MAP Kinase PrMPK9-1 Contributes to the Self-Incompatibility Response

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Mitogen-activated protein kinases (MAPKs) form important signaling modules for a variety of cellular responses in eukaryotic cells. In plants, MAPKs play key roles in growth and development as well as in immunity/stress responses. Pollen-pistil interactions are critical early events regulating pollination and fertilization and involve many signaling events. Self-incompatibility (SI) is an important mechanism to prevent self-fertilization and inbreeding in higher plants and also is known to utilize signaling to achieve incompatible pollen rejection. Although several pollen-expressed MAPKs exist, very little is known about their function. We previously identified a pollen-expressed MAPK (p56) from Papaver rhoeas that was rapidly activated during SI; several studies implicated its role in signaling to SI-induced programmed cell death involving a DEVDase. However, to date, the identity of the MAPK involved has been unknown. Here, we have identified and cloned a pollen-expressed P. rhoeas threonine-aspartate-tyrosine (TDY) MAPK, PrMPK9-1. Rather few data relating to the function of TDY MAPKs in plants currently exist. We provide evidence that PrMPK9-1 has a cell type-specific function, with a distinct role from AtMPK9. To our knowledge, this is the first study implicating a function for a TDY MAPK in pollen. We show that PrMPK9-1 corresponds to p56 and demonstrate that it is functionally involved in mediating SI in P. rhoeas pollen: PrMPK9-1 is a key regulator for SI in pollen and acts upstream of programmed cell death involving actin and activation of a DEVDase. Our study provides an important advance in elucidating functional roles for this class of MAPKs.

Cellular responses require an integrated signal perception and signal transduction network. Mitogen-activated protein kinases (MAPKs) form highly conserved signaling networks that are common to all eukaryotic cells, including animals, plants, and fungi. They are commonly used to transduce information from sensors to cellular responses. A MAPK cascade minimally consists of three kinases: a MAPKKK, a MAPKK, and a MAPK, which sequentially phosphorylate and activate each other. MAPKs are Ser/Thr kinases, and upon phosphorylation, which activates them, the MAPK can phosphorylate a range of target proteins, which include other kinases and transcription factors. This results, ultimately, in changes in gene expression, metabolism, cell division, and growth. In plants, they function in diverse signaling networks, including development, but perhaps the best characterized and well known involve responses to biotic stresses stimulated by interactions with pathogens, involving defense responses, and to a range of abiotic stresses, including wounding, drought, cold, heat, UV, touch, osmotic shock, and salt (Rodriguez et al., 2010; Meng and Zhang, 2013; Xu and Zhang, 2015). The involvement of MAPKs in signaling to the expression of defense genes, involving apoptosis and programmed cell death (PCD), is well documented (Pitzschke et al., 2009; Mase et al., 2012; Bigeard et al., 2015).

Arabidopsis (Arabidopsis thaliana) has 20 MAPK genes, and there are a similar number in the sequenced genomes of other plant species. Plant MAPKs have two types of activation motif: either a Thr-Glu-Tyr (TEY) activation motif or a Thr-Asp-Tyr (TDY) activation motif, which is unique to plant MAPKs (Ichimura et al., 2012; Hamel et al., 2006). Plant MAPKs are highly conserved between species and can be divided into four clades (A–D) based on sequence similarities. The plant...
TEY MAPKs can be classified into three groups (A–C), while the TDY MAPKs belong to a more distant clade (D; Ichimura et al., 2002; Hamel et al., 2006). Group A MAPKs are well characterized; many are functionally involved in stress responses and include the Arabidopsis MPK3 and MPK6 and their orthologs in other species, such as the stress-activated MAPK from alfalfa (*Medicago sativa*), salt-induced MAPK, tobacco (*Nicotiana tabacum*) salicylic acid-induced protein kinase, and wounding-induced protein kinase. The group B MAPKs (Arabidopsis MPK4 and MPK11) also have functions implicated in pathogen defense and stress responses and also play an essential role in cell division (for review, see Meng and Zhang, 2013). The functions of MAPKs in groups C and D are currently less well established (Meng and Zhang, 2013; Zhang et al., 2014).

Plants use PCD for a wide range of functions, including disease resistance and development as well as reproduction (for review, see Van Hautegem et al., 2015; Daneva et al., 2016; Van Durme and Nowack, 2016). Animal cells use a cascade of caspases (Cys proteases), which, when activated, cleave target proteins, resulting in cellular dismantling and, ultimately, death. Although there are no true caspase gene homologs in plants, there is good biochemical evidence for several caspase-like protease activities and their involvement in plant PCD (Bozhkov et al., 2004; Sanmartín et al., 2005). Caspase-like activities have been detected in plants through cleavage of the animal caspase-specific tetrapeptide substrates (e.g. Ac-DEVD-AMC for caspase-3; del Pozo and Lam, 1998; Richael et al., 2001; Danon et al., 2004; Thomas and Franklin-Tong, 2004; Thomas et al., 2006).

Pollination involves many interactions between the pistil and pollen grain/tube as it germinates and grows to achieve fertilization (for review, see Dresselhaus and Franklin-Tong, 2013). Many angiosperms face the possibility of self-fertilization and have evolved self-incompatibility (SI) to avoid this problem. This is an important genetically controlled system that has evolved independently several times; several different mechanisms regulate SI in different plant species (for review, see Takayama and Isogai, 2005; Franklin-Tong, 2008). SI is genetically controlled by a multiallelic S-locus that encodes linked pollen and pistil S-determinants. These allow recognition and rejection, so when male and female S-determinant allelic specificities match, self-(incompatible) pollen is recognized and rejected before fertilization can occur.

The SI system found in *Papaver rhoas* (the field poppy) has provided a model system in which to study the components involved in cell-cell recognition and rejection, in particular the signaling network downstream of the interaction between the pistil S-determinant, PrsS, and the pollen S-determinant, PrpS. *PrsS* encodes a small secreted protein (Foote et al., 1994), and *PrpS* encodes a small, novel transmembrane protein (Wheeler et al., 2009). The major focus for SI-induced signaling is the initiation of PCD (Thomas and Franklin-Tong, 2004; Bosch and Franklin-Tong, 2007). A long-standing model for SI in *P. rhoas* is that PrsS acts as a signaling ligand, initiating a network of signaling events within incompatible pollen that results in the rapid inhibition of pollen tube growth and, ultimately, PCD. A key target for SI signals is the actin cytoskeleton. Within a few minutes of SI initiation, F-actin in incompatible pollen is depolymerized, and later, F-actin reorganizes into punctate foci (Snowman et al., 2002; Poulter et al., 2010). These large-scale alterations to the actin polymerization status of incompatible pollen activate a signaling network resulting in PCD (Thomas et al., 2006). The predominant caspase-like activity during SI is a caspase-3-like/DEVDase activity (Thomas and Franklin-Tong, 2004; Bosch and Franklin-Tong, 2007). More recently, it has been demonstrated that reactive oxygen species (ROS) play a key role in signaling to alterations in actin and SI-PCD (Wilkins et al., 2011). How these events integrate to participate in SI-PCD is reviewed by Wilkins et al. (2014).

We previously showed that a MAPK named p56 was activated in SI-induced pollen (Rudd et al., 2003). This implicated MAPK signaling in *P. rhoas* SI. Activation of the p56-MAPK peaked ~10 min after SI, so it occurred after the inhibition of pollen tube growth, suggesting a function in later events. A further study showed that the inhibition of SI-induced p56 activation resulted in the alleviation of SI-induced caspase-3-like activity. This provided evidence that the MAPK p56 participates in initiating the PCD signaling cascade (Li et al., 2007). Here, we have identified and cloned a pollen-expressed *P. rhoas* MAPK, *PrMPK9-1*, that encodes the p56-MAPK. We provide evidence that it functions to participate in signaling to SI-mediated inhibition of growth and actin alterations that are key features of the SI response in *P. rhoas* and in the activation of a DEVDase, which is required for SI-PCD. The identification of *Pr-MPK9-1* provides an important step forward in identifying components involved in the SI signaling network. Moreover, our demonstration that this is a TDY-type MAPK and that it participates in signaling upstream of actin alterations and DEVDase activation in the PCD network provides an important example of the function of a cell-specific TDY MAPK, rather few of which have been characterized to date.

**RESULTS**

**Evidence Suggests That p56-MAPK Is Encoded by PrMPK9-1, an Ortholog of AtMPK9**

The strategy adopted to identify the gene encoding p56-MAPK was based on combining extant data on plant MAPKs, properties of the protein, and proteomic analysis. MAPKs comprise a large gene family with 20 members identified in the Arabidopsis genome. Although MAPKs are highly conserved, they fall into four groups: the TEY groups of MAPKs (A–C) are generally smaller (~42–45 kD) than the TDY group of MAPKs (group D), which are ~55 to 79 kD (Supplemental Fig. S1). This suggested that the poppy p56-MAPK was possibly a TDY group MAPK. Expression data from...
Genevestigator indicated that four Arabidopsis TDY MAPKs, AtMPK8, AtMPK9, AtMPK17, and AtMPK9, are expressed at high levels in pollen (Supplemental Table S1). Fourier transform-ion cyclotron resonance (FT-ICR) mass spectrometry of p56 isolated by SDS-PAGE fractionation of pollen proteins (see “Materials and Methods”) identified five peptides present in AtMPK9, comprising three peptides that were unique to AtMPK9, one peptide unique to AtMPK8, and two peptide sequences that were present in AtMPK8, AtMPK9, and AtMPK15 (Supplemental Table S2). Several other peptide sequences corresponding to TDY MAPKs from Brassica napus, rice (Oryza sativa), and Populus trichocarpa also were identified (Supplemental Table S2). Taken together, these data suggested that the poppy p56-MAPK was likely encoded by an AtMPK8/9 ortholog.

We next designed primers based on sequences from Arabidopsis TDY MAPKs with high expression in pollen (AtMPK8, AtMPK9, and AtMPK17). An ~950-bp fragment was cloned from poppy pollen, and sequencing of this revealed that it shared highest nucleotide identity with AtMPK8 and AtMPK9 (Supplemental Table S2). To obtain the full-length gene sequence, 5’ RACE and 3’ RACE were carried out on pollen cDNA (see “Materials and Methods”). An ~1.6-kb mRNA product was amplified, cloned, and sequenced. The pollen open reading frame was 1,479 bp long, predicted to encode a protein of 493 amino acids, with a molecular mass of 56.3 kD and a pI of 6.49. The full-length sequence showed highest homology to AtMPK8 and AtMPK9, sharing 79.4% identity with AtMPK9 and 65.5% identity to the AtMPK8 gene at the amino acid level. Therefore, we designated the poppy gene PrMPK9-1. To determine if the PrMPK9-1 sequence was the gene encoding the SI-activated p56-MAPK, we reanalyzed the FT-ICR mass spectrometry data using the predicted protein sequences obtained. The predicted PrMPK9-1 protein had two peptide matches that were highly significant (KGSYGVVASVDTHTEGKV and KVDPLALNLLERL; Supplemental Table S2).

We also cloned another pollen open reading frame, designated PrMPK9-2 (1,818 bp, encoding a predicted protein of 606 amino acids), that also showed high homology to AtMPK8 and AtMPK9 and homology with PrMPK9-1 (Supplemental Fig. S2). However, its predicted molecular mass of 68.95 kD was too large to be a good candidate for the gene encoding the SI-activated p56-MAPK. Comparing the PrMPK9-2 predicted protein sequences with the p56 pollen extract, FT-ICR peptide data revealed no significant matches (Supplemental Table S2). This discounted PrMPK9-2 as a candidate for the poppy p56-MAPK and confirmed that PrMPK9-1 was the best candidate.

The expression of PrMPK9-1 was examined using semiquantitative reverse transcription (RT)-PCR. Transcript was detected in mature pollen, with weak expression during late anther development; there was negligible expression in root, leaf, or stigma (Fig. 1A). This expression pattern is consistent with the known function of the p56-MAPK involvement in the SI response in mature pollen. We examined whether PrMPK9-1 was up-regulated after SI induction, as several MAPKs are up-regulated after stimulation, particularly stress treatments (Zhang et al., 2014). RT-PCR expression analysis of PrMPK9-1 revealed increased expression 10 min after SI induction in incompatible pollen specifically; compatible pollen challenged with the same PrsS did not show increased expression, nor did other control pollen samples (Fig. 1B). Thus, PrMPK9-1 also exhibits increased expression after SI induction.

**PrMPK9-1 Encodes a TDY MAPK**

Analysis of the predicted PrMPK9-1 protein sequence reveals the expected features of a MAPK, including 11 characteristic kinase domains, the ATP-binding site, the substrate-binding site, and the kinase interaction motif. The presence of a TDY motif, rather than a TEY motif, is characteristic of a group D MAPK (for review, see Rodriguez et al., 2010). Consistent with this, PrMPK9-1 possesses a long C-terminal extension of ~140 amino acids that is typical of group D MAPKs (Jonak et al., 2002). In addition, the protein lacks the C-terminal common-docking domain that is found in groups A, B, and C MAPKs but not in group D proteins. In addition, a phylogenetic tree (Supplemental Fig. S1) based on ClustalX analysis of the predicted PrMPK9-1 and PrMPK9-2 protein sequences with MAPK sequences from Arabidopsis, rice, *P. trichocarpa*, alfalfa, *Zea mays*, and *Homo sapiens* also placed the proteins in the large family of group D MAPKs.

**Figure 1.** Expression analysis of PrMPK9-1. A, Semiquantitative RT-PCR expression analysis of PrMPK9-1. PrMPK9-1 shows increasing expression during pollen development and low expression in other tissues. I, Immature anthers; −3/−2/−1/+1, stages of anther development (number of days from anthesis); P, hydrated pollen; R, root; L, leaf; S, stigma. GAPD shows control gene expression. B, RT-PCR expression analysis of PrMPK9-1 shows increased expression 10 min after SI induction in incompatible (SI) and compatible (COM) pollen or heat-denatured PrsS (DSI). CK, Control using water as a template; GM, control pollen growing in growth medium (GM). GAPD shows control gene expression.
clade of group D MAPKs. The poppy proteins exhibited highest homology with AtMPK9. Gene duplication is a prominent feature within both the eudicot and monocot MAPK gene families (Hamel et al., 2006; Rodriguez et al., 2010). For example, in *P. trichocarpa*, two paralogs of AtMPK16 have been identified (PtMPK16-1 and PtMPK16-2). The high similarity between PrMPK9-1 and PrMPK9-2 suggests this to be the case for the poppy MPK9. Thus, PrMPK9-1 and PrMPK9-2 appear to be paralogs of AtMPK9, although the latter is present only as a single copy in the Arabidopsis genome.

**Evidence of a Direct Link between PrMPK9-1 and p56-MAPK**

Although evidence indicated that p56-MAPK is not an ortholog of AtMPK3, we had shown previously that p56-MAPK cross-reacts with an anti-AtMPK3 antibody (Li et al., 2007). Therefore, we checked if the product of PrMPK9-1 was detected by the anti-AtMPK3 antiserum. We expressed the full-length His-tagged PrMPK9-1 protein in *Escherichia coli*. Western blotting confirmed that this recombinant protein could be detected with anti-His tag antiserum (Fig. 2A) and anti-AtMPK3 (Fig. 2B). Given this observation, we sought to obtain direct lines of evidence to demonstrate that PrMPK9-1 encodes the p56-MAPK.

Initially, we used western blotting to detect PrMPK9-1. As MAPKs share many conserved domains, we made an antibody raised against the divergent C-terminal region (103 amino acids) of PrMPK9-1, as the full-length protein was unlikely to be sufficiently specific. This C-terminal His-tagged PrMPK9-1C truncated recombinant protein (~16 kD) was detected with the anti-His tag antiserum (Fig. 2C). The PrMPK9-1C antiserum cross-reacted with the truncated PrMPK9-1C recombinant protein (Fig. 2D) and with full-length PrMPK9-1 recombinant protein (Fig. 2E). We also ascertained that it detected a protein migrating at 56 kD in crude pollen extracts from *P. rhoeas* (Fig. 2F). Preimmune serum did not cross-react with the PrMPK9-1C recombinant protein (Fig. 2G).

We then examined pollen extracts that had been SI induced (Fig. 3A) to see if we could detect an ~56-kD MAPK protein that was activated by SI. Western blotting using anti-pTXpY to detect activated MAPKs showed minimal levels of phosphorylated p56-MAPK activity in untreated pollen and increased activity in SI-induced samples (Fig. 3B); several activated MAPKs also were detected, but their activity was approximately the same in both samples. When the membrane was reprobed with anti-PrMPK9-1C (Fig. 3C), this antibody detected a protein at the same molecular mass as the phosphorylated p56-MAPK, but, as expected, it did not distinguish between phosphorylated and unphosphorylated samples. This provides good evidence that PrMPK9-1 corresponds with the p56-MAPK phosphoprotein. The top band at ~70 kD is a cross-reacting contaminant from the recombinant PrsS used for the SI induction (Supplemental Fig. S3).

We previously used calyculin A (a Ser/Thr protein phosphatase inhibitor) to obtain increased levels of phosphorylated MAPKs in pollen extracts and used a pTXpY antibody to detect the activated form of p56 (Rudd et al., 2003; Li et al., 2007). To determine that PrMPK9-1 corresponded to this phosphoprotein, we treated pollen with calyculin A. Equal amounts of untreated- and calyculin A-treated pollen extracts (Fig. 3D) were immunoprecipitated using biotinylated PrMPK9-1C antiserum and probed with anti-pTXpY antibody (Fig. 3, E and F). This revealed an activated ~56-kD protein immunoprecipitated by anti-PrMPK9-1C in the calyculin-treated sample (Fig. 3E) but not in the untreated sample (Fig. 3F). Corresponding immunoprecipitates of untreated and SI-induced samples probed with anti-pTXpY antisera (Fig. 3G) also gave an ~56-kD protein, present in the SI sample and not in the untreated sample. We believe the bottom band to be a degradation product. These data provide good evidence that PrMPK9-1 corresponds with a phosphoprotein that has the properties of the SI-activated p56-MAPK identified previously (Rudd et al., 2003; Li et al., 2007).

To unequivocally determine the identity of the protein in the calyculin A-treated pollen sample, a 56-kD band was excised from the sample immunoprecipitated by PrMPK9-1C antiserum (Fig. 3E) and analyzed using FT-ICR mass spectrometry. Importantly, this revealed that all the peptides present in this 56-kD band had highly significant matches with PrMPK9-1 (Supplemental Table S2). Together, these data provide compelling evidence that PrMPK9-1 encodes the p56-MAPK.

![Figure 2](image-url)
PrMPK-9 Is Cytosolic and Does Not Alter Its Localization after SI Induction

As some MAPKs translocate to the nucleus after activation (Cheong et al., 2003), we investigated the intracellular localization of PrMPK-9 in untreated pollen tubes and after SI induction using immunolocalization. Fixed pollen tubes were probed with the purified anti-PrMPK-9C antiserum and visualized using anti-rabbit IgG–fluorescein isothiocyanate (FITC) secondary antibody (Fig. 4). This revealed that PrMPK-9C appeared to have a largely cytosolic localization throughout untreated pollen tubes (Fig. 4, A–C). Examining localization after SI induction revealed that PrMPK-9C retained its mostly cytosolic localization (Fig. 4, D–F). Even several hours after SI induction, PrMPK-9C localization remained similar to the observed localization in normally growing pollen tubes. We conclude that, unlike some other MAPKs that have been shown to undergo rapid translocation to the nucleus (e.g. PcMPK3a/b and PcMPK6 during the innate immunity response in parsley [Petroselinum crispum] cells; Lee et al., 2004), PrMPK-9-1 does not alter its localization after activation.

Antisense Oligonucleotides for PrMPK-9-1 Block the SI Response in Pollen Tube Growth

Having obtained compelling evidence that PrMPK-9-1 is the poppy p56-MAPK, we wished to establish that PrMPK-9-1 was involved in the SI response. Although we had speculated earlier that p56 was unlikely to be involved directly in pollen inhibition, as its peak activation was 10 min after SI induction, this did not rule out a possible role in decision-making after the rapid tip inhibition. In order to establish whether the p56-MAPK was functionally involved in the early steps of the SI response, we used in vitro SI bioassays using antisense oligonucleotides. This approach has been used previously to demonstrate a functional role for a pollen-soluble inorganic pyrophosphatase (de Graaf et al., 2006) and for the PrpS pollen S-determinant (Wheeler et al., 2009) in SI, as they block the inhibition response. We hypothesized that if the PrMPK-9-1 MAPK is functionally involved in signaling to targets/mechanisms involved in SI, knockdown of its expression should result in the alleviation of pollen tube inhibition in an S-specific manner. Therefore, we induced SI in vitro in the presence of either antisense (as-ODNs) or sense (s-ODNs) oligonucleotides for PrMPK-9-1 to test this hypothesis.

SI induction in pollen grown in vitro, stimulated by the addition of recombinant PrsS proteins, resulted in highly significantly inhibited pollen tube growth (a reduction of 75.25% in length; $P = 2.55 \times 10^{-45}$, $n = 150$). Compatible pollen in combination with the same PrsS proteins did not result in any significant difference in lengths compared with compatible untreated pollen tubes ($P = 0.062$, not significant). When SI was induced in pollen pretreated with antisense MPK9-1 oligonucleotides (as-ODNs), we observed a significant alleviation of the SI-specific inhibition (Fig. 5). Addition of the
Antisense Oligonucleotides for PrMPK9-1 Block the Formation of SI-Induced Actin Punctate Foci

As we had shown previously that alterations in actin polymerization status can trigger PCD in pollen (Thomas et al., 2006) and that the formation of punctate F-actin foci is a key feature of SI induction (Geitmann et al., 2000), we wished to establish whether PrMPK9-1 was functionally involved in mediating the formation of these distinctive actin foci formed specifically in incompatible pollen. To examine this, we took a similar approach, inducing SI in vitro in the presence of either PrMPK9-1 antisense (as-ODNs) or sense (s-ODNs) oligonucleotides and imaging F-actin in pollen tubes after 2 h. SI triggered the formation of the F-actin foci (Fig. 6A), while untreated pollen tubes had normal F-actin configurations (Fig. 6B); as-ODNs in combination with SI induction rescued the pollen F-actin, which showed a normal configuration (Fig. 6C), while s-ODNs in combination with SI induction had no effect (Fig. 6D); control treatment with as-ODNs (Fig. 6E) or s-ODNs alone had no effect. Quantification of these data (Fig. 6F) revealed that pollen tubes pretreated with as-ODNs prior to SI induction had significantly fewer actin foci compared with SI alone ($P = 1.14 \times 10^{-10}$, $n = 200$), while s-ODN pretreatment prior to SI was significantly
Antisense Oligonucleotides for PrMPK9-1 Block SI-Induced PCD in Incompatible Pollen

We previously obtained data implicating a MAPK as being functionally involved in mediating PCD in incompatible pollen (Li et al., 2007). However, as this involved a pharmacological approach, which would inhibit all pollen MAPKs, and as the identity of p56 at that time was unknown, we could not link p56 to being functionally involved in mediating SI-induced PCD. Here, having cloned p56, we used the fluorogenic caspase-3/7 live-cell substrate, Image iT LIVE Green Caspase-3 and Green Caspase-7 Detection Kit (see “Materials and Methods”), in combination with the antisense PrMPK9-1 oligonucleotides to examine whether PrMPK9-1 was involved in mediating SI-induced PCD in incompatible pollen. We induced SI in vitro in pollen tubes that had been pretreated with either antisense (as-ODNs) or sense (s-ODNs) oligonucleotides and imaged caspase-3-like activation in pollen tubes after 4 to 5 h, when peak activity was expected (Bosch and Franklin-Tong 2007), to test this hypothesis. Untreated pollen tubes showed no FITC fluorescence indicating caspase-3-like activity (Fig. 7, A and B), while SI-treated pollen tubes had increased levels of fluorescence (Fig. 7, C and D); pollen tubes treated with as-ODNs prior to SI had background levels of fluorescence similar to untreated controls (Fig. 7, E and F), while the control treatment with s-ODNs prior to SI had no effect, with DEVDase activity still detected (Fig. 7, G and H). Quantification of these data (Fig. 7I) revealed that the as-ODNs resulted in a highly significant recovery of SI-induced tubes compared with SI-induced treatment alone ($P = 8.790 \times 10^{-10}$, n = 250), and s-ODN pretreatment prior to SI had a significantly different effect compared with that of the as-ODNs ($3.60 \times 10^{-8}$). The as-ODN and s-ODNs alone had no effect ($P = 0.409$, not significant, and $P = 0.250$, not significant, respectively). Together, these data demonstrate that PrMPK9-1 plays a key role in the signaling network resulting in caspase-3-like activation, which will induce PCD in incompatible pollen tubes.

DISCUSSION

MAPKs have been shown to be key players in regulating many signaling networks in plants (Pitzschke et al., 2009; Meng and Zhang, 2013; Xu and Zhang, 2015). Despite a good knowledge of the MPK gene families for some time now, the function of only a handful of MPK genes have been identified. Here, we have identified the pollen-specifically expressed PrMPK9-1, a developmentally expressed TDY MAPK, with high expression in mature pollen, as being involved in the SI response. We took an unusual backward approach, as we had a well-characterized biological phenomenon (SI) that we had shown previously to involve a MAPK activity (Rudd et al., 2003), but we did not know which of the 20 MAPKs was involved. To our knowledge, our studies are the first implicating a function for a MAPK that is expressed in pollen. Moreover, PrMPK9-1 falls in the (so far) rather poorly characterized group of TDY class (group D,
family V) MAPKs. Below, we discuss the implications of our findings.

Identity of PrMPK9-1 as a TDY MAPK

The *P. rhoes* MPK9-1 gene belongs to the large MPK clade D, which has a TDY motif instead of TEY and an extended C-terminal region relative to the other MAPKs (Ichimura et al., 2002). The group D MAPKs are unique, owing to their TDY motif in the activation loop and long C-terminal common-docking domain (Rodriguez et al., 2010). Although the existence of the TDY-type clade D MAPKs is well established and the fact that all plants have MAPKs in this group indicates their functional importance, relatively little is known about the function of MAPK members of clade D. Moreover, functional redundancy between MAPKs makes it difficult to employ a genetic approach to determine their functions. Thus, rather little is known about the function of TDY MAPKs in plants. A wealth of information relating to TEY MAPKs exists, and most of what we know about MAPK function relates to the TEY MAPKs, with studies largely focused on a relatively small subset of MAPKs, primarily MPK3/4/6, which are all in the A and B subgroups of TEY-type MAPKs. Early research on plant MAPKs focused on their functions in immunity and stress responses, as many of the TEY MAPKs were found to function in these (for review, see Meng and Zhang, 2013). More recent studies have revealed that many TEY MAPKs also play key roles in plant growth and development (for review, see Xu and Zhang, 2015).

Only a few members of subfamily D have been functionally characterized to date, so insights into functions for TDY MAPKs are limited. However, all four of those that have been characterized to date are phylogenetically closely clustered together in a group. The alfalfa MAPK, *TDY1*, was one of the first of the TDY-clade MAPKs to be characterized. High expression in root nodules and root and shoot apices suggested a possible role in tip growth initiation/development, and *TDY1* promoter studies revealed induction by mechanical and pathogen wounding (Schoenbeck et al., 1999). In rice, the TDY MAPK *BWMK1* (blast- and wound-induced MAPK) was shown to be induced by infection by both infection of the rice blast fungus *Magnaporthe grisea* and mechanical wounding (He et al., 1999). More recently, it was shown that *BWMK1* is activated by fungal elicitors, hydrogen peroxide, salicylic acid, and jasmonic acid (Cheong et al., 2003). Other studies in cotton (*Gossypium raimondii*) showed that *MPK9* (together with *MPK13* and *MPK25*) confer resistance to *Verticillium dahlia*, which causes defoliation (Zhang et al., 2014). These studies provide evidence that these TDY MAPKs play a role in signaling to defense signaling. In contrast, a landmark study in Arabidopsis revealed that *MPK9* was preferentially and highly expressed in stomatal guard cells and has a completely separate function. Studies revealed that *MPK9* is functionally redundant with *MPK12* (a TEY MAPK) and that together they acted as positive regulators of ROS-mediated abscisic acid-induced stomatal guard cell closure (Jammes et al., 2009). Although most of this study focused on *MPK12*, it clearly showed that *MPK9* and *MPK12* function together in regulating transpiration. More recently, it has been shown that these two MAPKs also function in methyl jasmonate signaling to induce stomatal closure (Khokon et al., 2015). Data indicate that *MPK9* and *MPK12* function upstream of *S*-type anion channel activation and downstream of ROS production, cytosolic alkalization, and \([Ca^{2+}]_{cyt}\) elevation in guard cells (Khokon et al., 2015). A further Arabidopsis TDY MAPK has been functionally characterized recently: Arabidopsis *MPK8* is activated by mechanical wounding, and it has been shown that the MPK8 pathway negatively regulates ROS accumulation by controlling the expression of...
the RbohD gene (Takahashi et al., 2011). Here, we have shown that PrMPK9-1, which is closely related to these TDY MAPKs, functions in signaling to SI in incompatible pollen. We speculate that different functions have evolved for these MAPKs in different cell types.

**PrMPK9-1 Functions in Pollen in the SI Signaling Network**

To our knowledge, to date, no known function for AtMPK9 in pollen has been found, although the Arabidopsis Affymetrix chip data indicate that AtMPK9 is expressed in pollen. This suggests that this MAPK has evolved a specific function within the context of SI. PrMPK9-1 exhibits increased expression after SI induction, and the protein is activated by phosphorylation after SI induction. Here, using an antisense oligonucleotide approach, we have demonstrated that PrMPK9-1 has a crucial role in the signaling network leading to the SI-induced S-specific pollen tube inhibition and PCD. Our study identifies a key role for PrMPK9-1 in signaling to characteristic SI-mediated actin cytoskeleton reorganization (Geitmann et al., 2000; Snowman et al., 2002; Poulter et al., 2010) and activation of a DEVDase activity that is required for PCD in incompatible pollen (Thomas and Franklin-Tong, 2004; Bosch and Franklin-Tong, 2007). Moreover, our previous studies on SI have shown that actin alterations are required for PCD (Thomas et al., 2006). Our data place PrMPK9-1 as a key player upstream of actin alterations and PCD. MAPK signaling to the actin cytoskeleton is well established (Samaj et al., 2004). Integrating our existing knowledge of the SI signaling network with our new data on PrMPK9-1, we can place PrMPK9-1 activation, which peaks at 10 min after SI induction (Rudd et al., 2003), downstream of the almost instantaneous increases in [Ca\(^{2+}\)]\(_{cyt}\) (Franklin-Tong et al., 1993, 1997), downstream of increases in ROS that peak at 5 min post SI (Wilkins et al., 2011), and upstream of the later formation of punctate actin foci and DEVDase activation. Thus, PrMPK9-1 occupies a critical position within the SI-PCD signaling network.

**Close Relatives AtMPK8 and AtMPK9 May Function in Similar Signaling Networks**

It is of considerable interest that two of the few Arabidopsis MAPKs belonging to the TDY group that have been functionally characterized so far, MPK8 and MPK9, are the closest relatives to the P. rhoeas PrMPK9-1 and have been shown to be involved in regulating ROS in different signaling networks (Jammes et al., 2009; Takahashi et al., 2011; Khokon et al., 2015). Thus, together, current data suggest that several TDY MAPKs, AtMPK8, AtMPK9, and PrMPK9-1, play a key role in regulating ROS homeostasis. As all three MAPKs are close relatives, this may not be a coincidence. It will be interesting to see if future studies show that further TDY MAPKs in this cluster generally share this phenomenon. Moreover, a study by Menges et al. (2008), using Gene Ontology overrepresentation analysis to analyze biological processes potentially involved in unknown MAPK functions, identified MPK9 as being potentially involved in cytoskeleton organization. Here, we have provided direct experimental evidence that the P. rhoeas PrMPK9-1 is upstream of and required for regulating the highly distinctive SI-induced actin reorganization into punctate foci. Indeed, it appears that the signaling network found in P. rhoeas pollen undergoing SI-PCD is rather similar (at least superficially) to that for MPK8 expressed in various tissues (Khokon et al., 2015). While the methyl jasmonate pathway in guard cells shares several signaling components with the abscisic acid pathway (ROS, [Ca\(^{2+}\)]\(_{cyt}\) alterations, and cytosolic alkalization), the SI-PCD network also involves ROS and [Ca\(^{2+}\)]\(_{cyt}\) increases and alterations in cytosolic pH, but a dramatic acidification is triggered (Wilkins et al., 2015). Future studies should explore whether other TDY MAPKs in this cluster generally share these key signaling components.

In summary, here, we show that PrMPK9-1 is a TDY MAPK that is expressed in a distinct cell type (pollen) and provide evidence that it has a cell type-specific function for PrMPK9-1, with a distinct role from AtMPK9. PrMPK9 is a key regulator for SI in pollen and acts upstream of PCD involving alterations in actin organization and activation of a DEVDase/caspase-3-like enzyme. Thus, the role of MPK9-1 expressed in pollen plays a role in a very different biological phenomenon to the other TDY MAPKs analyzed at this level to date (ROS, [Ca\(^{2+}\)]\(_{cyt}\) alterations, and cytosolic alkalization). However, the signaling network in which it is placed appears (at least superficially) similar to other closely related MAPKs that have been characterized to date. It will be interesting in the future to see what functions and signaling networks further cell type-specific MAPKs are involved in.

**MATERIALS AND METHODS**

**Cloning of Papaver rhoeas MPK9-1: Sequence Analyses and Affymetrix Analysis**

cDNA was synthesized using the Invitrogen SuperScript II Reverse Transcriptase kit using total RNA from P. rhoeas pollen (RNAeasy Plant Mini Kit; Qiagen). Initially, gene-specific primers based on Arabidopsis (Arabidopsis thaliana) MAPKs expressed in pollen (AtMPK8, AtMPK9, and AtMPK17) were used to obtain partial pollen-expressed P. rhoeas MPK cDNAs. An 880-bp cDNA fragment, amplified using primers MPK9 forward and reverse (MPK9F and MPK9R), was cloned and sequenced and shared highest identity with AtMPK8 and AtMPK9. Full-length cDNAs of PrMPK9-1 were obtained using 5' and 3' RACE PCR. 3' RACE amplification from P. rhoeas pollen cDNA used 3' RACE (3' RACE 17AP) and 5' gene-specific (PrMPK9-3R1) primers. The product was PCR purified and reamplified with 3' RACE primer (3' RACE UAP) and nested gene-specific primer (PrMPK9-3R2). For 5' RACE, cDNA was synthesized using a primer specific to the 5' end of the gene (PrMPK9-3R1) instead of the oligo(dT) primer. cDNA was cleaned using the QiAquick PCR Purification Kit (Qiagen). A poly(C) tail was added at the 5' end. PCR amplification employed a 5' RACE abridged primer (5' RACE AAP) and a second gene-specific 3' primer (PrMPK9-3R2). This amplification product was reamplified with a 5' RACE unbrided primer (5' RACE UAP) and a third nested gene-specific 3' primer (PrMPK9-3R3). Full-length sequence was confirmed by...
Proteomic and Bioinformatic Analyses

For mass spectrometry analysis of the p56 protein, total pollen proteins were separated by SDS-PAGE and stained with Coomassie Blue. A band corresponding to 56 kD was excised and digested with Trypsin Gold (Promega). Peptides were identified by FT-ICR mass spectrometry searching NCBI nr Green Plant database using the SEQUEST algorithm.

RT-PCR

Standard RT-PCR techniques were used for expression analysis. Total RNA was extracted from various tissues from P. rhoeas plants (anthers at various stages of development, mature pollen, stigma, leaf, and root; RNAeasy Plant Mini Kit; Qiagen) and cDNA was synthesized (Omniscript RT Kit; Qiagen). Gene-specific primers were used to amplify PrMPK9-1 transcripts during RT-PCR (PrMPK9-1RT-F/PrMPK9-1RT-R and PrMPK92gen5/PrMPK92gen3) for semi quantitative experiments; primers for P. rhoeas glyceroldehyde-3-phosphate dehydrogenase gene (PrGAPD5) and PrGAPD3 acted as controls (Table II).

In Vitro Kinase Activity Assays

Kinase assays using pollen protein were performed according to Rudd et al. (1996). Briefly, pollen was homogenized on ice in 50 mM Tris-HCl pH 7.5, and 0.1% Triton X-100 containing protease inhibitor cocktail, cell debris was removed by centrifugation, and supernatants were stored at −20°C. Leaf proteins were extracted in a similar way, after grinding with liquid N2. Protein concentration was estimated using the Bio-Rad assay.

Pollen Tube Growth and SI Induction

Pollen was grown and SI was induced as described (Wilkins et al., 2011, 1998). SI was induced by adding recombinant PrSi to (10 mg mL−1) to pollen of the appropriate S-haplotype to generate an incompatible combination (e.g. PrS6 and PrS5 with pollen of haplotype S6S5). For calycin A treatment, growing pollen was treated with 0.25 mM calyculin A (Sigma-Aldrich) for 10 min.

Table I. Primers for cloning of PrMPK9-1

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Table II. Primers for RT-PCR

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<td>PrGAPD3</td>
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Table III. Primers for amplification of PrMPK9-1

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<td>PrMPK9-1C_3′Xhol</td>
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<tr>
<td>PrMPK9-1C_PrinPoint</td>
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Production and Purification of Recombinant PrMPK9-1 Antisera

Polyclonal antibodies were raised in rabbits against full-length recombinant PrMPK9-1 (Biogenes) and also the C-terminal portion of PrMPK9-1 (residues 391–493; PrMPK9-1C) to obtain an antibody specific to PrMPK9 (Biogenes). The anti-PrMPK9-1C antibody was affinity purified using the biotinylated version of PrMPK9-1C (PrMPK9-1CPP) and the PinPoint Xa Protein Purification System (Promega). Antibody captured by the PrMPK9-1CPP-TetraLink Tetrameric Avdin resin (Pierce) was eluted using 100 mM citric acid (pH 3).

Biotinylation of anti-PrMPK9-1C Antibody and Immunoprecipitation

Purified anti-PrMPK9-1C antibody was biotin labeled using the EZ-Link Sulfo-NHS-LC-Biotinylation Kit (Pierce), following the manufacturer’s instructions for calculations (http://www.piercenet.com/haba/habacalc.cfm).
Biotin incorporation was confirmed using the Curvette Format. The biotinylated PrMPK9-1C antibody was linked to TetraLink Tetrameric Avidin Resin (Pierce). Biotinylated anti-PrMPK9-1C antibody-avidin resin was added to pollen extracts, with immunoprecipitation buffer (PBS + 1% 1 mg/ml PMSF), and incubated overnight at 4°C. The resin was washed and recovered by centrifugation, the supernatant was removed and incubated in 100 mM citric acid, pH 3, and proteins were eluted into Tris buffer, pH 8.

SDS-PAGE and Western Blotting

Proteins were separated using SDS-PAGE and electroblotted (Bio-Rad). Immunoblots were probed with primary antibodies (rabbit anti-His tag [1:1,000; Sigma-Aldrich], rabbit anti-AtMAPK3 antibody [1:1,000; Sigma-Aldrich], rabbit anti-full-length PrMPK9-1 antibody [1:1,000], rabbit anti-PrMPK9-1C antibody [1:1,000], and anti-ACTIVE MAPK polyclonal antibody [pTxPY; 1:12,000; Cell Signaling Technology]) in blocking solution (1× TBS and 5% milk powder). Blots were washed and then incubated with secondary antibody (goat anti-rabbit IgG-alkaline phosphatase; 1:5,000; Sigma-Aldrich). Proteins were detected using 5-bromo-4-chloro-3-indolyl phosphate/nitroblue tetrazolium alkaline phosphatase detection (Promega) or ECL Detection Reagent (Promega) with an AGFA CURIX 60 processor. To reprobe, blots were stripped in 0.05M sodium phosphate buffer (pH 6.5), 10M urea, and 0.1M SDS-PAGE and electroblotted (Bio-Rad).

Membrane fractions were incubated with 0.5% SDS and 15% glycerol in blocking solution (1× TBS and 5% milk powder). Blots were washed and then incubated with secondary antibody (goat anti-rabbit IgG-alkaline phosphatase; 1:5,000; Sigma-Aldrich). Proteins were detected using 5-bromo-4-chloro-3-indolyl phosphate/nitroblue tetrazolium alkaline phosphatase detection (Promega) or ECL Detection Reagent (Promega) with an AGFA CURIX 60 processor. To reprobe, blots were stripped in 0.05M sodium phosphate buffer (pH 6.5), 10M urea, and 0.1M SDS-PAGE and electroblotted (Bio-Rad).

Supplemental Figure S2. Phylogenetic tree of MAPKs.

Supplemental Figure S3. Explanation for ~72kDa band in SI-induced samples with PrMPK9-1C.

Supplemental Table S1. Expression of MAPKs in Arabidopsis pollen.

Supplemental Table S2. Peptides identified from the ~56-kD protein band using FT-ICR mass spectrometry.

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LITERATURE CITED


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