with modifications. Plant material (0.1 g) was homogenized in 200 µl binding buffer (25 mM MES [2-(N-morpholino)ethanesulfonic acid] pH 6.0, 3 mM MgCl2, 10 mM NaCl) containing protease inhibitor cocktail (1:100; Fermentas/Thermo Fisher Scientific). Lysates were centrifuged at 4°C for 15 min at 10,000 g. The pellet was resuspended in 100 µl binding buffer and filtered through Miracloth. Binding assays were incubated for 20 min on ice in a total volume of 100 µl with 46 fmol 125I-Y-GRIp65-84 either alone (total binding) or in the presence of 10 µM Y-GRIp65-84 or GRIp65-84 (non-specific binding) for standard assays (concentrations for radiolabeled or cold peptides in saturation and competition assays are indicated in the figures).

Protoplasts were lysed in binding buffer containing 1% (w/v) octylphenoxypolyethoxyethanol (Nonidet NP-40), 0.1% SDS and 0.5% (w/v) sodium deoxycholate as detergents. After 2 h shaking at 4°C, the lysates were centrifuged at 4°C for 15 min at 10,000 g, and the supernatant was used directly for binding assays or for immunoprecipitation with subsequent binding assays.

Membrane fractions or immunoprecipitates were collected by vacuum filtration on glass fiber filters (Macherey–Nagel MN GF-2; preincubated in binding buffer containing 1% bovine serum albumin, 1% bactopeptone, 1% bactotryptone, 1% polyethylenimine). Prior to peptide binding filters were rinsed with 1 ml binding buffer. For 125I-Y-GRIp65-84 after filtration, filters were washed under constant vacuum with 1 ml binding buffer, 10 ml wash buffer I (20 mM Tris pH 7.5, 5 mM EDTA, 100 mM NaCl, 1% Triton X-100) and 5 ml wash buffer II (20 mM Tris pH 7.5, 5 mM EDTA, 1 M NaCl, 1% Triton X-100) (Jonak et al., 2000). For 125I-Y-GRIp65-78, filters were washed under constant vacuum with 1 ml binding buffer and twice with 5 ml wash buffer I (20 mM Tris pH 7.5, 5 mM EDTA, 150 mM NaCl, 1% Triton X-100). Radioactivity retained on the filters was measured using a WallacWizard3 Gamma Counter. Specific binding was calculated by subtracting non-specific from total binding.

Western analysis of protoplasts transfected with PRK5-c-myc, PRK4-c-myc or YFP used anti-c-myc A-14 rabbit polyclonal and 9E10 mouse monoclonal antibodies (Santa Cruz), respectively.

In vitro interaction analysis and protein kinase assays

Recombinant glutathione-S-transferase (GST) or maltose-binding protein (MBP) fusion proteins of GRI, GRIp31-96 or the intracellular kinase domains of PRK5 and PRK4 were produced in Escherichia coli BL21 cells and purified according to manufacturer’s instructions. In vitro interaction tests of the extracellular domain of PRK5, PRK4 and FLS2 with GRI were performed as described (Nakagami et al., 2004). Western analysis for GST-fusion proteins was done using anti-GST antibody (mouse monoclonal antibody; Sigma Aldrich), anti-GRI antibody (rabbit polyclonal antibody raised against the epitope TRKCASCVKCEYGYC; Inbiolabs) or anti-GRI-pep (rabbit polyclonal antibody raised against the epitope VVDQEDDPEYYIL; Inbiolabs), respectively. Radioactive in vitro protein kinase assays using myelin-basic protein as an artificial substrate were performed as described (Idanheimo et al., 2014) in 10 mM HEPES pH 7.4, 1 mM dithiothreitol with either 10 mM MgCl2 or MnCl2.

Microscopy

PRK5 subcellular localization was analyzed by confocal microscopy on a Leica SP5 II HC5 A inverted confocal microscope using a solid state blue laser for CFP, YFP and chloroplast autofluorescence (detection with 465–510, 521–587 and 636–674 nm range, respectively).

In vitro AtMC9 cleavage assay

Recombinant His-6 purified AtMC9 protease (Vercammen et al., 2004) and the inactive AtMC9C147AC29A mutant (Belenghi et al., 2007) were pre-activated in assay buffer containing 50 mM MES (pH 5.5), 150 mM NaCl, 10% (w/v) sucrose, 0.1% (w/v) CHAPS and 10 mM DTT for 15 min at room temperature. The proteases were then mixed with the substrate in several pmol quantity ratios and incubated at 30°C for 30 min. The reaction was terminated by addition of Laemmli–SDS–PAGE loading buffer and heating to 95°C for 5 min. Proteins were separated on 12% SDS–PAGE gels and transferred to Immobilon P (Millipore) membrane for Western blot analysis. AtMC9 was probed with a rabbit polyclonal antibody (Vercammen et al., 2004) and MBP-tagged substrates with a MBP-tag rabbit polyclonal antibody (Santa Cruz) and visualized by chemiluminescence (Western Lightning Plus-ECL; PerkinElmer). In-solution acetyl-2H(3) labeling and subsequent MS/MS analysis of neo N-termini was performed as described (Melzer et al., 2012).

Mass spectrometric analysis

In-solution triadeutero-acetyl (<AcD3->)-labeling and subsequent MS/MS analysis of neo N-termini was performed as previously described (Helsens et al., 2008) with minor modifications. Approximately 5 µg of AtMC9 and MBP-GRI125–168 (total amount in the protein mix) were reacted for 90 min at 30°C in AtMC9 assay buffer supplemented with 2 mM TCEP. The reaction was stopped by raising the pH to 8.0 with NaOH and alklylation of cysteines with 10 mM iodoacetamide for 1 h at 30°C in the dark. The buffer was exchanged to 50 mM triethylammonium bicarbonate buffer. Labeling was performed in solution with a threefold molar excess of N-hydroxysuccinimide ester of triadeutero-acetate (produced in-house), twice for 1 h at 30°C. To quench remaining NHS-ester, a fourfold molar excess (over NHS-ester) of glycine was added for 10 min at 30°C. Tryptsin digestion was performed overnight, after which the digest was incubated with a fourfold molar excess of hydroxylamine for 10 min at 30°C and was subsequently acidified with trifluoroacetic acid (TFA). Peptides were analyzed by LC-MS/MS using a Thermo LTQ Orbitrap XL mass spectrometer. Spectra were identified with the Mascot search algorithm in the TAIR10 database (concatenated with MBP-GRI125–168 sequence).

The Mascot search parameters and all identified spectra matching the MBP-GRI125–168 sequence were grouped in Supplementary Set1.

In vitro GRIp31-96 peptide cleavage by AtMC9 and separation by RP-HPLC

The GRIp31-96 peptide was dissolved to a concentration of 1 mM in 5% formic acid and adjusted to pH 3.8 with NaOH. 200 µM GRIp31-96
peptide was incubated per 40 \( \mu l \) reaction mixture (pH of the reaction mixtures was adjusted to pH 5.5 with NaOH) containing increasing concentration of recombinant AtMC9 (0, 31, 125 or 500 nM rAtMC9) in AtMC9 assay buffer (supplemented with 40 mM DTT and 40 mM MES buffer). After incubation for 30 min at 30\(^\circ\)C, the reaction was stopped by addition of 5 \( \mu l \) 10\% TFA. Cleavage products in the samples were separated by reverse-phase high-performance liquid chromatography (RP-HPLC, Agilent Technologies 1200 series) on a 2.1 mm (internal diameter) C18 column in solvent A (2/98\% ACN/H\(_2\)O, 0.1\% TFA) with a gradient increase of 1\% solvent B (70/30\% ACN/H\(_2\)O, 0.1\% TFA) per minute. Buffer controls were run with the same parameters. Peptide elution was monitored by measuring UV absorbance at 280 nm, and 1 min fractions were collected from 24 to 120 min in a 96-well plate. Fractions corresponding to each peak in the 500 nM rAtMC9 sample were measured by MALDI-TOF MS (Ultraflex, Bruker), and the measured masses were linked to GRIp\(^{31-96} \) peptide fragments. The fractions of the 0 nM rAtMC9 sample corresponding to the expected full-length GRIp\(^{31-96} \) peptide were analyzed by LC-MS/MS using a Thermo LTQ Orbitrap XL mass spectrometer, and the correct GRIp\(^{31-96} \) mass was deduced from the MS precursor masses. Detected peptides are listed in Supplementary Dataset S1.

**Primer sequences**

Primers used for cloning are listed in Supplementary Table S1.

**Sequence analysis**

Sequences were aligned using PSI-Coffee (Di Tommaso et al., 2011) at the T-Coffee web server (http://tcoffee.crg.cat/apps/tcoffee/index.html).

**Protein structure predictions**

Protein structure predictions were done using I-TASSER (Roy et al., 2010) (http://zhanglab.ccb.med.umich.edu/I-TASSER/) or Phyre2 (http://www.sbg.bio.ic.ac.uk/phyre2/html/page.cgi?id=index) (Kelley & Sternberg, 2009).

**Statistical analysis**

Statistical analysis was performed in IBM SPSS Statistics (version 22). Ion leakage and binding data were analyzed using one-way ANOVA using Sidak’s post hoc test. Bacterial growth was analyzed using two-way ANOVA using Tukey’s HSD post hoc test. Plots were created in Sigmaplot and in R.

**Supplementary information** for this article is available online: http://emboj.embopress.org

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**Author contributions**

MW and JPV contributed equally to this work. SS, LT and HHRR contributed equally to this work. MW, JPV, SS, LT, HHRR, HT, KG, FVB, YH and JK designed research, and MW, JPV, HHRR, SS, LT, AG, DK, AL, AS and BB carried out experiments. MW, JPV and JK wrote the paper. All authors discussed the results and commented on the manuscript.

**Conflict of interest**

The authors declare that they have no conflict of interest.

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