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**Arabidopsis** MKS1 Is Involved in Basal Immunity and Requires an Intact N-terminal Domain for Proper Function

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**Abstract**

**Background:** Innate immune signaling pathways in animals and plants are regulated by mitogen-activated protein kinase (MAPK) cascades. MAP kinase 4 (MPK4) functions downstream of innate immune receptors via a nuclear substrate MKS1 to regulate the activity of the WRKY33 transcription factor, which in turn controls the production of anti-microbial phytoalexins.

**Methodology/Principal Findings:** We investigate the role of MKS1 in basal resistance and the importance of its N- and C-terminal domains for MKS1 function. We used the information that mks1 loss-of-function partially suppresses the mpk4 loss-of-function phenotype, and that transgenic expression of functional MKS1 in mpk4/mks1 double mutants reverted the mpk4 dwarf phenotype. Transformation of mks1/mpk4 with mutant versions of MKS1 constructs showed that a single amino acid substitution in a putative MAP kinase docking domain, MKS1-L32A, or a truncated MKS1 version unable to interact with WRKY33, were deficient in reverting the double mutant to the mpk4 phenotype. These results demonstrate functional requirement in MKS1 for the interaction with MPK4 and WRKY33. In addition, nuclear localization of MKS1 was shown to depend on an intact N-terminal domain. Furthermore, loss-of-function mks1 mutants exhibited increased susceptibility to strains of *Pseudomonas syringae* and *Hyaloperonospora arabidopsidis*, indicating that MKS1 plays a role in basal defense responses.

**Conclusions:** Taken together, our results indicate that MKS1 function and subcellular location requires an intact N-terminus important for both MPK4 and WRKY33 interactions.


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**Introduction**

Plants are constantly exposed to a broad range of microbes and have evolved an innate immune system to defend against invading pathogens [1,2]. Part of this system is based on the perception of pathogen- or microbe-associated molecular patterns (PAMPs or MAMPs) through pattern recognition receptors (PRRs) at the cell surface. A common mechanism to transduce such signals into cellular responses is the activation of mitogen-activated protein kinase (MAPK) cascades. These cascades consist of MAPKKK-MAPKK-MAPK modules that link upstream receptors and downstream targets leading to rapid activation of defense responses upon recognition of invading pathogens [3,4].

Loss of *Arabidopsis* MAP kinase 4 (MPK4) activity leads to dramatic changes in gene-expression, elevated levels of the phytohormones salicylic-acid (SA), increased resistance to biotrophic pathogens, and mpk4 loss-of-function mutants are extreme dwarfs [5]. The resistance-associated phenotypes of mpk4 are suppressed by mutations in two defense regulators, ENHANCED DISEASE SUSCEPTIBILITY 1 (EDS1) and PHYTOALEXIN DEFICIENT 4 (PAD4) [6]. In contrast, MPK4 seems to be required for the expression of defense genes that rely on the phytohormones ethylene and jasmonate (ET/JA) and efficient resistance against necrotrophic pathogens. Interestingly, EDS1 was found to be responsible for blocking PDF1.2 expression in mpk4 single mutants, because mpk4/eds1 double homozygotes express PDF1.2 in response to jasmonate [6].

MAP kinase substrate 1 (MKS1) was previously identified as a MPK4 substrate, and analysis of transgenic plants, and transcript profiling indicated that MKS1 was required for full resistance in mpk4 mutants [7]. MKS1 was also found to interact in vivo with the transcription factor WRKY33, and may function as an adaptor linking MPK4 activity to WRKY-regulated gene expression [8]. WRKY transcription factors constitute a family of defense-related factors that bind W-box sequences in the promoters of pathogen-induced genes, including WRKY genes themselves [9,10]. It was
shown that MPK4 and MKS1 associate in a complex with WRKY33, and that activation of MPK4 and phosphorylation of MKS1 upon infection leads to release of MKS1 and WRKY33 from MPK4. Consequently, WRKY33 targeted the promoter of PHYTOALEXIN-DEFICIENT3 (PAD3), encoding a cytochrome P450 monoxygenase required for the production of the antimicrobial phytoalexin camalexin [8].

MKS1 contains a plant-specific VQ motif that is found in about 35 predicted Arabidopsis proteins [11]. These proteins are generally small and share little significant similarity to other sequenced or predicted proteins. Other than the regions containing the conserved VQ motif, their primary structures also appear to be highly diverse [11].

MAP kinases phosphorylate their substrates on conserved Ser/Thr-Pro phosphoacceptor sites [12]. However, targeting of a MAP kinase to a specific substrate does not only depend on the phosphoacceptor site, but is also mediated by physical interaction between the kinase and MAP kinase docking domains present on substrate protein [13]. Docking domains have been identified in numerous MAP kinase substrates, and consist of a K/R1-X1-R/Q1-X2-R/Q2 module, where R/Q1 and R/Q2 are hydrophobic residues (leucine, isoleucine or valine) [13].

MKS1 contains 12 Ser-Pro, and our initial analyses indicated that MPK4 phosphorylated MKS1 in vitro on Ser30 and/or Ser72 and perhaps on other Ser–Pro sites throughout MKS1 [7]. In a more recent paper we used mass spectrometry to identify in planta activated MPK4 phosphorylation of MKS1. However, using this technique we did not detect phosphorylation of Ser30, but only phosphorylation of Ser72, Ser108, and Ser120 [14].

Here we show that MKS1 plays a pivotal role in basal defense responses in Arabidopsis as loss-of-function mks1 mutants exhibit increased susceptibility to strains of Pseudomonas syringae and Hyaloperonospora arabidopsidis. In addition, we show that MKS1 function and subcellular location requires an intact N-terminus important for both MPK4 and WRKY33 interactions.

Results

mks1 suppresses the mpk4 dwarfism phenotype

We previously demonstrated that reduced accumulation of MKS1 mRNA via RNAi (MKS1-RNAi) partially suppressed the dwarfism and disease resistance conferred by mpk4 mutation in homozygous mpk4 expressing MKS1-RNAi [7]. However, the resistance phenotype of MKS1-RNAi was not significantly different from wild-type [7]. This may have been because MKS1 does not contribute to basal defense, or that the levels of MKS1 mRNA in MKS1-RNAi plants were sufficient to mask such a phenotype. To distinguish between these two possibilities, we obtained an MKS1 Ds-insertion line (GT.108403). RT-PCR identified MKS1 transcripts in the parental wild-type background Ler but not in the mks1 insertion mutants (Figure 1A). Furthermore, immune-blots with an MKS1-specific antibody [7] demonstrated the presence of MKS1 protein in Ler and in transgenic in which MKS1 expression is controlled by the CaMV 35S promoter, but failed to detect MKS1 protein in the mks1 insertion line (Figure 1B). The mks1 null mutant was expected to suppress the mpk4 phenotype at least to the same level as seen with MKS1-RNAi [7]. Therefore, the mks1 insertion allele was crossed into the mpk4 background and double mutant mpk4/mks1 progeny confirmed by PCR (data not shown). Notably, the suppression of mpk4 dwarfism and leaf epinasty by the mks1 insertion allele was stronger than what we originally found with MKS1-RNAi (Figure 1C).

mks1 mutants exhibit decreased basal resistance to pathogens

Since the mks1 mutant is a stronger suppressor of mpk4 than MKS1-RNAi, MKS1 could be engaged in cellular processes, including general plant defense responses, not detected via the RNAi approach. We therefore monitored the disease susceptibility of mks1 infected with P. syringae Pst DC3000. Time-course replicate assays revealed that, 2 and 4 days after inoculation with virulent Pst DC3000, bacterial growth in leaves of soil grown mks1 mutant plants was up to 10-fold higher compared to Ler wild-type (Figure 2A). To verify this finding, we extended the analysis with another pathogen class by inoculating mks1 mutants with a virulent isolate (Cala 2) of the oomycete Hyaloperonospora arabidopsidis. Colonization by the virulent Cala 2 isolate was considerably more pronounced in mks1 compared to Ler, as revealed by the number of spores per plant (Figure 2B) and by macroscopic disease symptoms (data not shown). This suggests that loss of MKS1 affects induced defense responses. We therefore examined the accumulation of the pathogenesis-related marker PRI1 mRNA by real-time RT-PCR in mks1 mutants after challenge with virulent P. syringae. However, PRI1 accumulated to much lower levels in mks1 compared to wild-type Ler leaves 2 days after infection (Figure 2C). These results indicate that MKS1 plays a role in maintaining basal resistance.

Overexpression of MKS1 leads to susceptibility to the necrotrophic pathogen B. cinerea

To further characterize the role of MKS1 in disease resistance, we included a necrotrophic pathogen in our analysis and inoculated both mks1 mutants and transgenic plants overexpressing MKS1 (35S:MKS1) with the fungus B. cinerea. The 35S:MKS1 plants displayed severe tissue damage 5 days after inoculation (DAI) compared to both mks1 and the Ler wild-type (Figure 3A). The size of disease lesions on inoculated leaves of 35S:MKS1 was increased compared to Ler wild-type (Figure 3B) and mks1 (data not shown). Moreover, fewer spreading lesions appeared in mks1 plants than in...
35S::MKS1 or Ler wild-type after inoculation (data not shown). To determine whether enhanced susceptibility to B. cinerea in 35S::MKS1 is associated with altered defense responses against necrotrophs, we determined the expression of the defense marker gene PDF1.2 following B. cinerea inoculation. The expression of PDF1.2 was significantly reduced in 35S::MKS1 compared with wild-type, whereas PDF1.2 was highly elevated in mks1 (Figure 3C). Collectively, these data indicate that MKS1 negatively regulate resistance responses required to combat the necrotrophic pathogen B. cinerea.

MPK4 and WRKY33 interact with different regions of MKS1

We previously showed that MKS1 interacts in vivo with MPK4 and WRKY33 [7,8]. To further specify which domains of MKS1 are important for these interactions, we performed a directed yeast two-hybrid analysis with two N-terminal deletions and three C-terminal deletions (Figure 4). N-terminal deletion 1, MKS1DN1, lacks domain 1 containing a putative MAP kinase docking domain [13]. MKS1DN2, lacks both domain 1 and domain 2 (containing a conserved VQ motif) [7]. MKS1DC3, contains only domain 1 and part of domain 2. MKS1DC2 consist of both domains, while MKS1DC1 only lacks the 27 most C-terminal amino acids of MKS1. Table 1 summarizes the results of the yeast two-hybrid screen. Unfortunately, the MKS1DN2 truncation was self-activating and was therefore omitted from further analysis. Nevertheless, we found that MPK4 interacted with all C-terminal truncations, but not with MKS1DN1, indicating that domain 1 of MKS1, containing the putative MAP kinase docking domain, is necessary for interaction of MPK4 with MKS1 (Figure 4).

Figure 2. The mks1 mutant is hypersusceptible to P. syringae and H. arabidopsidis. (A) Susceptibility of Ler, mks1 and 35S::MKS1 plants to Pst DC3000. (B) Number of asexual spores 6 days after inoculation by spray of virulent H. arabidopsidis Cala 2 isolate (10^5 spores/mL). Similar results were obtained in independent experiments. (C) PR1 mRNA levels measured by real-time PCR in Ler and mks1 after Pst DC3000 infection. Means ± SD are shown. dpi: days post infection.

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Figure 3. Overexpression of MKS1 is susceptible to B. cinerea. (A) Disease symptoms showing fungal growth after inoculation with 2.5 × 10^5 B. cinerea spores/mL. (B) Area of spreading lesions was determined after 60 h. Data represent average area of >10 lesions ± standard error. (C) Real-time PCR detection of PDF1.2 mRNA after inoculation with B. cinerea. Samples were tested in triplicate and normalized to ACTIN2. Means ± SD are shown.

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MKS1 only interacts with an intact N-terminal domain of MKS1

To investigate the importance of the protein sequence in the putative MAP kinase docking domain of MKS1, we made 18 alanine substitutions (Figure 3A) and conducted a directed yeast two-hybrid assay with MPK4 as bait. The amino acids to be substituted were selected by their level of conservation among different plant MKS1 homologs (Figure S1). Of the 18 alanine substitutions, six were found to be important for interaction (Figure 3B). Two possible $\phi_A$-$X$-$\phi_B$ motifs exist in the N-terminus of MKS1: Leu22-Gln23-Ile24 and Leu32-Ser33-Val34 (Figure 3A). The $\phi_A$-$X$-$\phi_B$ motif inserts into the docking groove on the MAP kinase, and alanine substitutions in this motif have been shown to block activation of the MAPK p38 in mammalian cells [15]. Since substituting Leu22 with alanine caused disruption of binding and no such effect is observed for substitutions of Leu22, Gln23 or Ile24, it is likely that Leu32-Ser33-Val34 constitutes the relevant $\phi_A$-$X$-$\phi_B$ motif. This is also supported by the observation that Leu32 and Val34 are highly conserved among the different MKS1 homologs, whereas Leu22 shows no conservation at all (Figure S1). This points to the existence of a docking domain at the N-terminus of MKS1 fitting the $K/R_{1-4}$-$X_{1-6}$-$\phi_A$-$X_{-}$-$\phi_B$ module [16]. However, we previously showed that MPK4 phosphorylates MKS1 in vitro on Ser30 [7], and mammalian studies have shown that the classical docking motif binds to a region that lies on the other side of the protein to a phosphorylation site [17]. These results would exclude a classical docking domain within a phosphorylation site. However, a recent study shows that in planta activation of MPK4 by inoculation with P. syringae DC3000 expressing the AvrRpm1 avirulence factor only phosphorylates MKS1 on Ser72, Ser108, and Ser120, and not on Ser30 [14]. If this is the case, it is probable that the N-terminus of MKS1 contains a ‘classical’ docking domain.

Table 1. Yeast two-hybrid analysis for MKS1, MPK4, WRKY25 and WRKY33 proteins.

<table>
<thead>
<tr>
<th>pBD/pAD vector</th>
<th>MKS1 N1</th>
<th>MKS1 N2</th>
<th>MKS1 C1</th>
<th>MKS1 C2</th>
<th>MKS1 C3</th>
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<tr>
<td>MPK4</td>
<td>-</td>
<td>N/A</td>
<td>+</td>
<td>+</td>
<td>+</td>
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<tr>
<td>WRKY25</td>
<td>+</td>
<td>N/A</td>
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<td>-</td>
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<tr>
<td>WRKY33</td>
<td>+</td>
<td>N/A</td>
<td>+</td>
<td>+</td>
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</tr>
</tbody>
</table>

Yeast was spotted onto 3D-2 medium lacking trp and leu and 3D-4 medium also lacking ade and his, and all combinations that grew on both media were scored as interaction (+). No interaction is indicated by (-).

N/A not applicable.

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Figure 4. Yeast two-hybrid analysis for MKS1, MPK4 and WRKY33 proteins. Schematic representation of MKS1 truncations used in this study. MKS1: full length MKS1, N1: MKS1ΔN1, N2: MKS1ΔN2, C1: MKS1ΔC1, C2: MKS1ΔC2, C3: MKS1ΔC3. Summary of yeast two-hybrid analysis, MPK4 interacts with domain 1 (#1) of MKS1, WRKY33 interacts with domain 2 (#2) of MKS1. doi:10.1371/journal.pone.0014364.g004

An intact N-terminus is required for MKS1 nuclear localization

MKS1 is exclusive localized in nuclei and MPK4 primarily localizes to the nucleus, consistent with their ability to interact in vivo [7]. To examine the subcellular localization of the different mutant versions of MKS1, we analyzed the localization of the MKS1-L32A point mutation and the five different truncations of MKS1 by gene fusions to green fluorescent protein (GFP). To confirm that intact GFP-MKS1 fusion proteins were produced, immunoblot were performed using anti-GFP antibody (Figure S2). Full length MKS1 produces strong GFP fluorescence in the nucleus (Figure 6, MKS1). The C-terminal truncations MKS1ΔC1 and MKS1ΔC2 also localized almost exclusively in nuclei (Figure 6, ΔC1 and ΔC2), whereas MKS1ΔC3 and the two N-terminal truncations, MKS1ΔN1 and MKS1ΔN2, displayed strong fluorescence in both nuclei and cytoplasm (Figure 6, ΔC3, ΔN1 and ΔN2). Interestingly, MKS1-L32A only seemed to display weak fluorescence in the nucleus and was primarily localized to the cytosolic compartment (Figure 6, L32A). These results indicate that the region of MKS1 including residues 129-223 are dispensable for its specific nuclear localization. On the other hand, residues 1-74 (MKS1ΔC3) alone do not produce specific nuclear localization. These indicates that the putative docking domain alone does not specify nuclear localization, but that the VQ domain is needed together with the docking domain for nuclear localization.

An intact N-terminus is required for MKS1 function

To examine the biological significance of the MKS1-L32A point mutation and the five different truncations of MKS1, we transformed these six constructs into mpk4/mks1 double mutant to assess their ability to complement mks1. As noted in Figure 1C, mks1 partially suppressed the mpk4 phenotype, and re-introducing functional MKS1 reverted mpk4/mks1 to the mpk4 dwarf phenotype. As can be seen in Figure 7A, only MKS1ΔC1 or MKS1ΔC2 truncations of MKS1 reverted the mpk4/mks1 phenotype to the mpk4 dwarf phenotype. These results indicate
that a functional MKS1 protein requires an intact N-terminus important for both MPK4 and WRKY33 interactions. To confirm that intact proteins were produced in these experiments, immuno-bLOTS were performed using anti-MKS1 (Figure S3). However, MKS1D1 and MKS1D2 are truncated within the N-terminal sequence against which the anti-MKS1 antibody was raised and are therefore not recognized. MKS1D3 was also not recognized by the anti-MKS1 antibody, although this truncation includes the sequence used to raise the anti-MKS1 antibody. An explanation may be that MKS1D3 is not folded correctly and therefore not recognized by the antibody, because MKS1D3 expressed in E. coli was also not recognized although the mRNA was detected by RT-PCR (data not shown).

Because overexpression of MKS1 leads to increased expression of PR1 [7], we examined whether ectopic expression of the point mutation construct MKS1-L32A or the truncations of MKS1 would have any effect on PR1 expression (Figure 7B). Only transgenic plants overexpressing the C-terminal truncations MKS1ΔC1 and MKS1ΔC2 exhibited high PR1 expression, with levels comparable to those in mpk4 or 35S:MKS1, whereas MKS1ΔC3, MKS1ΔN1, MKS1ΔN2 and MKS1-L32 all showed similar PR1 expression levels as mpk4/mks1 or Ler wild-type (Figure 7B). To confirm that PR1 expression does not correlate with transgenic MKS1oe levels, we next analyzed the expression levels of the different transgenic MKS1oe versions. This showed that PR1 mRNA levels are independent of the mRNA levels produced by the transgenic MKS1oe constructs, indicating that the increased PR1 mRNAs do not simply reflect the levels of the transgenic MKS1oe mRNAs (Figure 7C).

**Discussion**

We show that a loss-of-function mks1 insertion allele is a much stronger suppressor of mpk4 than MKS1-RNAi. In addition, we found that this mks1 mutant exhibits decreased basal resistance to biotrophic pathogens, an effect not seen in plants with reduced accumulation of MKS1 mRNA via RNAi. These observations are important because they demonstrate that MKS1 plays a role in maintaining basal resistance at levels similar to that found for other resistance signaling proteins like EDS1 and PAD4 [18]. That MKS1 plays important roles in plant resistance responses is further supported by the recent finding that the snc4-1D mutant, which exhibits increased resistance responses, is partially suppressed by mks1 [19].

MKS1 interacts with both MPK4 and WRKY33. Using directed yeast two-hybrid screens with different MKS1 deletion forms, we found that MKS1 interacts with MPK4, whereas WRKY33 was found to interact with a plant-specific VQ motif-containing domain. MKS1 is a member of a small protein family sharing this conserved VQ motif of unknown function, but other than this region their primary structures are highly diverse. Two other VQ motif-containing proteins have been characterized: SIB1 is a nuclear-encoded protein that is targeted to chloroplasts and interacts specifically with plastid RNA polymerase σ-factor Sig1 [20], and AtCaMBP25 is a calmodulin-binding protein involved in abiotic stress tolerance [21]. Interestingly, SIB1 was also found to be induced by SA [22], and to be involved in disease resistance [11]. Thus, the sib1 loss-of-function mutation is
compromised in the induction of some defense-related genes triggered by pathogen infection, whereas over-expression of SIB1 activates defense-related gene expression following pathogen infection, leading to enhanced resistance to infection by P. syringae. It is thus tempting to speculate that like MKS1 and SIB1, other VQ domain-containing proteins also play roles in basal resistance. Future studies, including double mutant analysis and protein interaction experiments, will clarify the role this protein family may exert in plant immunity and whether MKS1 and SIB1 play similar roles in the MPK4 regulatory node.

We previously showed that MKS1 is localized in nuclei and interacts with MPK4 in this compartment [7,8]. The in-depth analysis of MKS1 constructs presented here demonstrates that the N-terminal part of MKS1 is important for MPK4 interaction. In addition, a single amino acid change, L32A, within the putative MPK4 docking motif of MKS1, is sufficient to reduce MKS1 and MPK4 interaction and to exclude MKS1 from nuclei. In addition, expression of MKS1 L32A fails to revert the phenotype of the mpk4/mks1 double mutant to that of the single mpk4 mutant. Therefore, Leu32 of MKS1 appears to be essential for all known aspects of MKS1 function, indicating that the integrity of the MKS1 N-terminal is essential for proper function.

An intact N-terminus including a putative MAPK docking domain and a VQ motif seems to be required for MKS1 to revert mks1/mpk4 to the mpk4 dwarf phenotype as visualized by the phenotypic inspection of mks1/mpk4 plants expressing MKS1-L32A, MKS1ΔN1, MKS1ΔN2 and MKS1ΔC3. In contrast, amino acids 127-223 comprising the C-terminus are dispensable for this effect. These results solidify the importance of the N-terminal region for MKS1 function. As noted above, domain 2 contains a VQ motif and is required for interaction with WRKY33, suggesting that WRKY33 is involved in the mpk4 dwarf phenotype. As observed in the reversion effects for mks1/mpk4, correct MKS1 nuclear localization also depends on an intact docking domain, as evidenced by the increased cytoplasmic localization of MKS1-L32A, MKS1ΔN1, MKS1ΔN2 and MKS1ΔC3.

Materials and Methods

Plant Materials and Growth Conditions

mpk4 [5], mks1 [GT.108403; [8]] and the mpk4/mks1 double mutant, all in Landsberg (Ler) background, were grown in chambers under short-day (8 h light/16 h darkness). Day and night temperatures were 21 and 16°C, respectively.
Genotyping

The following gene-specific primers were used for PCR-based genotyping for *mpk4*: MPK4fwd: 5’-CAGAGATGCTGATGAT-TAGTAACA-3’ and MPK4rev: 5’-GGATCCATGTCGGCG-GAGAGTTGTTC-3’. For *mks1*: MKS1fwd: 5’-ATCTGGCGGCGGTGGAGATGT-3’ and MKS1rev-3’UTR: 5’-GCTACTACATTGGATATGTCA-3’. Ds1: 5’-GTTTTTCGT-TTCCGTCCCGCAAG-3’ recognizes the Ds transposon insertion in *mpk4* and *mks1*. For genotyping the MKS1 truncations and the MKS1-L32A point mutation, the following primers were used: MKS1fwd: 5’-ATCTGGGGGCGGATGATGT-3’ and MKS1rev-3’NOS 5’-CGGCAACAGGATTCAATCTT-3’. For

Figure 7. Effects of transgenic expression of MKS1 constructs in *mpk4/mks1*. (A) Phenotypes of three-week-old plants with the indicated genotypes were grown under short-day conditions. MKS1-L32A, MKS1 ΔN1, MKS1 ΔN2, MKS1 ΔC1, MKS1 ΔC2 and MKS1 ΔC3 are overexpressed with the constitutive 35S promoter in *mpk4/mks1* double mutants. Plants were grown on soil at 22 °C and photographed 3 weeks after planting. (B) and (C) Real-time PCR detection of PR1 (B) and MKS1oe (C) mRNA. Samples were tested in triplicate and normalized to ACTIN2. Means ± SD are shown. doi:10.1371/journal.pone.0014364.g007
the truncation MKS1ΔC3, MKS1Δ4ΔC3: 5′-TCCTTCCGATT-CACGAGAACGAGAAG-3′ and MKS1rev3-NOS 5′-CGGC-AACGAGTCAATCTT-3′ were used.

**Bacterial Growth Assays**

Five-week-old plants were infiltrated with *Pseudomonas syringae* tomato DC3000 and growth assays performed according to [23]. Infections with *Hyaloperonospora arabidopsidis* were performed using 10^5 conidia/mL under conditions described previously [24].

**Plasmid Construction and *Arabidopsis* Transformation**

For yeast two-hybrid, the five truncated versions of MKS1, MPK4 and WRKY33 cDNA were amplified by RT-PCR from wild-type Ler using the primers listed in Table S1. Hereafter, the truncated versions of MKS1 were cloned into the *NdeI* and *EcoRI* sites of pGBK7 and MPK4, WRKY25 and WRKY33 cDNA were cloned into the *NdeI* and *EcoRI* sites of pGADT7.

For transgenic analyses, the five truncations of MKS1 and the MKS1-L32A point mutant were cloned into the *XmaI* site of the binary vector pJL12 using primers listed in Table S2. The pJL12 vector was derived from the binary vector pCB302-3 [25]. pCB302-3 contains vector pJL12 and MPK4, WRKY25 and WRKY33 cDNA were cloned into the *NdeI* and *EcoRI* sites of pGADT7.

For transgenic analyses, the five truncations of MKS1 and the MKS1-L32A point mutant were cloned into the *NdeI* site of the binary vector pJL12 using primers listed in Table S2. The pJL12 vector was derived from the binary vector pCB302-3 [25]. pCB302-3 contains two *NdeI* sites, one in MCS2 and another in the vector backbone. In pJL12, the *NdeI* site in the vector backbone has been deleted by a silent mutation. The six different pJL12-MKS1 vectors were transformed into *Agrobacterium* and subsequently into *mpk4*/*mks1* doubly homozygous plants by floral dipping [26]. Plants carrying the transgene were identified with BASTA® selection and PCR.

For GFP fusion constructs, the five different truncations of MKS1 were cloned into the *XmaI* and *NdeI* sites of pEGFP using primers listed in Table S3.

**Site-directed Mutagenesis**

Full-length MKS1 cDNA was in the pGBK7 vector. Site-directed mutagenesis PCR was performed using Pfu polymerase (Promega) according to the manufacturer's protocol (Stratagene).

**Yeast Two-Hybrid Assays**

MKS1 truncated versions were in the bait vector (pGBK7) and MPK4, WRKY25 and WRKY33 were in the prey vector (pGADT7). For the 18 alanine substituted constructs, MKS1 was in the prey vector (pGADT7) and MPK4 in the bait vector (pGBK7). Transformation of yeast strain AH109 and yeast two-hybrid assays were performed as described by Clontech.


