Constitutive Activation and Transgenic Evaluation of the Function of an Arabidopsis PKS Protein Kinase*

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A novel family of SOS2 (salt overly sensitive 2)-like protein kinase genes (designated PKSes) have been recently identified in Arabidopsis. The biochemical characteristics as well as in vivo roles of most of the PKSes are unclear at present. In this work, we isolated and characterized one of the PKSes, PKS18. PKS18 was expressed in leaves of mature Arabidopsis plants. The glutathione S-transferase (GST)-PKS18 fusion protein was inactive by itself in substrate phosphorylation. An activation loop Thr<sup>169</sup> to Asp mutation, however, highly activated this kinase in vitro (designated PKS18T/D). Kinase activity of the PKS18T/D preferred Mn<sup>2+</sup> to Mg<sup>2+</sup>. The activated kinase showed a substrate specificity, and high catalytic efficiency for a peptide substrate p3 and for ATP. Interestingly, PKS18T/D transgenic plants were hypersensitive to the phytohormone abscisic acid (ABA) in seed germination and seedling growth, whereas silencing the kinase gene by RNA interference (RNAi) conferred ABA-insensitivity, indicating the involvement of PKS18 in plant ABA signaling.

In eukaryotic organisms, protein kinases are involved in a large number of distinct signal transduction pathways, and thus proper regulation of the catalytic activity is of crucial importance to cellular growth and development and in response to various hormonal and stress signals. In animals, calcium/calmodulin-dependent protein kinases are a major type of kinase that decode calcium signals. In plants and prokaryotes, calcium-dependent protein kinases contain a kinase catalytic domain fused with a calmodulin-like regulatory domain and are directly activated by cytosolic calcium (1, 2). The Arabidopsis genome contains a large number of protein kinase genes (3). We have recently identified a novel family of 24 salt overly sensitive 2 (SOS2)<sup>1</sup>-like protein kinase genes (designated PKSes) from Arabidopsis (4, 5). The biochemical characteristics and in vivo roles of most of these kinases are still unknown at the present time. These PKSes are Ser/Thr protein kinases that comprise an N-terminal kinase catalytic domain similar to SNF1/AMPK and a unique C-terminal regulatory domain (4, 5). The PKS kinases can be classified into the SnRK3 subgroup of plant SNF1-related protein kinases (6). The founding member, SOS2, is known to function in salt tolerance in plants (4). We have also defined a novel family of SOS3-like EF-hand-type calcium sensors that may sense the calcium signal elicited by salt stress and other stimuli (5, 7, 8). SOS3 interacts with and activates SOS2 via the autoinhibitory FISL motif within the regulatory domain of SOS2 (5, 9). An up-regulation of the putative plasma membrane Na<sup>+/</sup>H<sup>+</sup>-antiporter SOS1 gene by salt stress is partially controlled via SOS2/SOS3 and SOS3 (10). Recently, both SOS3 and SOS2 have been shown to be required for the activation of Na<sup>+</sup>/H<sup>+</sup> exchange activity of SOS1 (11).

Most PKS proteins, including PKS18, when expressed and isolated from bacteria, do not seem to exhibit substrate phosphorylation activity in the absence of specific SOS3-like calcium sensors. To determine the biochemical characteristics and in vivo roles of the novel kinases, we wanted to create constitutively active forms of these proteins. Here we isolated and characterized a novel Arabidopsis PKS gene, PKS18. PKS18 was expressed in leaves of mature plants. Substitution of a threonine residue with aspartic acid within the activation loop resulted in a highly activated PKS18 mutant (designated PKS18T/D), suggesting an important role of the activation loop phosphorylation in the regulation of PKS18 activity. This constitutively active PKS18 mutant was then utilized to determine cofactor preference, pH dependence, substrate specificity, and kinetic properties of the kinase in vitro. To investigate the in vivo function of PKS18, we generated transgenic Arabidopsis plants ectopically expressing the PKS18T/D or dominant negative mutant by RNA interference (RNAi). PKS18T/D transgenic plants were hypersensitive to the phytohormone abscisic acid (ABA) in seed germination and seedling growth, whereas silencing the kinase gene via RNAi conferred ABA-insensitivity.

EXPERIMENTAL PROCEDURES

Northern Blot Analysis—Seeds of the Arabidopsis wild type plants (Columbia ecotype) were germinated, and seedlings were grown on Murashige and Skoog (MS) (12) agar plates under continuous light (13). Ten-day-old seedlings were treated with NaCl, cold, and drought as described previously (10, 14). Total RNA isolation and Northern blot analysis were performed as described previously (15). To analyze transgene expression, total RNA was isolated from 2-week-old seedlings grown on MS agar plates containing 0.3 μM ABA. Thirty micrograms of total RNA were used, and the blot was hybridized with a PKS18 gene-specific DNA probe.

Reverse Transcription-Polymerase Chain Reaction and Site-directed Mutagenesis—A cDNA containing the complete open reading frame (ORF) of PKS18 was obtained by reverse transcription (RT)-PCR. The PKS18-specific primers were 5′-CGGGATCCATGGATAAAAACGGCA-TAGTTTTGATGC-3′ (forward, BamHI site underlined) and 5′-CCGCC-TATCTTAATGTATCACTTCAATCTTCTCATTG-3′ (reverse, KpnI site underlined) (MWG-Biotech, High Point, NC). The PCR product was purified from the agarose gel, digested with BamHI and KpnI, and cloned into a modified pGEX-2T-CMS vector and sequenced from both strands. For analysis of the PKS18 gene expression in wild type plants

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1 The abbreviations used are: SOS2, salt overly sensitive 2; RNAi, RNA interference; ABA, abscisic acid; AMPK, AMP-activated protein kinase; GST, glutathione S-transferase; MS, Murashige and Skoog; ORF, open reading frame; RT, reverse transcription; PKS, SOS2-like protein kinase; SNF1, sucrose-non-fermenting protein kinase.
and RNAi lines, the first strand cDNAs were synthesized from total RNA samples of wild type, pks18-1, pks18-3, pks18-5, and pks18-8 RNAi plants. RT-PCR was performed by using the PKS18 gene-specific primers as described above. PKS6 and PKS11 gene-specific primers were used in the control PCR reactions.

Site-directed mutagenesis was used to construct Thr to Asp changes or a FISL motif deletion mutant of PKS18 (designated PKS18FD). The mutagenic primers were as follows: 5'-CACATGTCGGGCTCATCAGGCAAACATCTTG-3' (pPKS18T/F-forward), 5'-ACATGTCGTTCCAATGTCAGAACGACACGATC-3' (pPKS18T/R-reverse), 5'-ACCGATCCATGTAAGAGAGAGACTGAAGACTGTTGC-3' (pPKS18RD-forward), and 5'-CTCCTCTTCAGACGATCCGATGGTG-3' (pPKS18RD-reverse). PCR reactions were carried out on the plasmid DNAs with an enzyme mix (1:1) of Taq polymerase (ShoBio, Seoul, Korea) and Turbo DNA polymerase (Stratagene, La Jolla, CA). The gel-purified PCR products were digested with DpnI and transformed into DH5α competent cells. The mutated sequences and fidelity of the rest of the DNA in these constructs were verified by sequencing.

Fusion Protein Expression and Assays—All GST fusion constructs were transformed into Escherichia coli BL21 codon plus cells (Stratagene). The transformed cells were grown at 37 °C in Luria-Bertani medium with ampicillin (100 μg/ml) and chloramphenicol (50 μg/ml) until the OD600 reached 0.8. Recombinant protein expression was induced by 0.6 mM isopropyl β-D-thiogalactopyranoside for 4 h at 37 °C. Bacterial pellets were resuspended in a phosphate-buffered saline buffer (pH 7.5) containing 10% (v/v) glycerol, 5 mM dithiothreitol, 2 μg/ml leupeptin, 2 μg/ml aprotinin, and 2 mM phenylmethylsulfonfluoride. GST fusion proteins were purified by glutathione-Sepharose 4B (Amersham Biosciences), and analyzed by 10% (w/v) SDS-PAGE gels.

Kinase Assays—Peptide phosphorylation with a synthetic peptide p3 (ALARAASAAALARRR, Research Genetics, Huntsville, AL) was assayed as the incorporation of radioactivity from [γ-32P]ATP (PerkinElmer Life Sciences, Foster City, CA) into the peptide substrate. The peptide phosphorylation was performed in kinase assay buffer containing 20 mM Tris-HCl (pH 7.2), 2.5 mM MnCl2, 0.5 mM MgCl2, 0.5 mM CaCl2, 10 μM ATP, and 2 mM dithiothreitol. Forty microliters of kinase reaction was started by adding 150 μM p3 and 5 μCi of [γ-32P]ATP (specific activity of 600 cpm/pmol), and reaction mixtures were immediately incubated at 30 °C with gentle shaking for 30 min. Reactions were terminated by adding 1 μl of 0.5 M EDTA, and the glutathione-Sepharose beads were pelleted. To measure peptide phosphorylation, 15 μl of the supernatant was spotted onto P-81 phosphocellulose paper (Whatman, Clifton, NJ), and the phosphorylated peptide was eluted by washing with a phosphate-buffered saline containing 0.1 M NaCl, 0.05 M Tris, and 0.05% (v/v) SDS. The eluted phosphopeptide was dried and exposed to a Kodak x-ray film.

Expression of PKS18 in Arabidopsis Plants—A cDNA containing the ORF of PKS18 was amplified by RT-PCR and completely sequenced. The deduced amino acid sequence of PKS18 was identical to the computer annotation in the data base. The PKS18 cDNA contains an ORF of 1320 bp and encodes a polypeptide of 440 amino acid residues with an estimated molecular mass of 50.2 kDa. The PKS18 gene is located on chromosome 5 based on the Arabidopsis genome sequence database (www.arabidopsis.org). Blots of total RNA from different tissues of adult Arabidopsis plants were hybridized to a gene-specific DNA probe for PKS18. PKS18 was expressed in leaves of adult plants, but its expression was not detectable in any of the other tissues examined (Fig. 1). We also tested potential regulation of the PKS gene by salt, cold, and drought in young Arabidopsis seedlings. PKS18 mRNA accumulation was not significantly affected by any of the treatments (data not shown).

Substitution of a Threonine with Aspartic Acid in the Activation Loop Activates PKS18—The GST-PKS18 fusion protein in which the bacterial GST was fused in-frame to the N-terminal end of PKS18, had little kinase activity when expressed and isolated from bacteria (data not shown). To determine its biochemical characteristics, we attempted to construct constitutively active forms of the kinase. We have recently found that SOS2 could be activated either by a Thr to Asp mutation in the putative activation loop or deletion of the regulatory domain (5). Like SOS2, PKS18 contained an N-terminal SNF1-like kinase catalytic domain and a novel C-terminal regulatory domain (Fig. 2A). The deduced amino acid sequences of PKS18 and SOS2 were highly conserved throughout the entire length. Interestingly, PKS18 also contained a conserved putative activation loop in the catalytic domain and a FISL motif in the regulatory domain (Fig. 2B). A residue, Thr169, in the activation loop of PKS18 is conserved (Fig. 2B and data not shown). We hypothesized that the...
The threonine residue could be one critical target site for activation by a putative upstream kinase(s). We therefore substituted the residue with aspartic acid by site-directed mutagenesis to construct an activation loop mutant of PKS18 (PKS18T/D). A FISL motif deletion mutant (PKS18FD) was also produced by removing the FISL motif between Tyr295 and Glu316. We expressed and purified the PKS18T/D and PKS18FD mutant proteins as well as the wild type protein (designated PKS18WT) from bacteria. SDS-PAGE analysis of these purified proteins showed a single band of 80 kDa in agreement with the calculated mass (Fig. 3A). As shown in Fig. 3B, both mutant proteins exhibited higher autophosphorylation activity compared with PKS18WT. SOS2 is known to phosphorylate a synthetic peptide p3 (AMARAASAAALARRR) in the presence of SOS3 (9). With the p3 as a substrate, PKS18T/D mutant was extremely active, with a 113-fold higher activity in p3 phosphorylation than PKS18WT (Fig. 3C). PKS18FD also displayed a 2-fold increase in p3 phosphorylation compared with PKS18WT (Fig. 3C). We subsequently used the active form of PKS18, PKS18T/D, to analyze some of the biochemical properties of this kinase.

Biochemical Properties of PKS18T/D—A divalent cation is required by kinases and other phosphotransferases for coordinating the phosphate groups of the nucleotide triphosphate substrate. These enzymes may also be activated or inactivated by binding of a cation to an additional site of interaction (18). Both autophosphorylation and peptide substrate phosphorylation activities of PKS18T/D required the divalent cation Mg$^{2+}$ or Mn$^{2+}$ as a cofactor (Fig. 4, A and B). Interestingly, this kinase seemed to prefer Mn$^{2+}$ to Mg$^{2+}$ as a cofactor for either autophosphorylation or peptide phosphorylation. Mg$^{2+}$ only weakly activated the kinase, and the activation required millimolar concentrations of Mg$^{2+}$, but Mn$^{2+}$ activated the kinase even in the micromolar range. The optimal concentrations were at 2.5 mM for Mn$^{2+}$ and 5 mM for Mg$^{2+}$. Mn$^{2+}$ concentration at 5 mM or higher became inhibitory to peptide phosphorylation activity of the kinase. In contrast, Mg$^{2+}$ concentration up to 20 mM did not inhibit the phosphorylation activity of the kinase (Fig. 4, A and B).

P3 phosphorylation by the kinase was determined over the pH range of 6.5–9.5 (Fig. 5A). The optimal pH for the kinase was observed to be 7.5, and this kinase seemed to be tolerant of slightly alkaline pH. In addition to p3, another serine-containing peptide p1 (LRRASLG) and a threonine-containing peptide p2 (VRKTRLRLR) could also be phosphorylated by SOS2 (9). Kinase assays with these three peptides showed that PKS18T/D did phosphorylate both p1 and p3, with p3 giving higher activity than p1, but it did not have any significant activity with p2 (Fig. 5B). To further evaluate its affinity toward the preferred peptide substrate p3 and ATP, we conducted a kinetic study for the kinase. The dependence of kinase activity of PKS18T/D on either p3 or ATP exhibited a typical Michaelis-Menten kinetics (Fig. 6, A and B). The apparent $K_m$ values of PKS18T/D for p3 and ATP were determined to be 29

![Fig. 2. Amino acid sequence alignment of PKS18 with SOS2. A, a schematic diagram of the domain structure of SOS2. FISL, FISL motif. B, an alignment of the deduced amino acids of PKS18 and SOS2. PKS18 is identical to the gene product with the GenBankTM accession number: BAB09310. Amino acids are numbered on the left. Identical residues and conservative replacements are shown with black and gray shading, respectively. Marked is the putative activation loop between the conserved DFG and APE motifs (dots) and the conserved Thr residue (asterisk). Also marked is the conserved FISL motif in the C-terminal regulatory domain. Dashed lines represent spaces that were introduced to maximize alignment.](image-url)
Fig. 3. Expression of recombinant GST fusion proteins and activation of PKS18 in vitro. A, PKS18 wild type (PKS18WT), FISL motif deletion (PKS18FD), and activation loop mutant (PKS18T/D) were expressed as GST fusion proteins in E. coli BL21 (codon plus), and puriﬁed by glutathione-Sepharose afﬁnity chromatography. Expressed proteins were analyzed by SDS-PAGE, and the gels stained with Coomassie Brilliant Blue R-250. Lanes 1, 3, and 5, induced PKS18WT, PKS18FD, and PKS18T/D, respectively; lanes 2, 4, and 6, afﬁnity-puriﬁed PKS18WT, PKS18FD, and PKS18T/D, respectively. The protein size standards were rabbit phosphorylase b (97 kDa), bovine serum albumin (66 kDa), and ovalbumin (45 kDa). B, autophosphorylation activities of PKS18WT (lane 1), PKS18FD (lane 2) and PKS18T/D (lane 3). C, peptide phosphorylation activities of PKS18WT, PKS18FD, and PKS18T/D. Kinase activity was assayed using 150 μM p3 as a substrate, 10 μM ATP, and 5 mM MgCl₂ as described under “Experimental Procedures.” The number on top of each bar is a fold increase over wild type control. Results represent the means ± S.D. from three experiments.

and 0.88 μM, respectively (data not shown). The ratio of $k_{cat}$ to $K_m$ is a good overall measure of substrate preference. The $k_{cat}/K_m$ values of PKS18T/D for p1 and p3 were 0.76 and 2.2 M⁻¹s⁻¹, respectively (data not shown), indicating a preference of p3 over p1. In addition, the activity of PKS18T/D was slightly inhibited by high concentrations of ATP. At 25–100 μM concentrations of ATP, the activity was reduced by ~5% compared with the peak activity at 10 μM ATP. At 1 mM ATP, the kinase still had ~75% of the peak activity (data not shown).

Overexpression of PKS18T/D Confers ABA Sensitive Growth Phenotypes—SOS2 kinase is known to function in plant salt tolerance (4). To attribute in planta functions to PKS18, we used both gain-of-function and loss-of-function approaches. The coding region of the PKS18T/D was fused to the superpromoter and used to transform Arabidopsis plants. Over 20 T₂ and T₃ homozygous lines were recovered, and lines with high transgene expression levels were selected for more detailed analyses. The expression levels of the kinase gene in the PKS18T/D transgenic plants was determined by Northern blot analysis using a gene-specific probe. The results (Fig. 7A) showed that all the transgenic lines tested (at 0.3 μM ABA) expressed the transgene at various levels. In contrast, there was little PKS18 transcript expression in wild type seedlings under the same conditions.

We tested the transgenic lines under various treatment conditions such as ABA, salt stress, high mannitol, sucrose or glucose, and extreme pHs. We found that the lines had a clear phenotypic change under ABA but not other treatments. To evaluate the effect of PKS18T/D overexpression on the ABA sensitivity in transgenic plants, seeds of the PKS18T/D transgenic plants were germinated and seedlings were grown on MS media containing various concentrations of ABA. When ABA concentration was 0.3 μM or higher, both seed germination and seedling growth including root growth and cotyledon greening/expansion were severely inhibited (Fig. 8A and data not shown). In contrast, seeds of the nontransformed wild type...
plants germinated and seedlings grew normally, although at a slower rate than on ABA-free MS media. Quantitation of seed germination (Fig. 8B) showed that percentage of seedlings with green cotyledons in two transgenic lines, PKS18T/D-1 and PKS18T/D-9, were only 8 and 4%, respectively, at 0.3 μM ABA, whereas the percentage in wild type plants was 55% under the same conditions. Measurement of root length showed that root growth of these two transgenic lines on 0.3 μM ABA medium was less than 20% of that on ABA-free medium (Fig. 8C). In contrast, root growth of wild type plants was 70% of that on ABA-free medium.

In a dose response assay, root growth of the transgenic seedlings was found to be hypersensitive to ABA at all concentrations tested (Fig. 8D and data not shown). Furthermore, when young seedlings germinated on ABA-free MS plates were transferred to MS plates containing 60 or 100 μM ABA, root growth of the PKS18T/D transgenic lines was only ~40% of that in the wild type plants (data not shown). These observations indicated that both germination and postgermination growth of the PKS18T/D transgenic plants were hypersensitive to ABA.

Silencing of PKS18 Confers ABA Insensitive Growth Phenotypes—To further search the in vivo role of PKS18, we also generated dominant negative PKS18 mutant lines (designated pks18) by RNAi. The expression of PKS18 transcript was examined in 4 randomly chosen, independent pks18 RNAi lines including pks18-5 and pks18-8. The results showed that PKS18 was silenced in all these pks18 RNAi lines to various extents (Fig. 7B). Control RT-PCRs showed that expression of either the PKS6 or PKS11 gene that is closely related to PKS18 (data not shown) was not affected in these pks18 RNAi lines (Fig. 7B). There was no PCR product amplified from RNA samples without reverse transcription (data not shown), indicating an absence of contaminated DNA.

Over 20 independent T2 and T3 pks18 RNAi lines were tested for ABA responses, and 2 representative T3 homozygous lines (i.e. pks18-5 and pks18-8) were presented here. When seeds were planted on ABA-free MS agar media, seed germination of these RNAi lines was similar to that of the wild type. However, with supplementation of 0.3 μM ABA in the media, seed germination of the pks18 RNAi lines was earlier than the wild type (data not shown), and cotyledon greening/expansion and root growth were less inhibited as compared with the wild type (Fig. 9A). In these pks18 RNAi lines, percentage of seedlings with
green cotyledons was much higher than that in the wild type on 0.3 μM ABA medium (Fig. 9B). Roots of these RNAi lines at 0.3 μM ABA also grew significantly better than those of the wild type (Fig. 9C). ABA dose response of these RNAi lines was also examined. As compared with the wild type, roots of these transgenic lines grew better under all ABA concentrations tested (Fig. 9D, pks18-8 data not shown). Furthermore, root elongation of these pks18 RNAi seedlings after transfer from ABA-free MS media was faster than the wild type on MS plates containing either 60 or 100 μM ABA (data not shown). These results suggest that both germination and postgermination growth of the pks18 RNAi lines were less sensitive to ABA.

**DISCUSSION**

PKS18 is a novel leaf-specific PKS protein. The PKSes are a novel subfamily of SNF1/AMPK protein kinases. Like most kinases including SOS2, PKS18 contains a putative activation loop in the catalytic domain. In most kinases, this activation loop is phosphorylated when the kinase is active. Phosphorylation of the activation loop stabilizes it in an open conformation that is permissive for substrate binding and catalysis (19). In the present study, we found that a threonine to aspartic acid mutation in the activation loop of PKS18 (Fig. 3). SOS2 was also activated by substitution of a threonine residue with aspartic acid in its activation loop (5). The yeast SNF1 kinase was activated by the phosphorylation of a conserved threonine residue in the activation loop of the catalytic subunit (20). These results strongly suggest that PKS18 may be activated *in vivo* through activation loop phosphorylation at the threonine residue. Two residues, Ser244 and Ser248, in the activation loop of protein kinase D were phosphorylated during its activation (21). The use of site-specific antibodies identified a serine, Ser176, within the C-terminal region of human protein kinase D2 as a phosphorylation site (22). PKS18 contains a serine residue that is absolutely conserved in the activation loop of the *Arabidopsis* PKSes (Fig. 2B and data not shown). It remains to be determined whether PKS18 can also be activated by substitution of the serine residue with aspartic acid or glutamic acid.

Protein kinases have diverse responses to diurnal cations. In this study, we observed a preference of manganese over magnesium of PKS18T/D for both autophosphorylation and peptide phosphorylation activity (Fig. 4). PKS18T/D was activated by micromolar amounts of Mn²⁺, the physiological concentrations in plant cells, indicating possible activity regulation of the kinase by Mn²⁺ *in vivo*. Activation of some kinases by Mn²⁺ has been considered to reflect its involvement in a kinase complex (23). PKS18 may be cytosolic, as suggested by its amino acid sequence. The pH optimum of PKS18T/D activity (Fig. 5A) was within the range of cytosolic pH values, and was similar to that of a spinach SNF1-like protein kinase (pH between 7.0 and 7.5 in the presence of 2 μM Mg²⁺) (24). PKS18 phosphorylated two serine-containing peptides but not the threonine-containing peptide (Fig. 5B). SOS2 did not phosphorylate commonly used protein substrates, such as myelin basic protein, histone H1, and casein, but did phosphorylate these peptide substrates (9). These observations suggest that the PKS isoforms have strict substrate selectivity. In this study, p3 (ALARAASALALLRR) was found to be the preferred peptide substrate for PKS18T/D. A synthetic peptide, AMARA (AMA- RAAASALALLRR), which contains the (hydrophobic)-(X-hy- (hydrophobic) residue, was found to be a minimal recognition motif (25) for a cauliflower AMPK/SNF1 homologue (26). This peptide was also used in the purification of two SNF1-like protein kinases from spinach leaves (27). Therefore, the presence of the hydrophobic and basic residues may be a determinant for the specific substrate of the PKS. However, further systematic analysis of phosphorylation motifs using a series of variants of the p3 peptide is needed to define the importance of these residues for each PKS isoform.

In this study, we found that PKS18T/D was slightly inhibited by high concentrations of ATP. ATP inhibition has been demonstrated in other kinases, such as the phosphofructo-1 kinase (PFK) (28). Mammalian PFK has a separate ATP inhibition site (29), whereas PFK from *E. coli* shows a mechanism-based, nonallosteric inhibition by ATP (30). The mechanism of ATP inhibition in PKS18 is still unclear. In addition, some protein kinases are known to utilize GTP as well as ATP as a phosphate donor (31). Whether PKS18 has distinct phosphate donor specificity is unclear.

SOS2 plays a specific role in plant adaptation to high sodium and low potassium stresses (4). Different members of the kinase subfamily could have distinct roles in plants. In this study, we investigated PKS18 function *in vivo* by both overexpression and loss-of-function approaches. Overexpression of PKS18 might affect the functions of other PKSes, and thus overexpression phenotypes need to be interpreted with caution. We therefore further confirmed PKS18 function by using RNAi to silence PKS18 gene expression. The ABA hypersensitive phenotype of the transgenic plants overexpressing PKS18T/D and ABA hyposensitive phenotype of PKS18-silenced plants provide a strong case for the involvement of PKS18 in ABA.
signaling pathway in vivo (Figs. 8 and 9). Our results demonstrate an important role of the SnRK3 protein kinase subgroup in plant ABA signaling pathway.

A SnRK2 protein kinase, PKABA1, has been found to be involved in ABA signaling in wheat (32). PKABA1 was transcriptionally up-regulated by ABA (32), and this kinase may suppress gibberellic acid induced gene expression during cereal grain germination (33). Another Ser/Thr protein kinase gene (Esi47) from wheatgrass might also be involved in the same signaling pathway as that for PKABA1 (34). A guard cell-specific, ABA-activated Vicia faba Ser/Thr protein kinase, AAPK, has been shown to control the activity of plasma membrane anion channels (35). Two Arabidopsis protein Ser/Thr phosphatase 2C-type genes, ABI1 and ABI2 (ABA-insensitive 1 and 2), are known to function in controlling plant ABA sensitivity during seed germination and vegetative growth (36–38). Some of the protein kinases in ABA signaling may interact with the ABI phosphatases. An Arabidopsis protein phosphatase is known to interact with a Ser/Thr receptor-like kinase (39). These and our results strongly support the notion that protein phosphorylation plays an important role in ABA signaling pathway in plants.

Recent studies have identified a number of transcription factors such as ABI5 and AREBs that are phosphorylated in response to ABA (40–42). The constitutive overexpression of the ABRE (ABA-responsive elements) binding factor, ABF3 or ABF4, in Arabidopsis resulted in ABA hypersensitivity phenotypes (43), although the gene knockout/silencing phenotype of either of them is not known yet. Whether the function of PKS18 in plant ABA signaling is mediated by phosphorylating and activating these transcription factors is not known. The involvement of a PKS protein in ABA signaling is not surprising as the PKS family of kinases are known to interact with the SOS3 subfamily of calcium sensors, and as such are involved in calcium signaling (5). Although the calcium sensor(s) that interacts with PKS18 has yet to be identified, the presence of a FISL motif in PKS18 suggests that this kinase binds to one or more of the calcium sensors (5). Ca2+ is a second messenger mediating cellular responses to ABA (37). ABA has been recently found to activate multiple Ca2+ fluxes in stomatal guard
cells in Commelina communis (44). ABA treatment might result in a strong and transient increase in cytosolic [Ca²⁺], which may be perceived by a specific calcium sensor(s). Therefore, we propose that PKS18 functions in mediating calcium signaling in response to ABA signals. Identification of PKS18 interacting partners and substrate proteins will help clarify the precise role of this kinase in ABA signaling pathway in plants. Additionally, it is possible that PKS18 may control plant responses to external ABA by regulating the phosphorylation state of an ABA transport system either in the plasma membrane or vacuole. We have recently demonstrated that SOS2 phosphates and regulates the activity of the plasma membrane sodium/proton antiporter SOS1 (45).

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